us-09-826-581-3.rge

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GenCore version 5.1.6
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June 14, 2003, 11:14:11 ; Search time 4487 Seconds (Without alignments) 11168.939 Million cell updates/sec
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TGGCCTGACTCTGGCTCTTTCTGCAGGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGT
                                     CICCATCICICETAATGATAGGIGGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCC
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/organism="Homo sapiens"
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123597 137837; contig of 14441 bp in length
137838 137937; gap of 100 bp
137938 152129; contig of 14192 bp in length.
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51285; contig of 4820 bp in length
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17224. .19466
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/db_xref="taxon:9606"
                                                                                                    19566: gap of 10
21928: contig of
            gap of 1
23: contig of
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113091 113190; gap of
113191 123496; cont
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46365: conf
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66595; cont
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38179: cont
                                        .7123:
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Guskett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dara, T.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Carduc, G., Ginde, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Klein, J., Lakocque, K., Lamaers, R., Landers, T., Lehoccky, J., Lenn, J., Lakocque, K., Lamaers, R., Landers, T., Lehoccky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McDarthy, M., McDwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Waylor, J., Minova, T., Minanda, C., Menga, Y., Morrow, J., Nenly, T., Waylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Young, G., Zainoun, J., Zimmer, A., Travers, M., Trigillo, J., Young, G., Zainoun, J., Zimmer, A., Travers, M., Trigillo, J., Subrattick, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (39-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center clone name: 17458
Center clone name: 504_G_11
Consensus quality: 135376 bases at least Q40
Consensus quality: 14503 bases at least Q30
Consensus quality: 14503 bases at least Q20
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
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contig of 1297 bp in length
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648 9983: contig of 2336 bp in length
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2657 15043: contig of 2387 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1005; contig of 1005 bp in length
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3924 5020; cor
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1106 2402: co
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                 AUTHORS
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FEATURES
                                                   Direct Submission
Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                             PRI 09-JAN-2002
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                                                                                                         1621 CATCCTGACTGCACTGGACATCTTTGTGGACCGGGGTGTGTCTGCACTGCCTGTGGTCAA 1680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                  TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center, Washington 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                            2, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Nov 8, 2001 this sequence version replaced gi:13431203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris, A. and Cotton, M. The sequence of Homo sapiens BAC clone RP11-459119
                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                     34938 CGAATGTGGTACCCACCCCAGGATGAGAGGCTCGGCTGG 34898
                                                                                                                                                                                  1681 CGAATGTGGTACCCACCCCAGGATGAGAGGCTCGGGCTGG 1721
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                     206854 bp DNA
Homo sapiens BAC clone RP11-459119 from
AC009974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-NOV-2001) Genome University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 206854)
Sulston, J.E. and Waterston, R.
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Waterston, R. H.
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4 (bases 1 to 206854)
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5 (bases 1 to
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SOURCE
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Louis Mapping information for this clone was provided by Dr. John D. McPherson. Department of Genetics, Mashington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) The RPCI-11 human BAC library was made from the blood of one male donor, as described by Gosegawa.K., Woon.P.T., Zhao,B., Frengen,E., Tateno,M., Catanese,J.,J. and Ge Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome

VECTOR: pBACe3,6 NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

and Ā Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 AC009974. A single plasmid region exists beteen 38812-38903. Runresclyed tandem in the HERY SYR exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

Location/Qualifiers source

/organism="Homo sapiens" /db_xref="taxon:9606" /clone="RP11-459119" /clone_lib="RPCI-11" /chromosome-"2" /map="2

misc_feature

(NID:98364652) tz39c01.y1" 'note="match to EST AL567345 (NID:g12920610)" /note="match to EST AW880850 (NID:g8042860)" 1. .37 /note="match to EST BE047599 .37 misc_feature misc_feature misc_feature

'note="match to EST BF183086 (NID:g11061273)" /note="match to EST BE314060 (NID:99134719)" misc_feature misc_feature

'note="match to EST BG477625 (NID:913409904)" .37 /note="match to EST BI059713 (NID:g14467240)" /note="match to EST BF304755 misc_feature misc_feature

/note="similar to Homo sapiens EST BI114348 (NID:914565249)" misc_feature

misc_feature

/note="match to EST A1670836 (NID:94850567) wa04g10.x1" 'note="match to EST BE908408 (NID:g10402954)" /note="match to EST C05773 (NID:g1502549)" misc_feature misc_feature

281. .344 /note="match to EST A1670836 (NID:94850567) wa04910.x1" /note="match to EST BG470047 (NID:g13402322)" misc_feature

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

Center project name: H_NHO459119

between neighboring data submissions.

to EST BG477625 (NID:g13409904)" to EST BI059713 (NID:g14467240)" II to Homo sapiens EST BI114348 19)" to EST BG470047 (NID:g13402322)" to EST AA043371 (NID:g1521226) zk53e10.r1 to EST 764073 (NID:g667938) yc05d12.r1" to EST B1059713 (NID:g14467240)" to EST AA043371 (NID:g1521226) zk53e10.r1 to EST AA043371 (NID:g162726)" to EST AA0880850 (NID:g10402954)" to EST BE908408 (NID:g10402954)" to EST BF183086 (NID:g11061273)" to EST BF183086 (NID:g11061273)"
to EST BG470647 (NID:g13402322 to EST BG477625 (NID:g13409904 9)" to EST BE047599 (NID:g8364652) to EST BE047599 (NID:g8364652) to EST AL567345 (NID:g9134719) to EST AL567345 (NID:g210913) to EST AA481361 (NID:g2210913) to EST AA481361 (NID:g514574) r to Mus musculus EST AI196847 to EST BG992568 (NID:g4740791) to EST A1656812 (NID:g1396538 to EST AA043371 (NID:g1521226) ir to Homo sapiens EST BI114348 9)"

166398 166278 166277 ACTIGICCTGTTCCCACAGTCCCCACTGTGTCTCAGCACAGAAGACACTGGCAGGGTGGGGA 166218 166099 165919 165800 165740 166638 166338 3 900 780 840 900 420 480 540 99 720 960 240 300 180 360 9 661 AGGGGAGTCCTCCTGGAGCCTGGTGCCCTAGAAGCCCACGTCTTTCTGACTTCTGGAGTC 781 GGGTGAGTGGGGAGAGGAACCCGGAAAGGGGCTGTTGGTGATGGTGGCCCAGGGCTTAAG CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGC 61 CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGGGCTGGGGAGGTGAAG 241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT 301 AIGACCAGCIGACACCITICACCICCGCIACIGCAIGGCCCIGIGCCAIAGGIGCIAGGG ACTGTCCTGTTCCCACAGTCCCCACTGTGTCTCAGCACAAGGACACTGGCAGGGTGGGGA 481 GGGGATCTGACCCTCAACCTGCCTTCCACCCAAAGGCCCCGGGCTGACCTCCTCCCCCGCC 541 CCTCCCCTGCAGGGATGCTGACCATCACTGACTTCATCCTGGTGCTGCATCGCTACTACA CTGTCGATGTCTAGGTCCAGATCTATGAGATTGAACAACATAAGATTGAGACCTGGAG 901 GGTGCCTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTGACCGGCTCCCC 961 TGGCCTGACTCTGGCTCTTTCTGCAGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGT GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT ACCAAATGGGGGGGGGGGAGAGAGAGAGCCCCCACTTCTCAGGCCTGGGGGGCTGCCCC ACCACAGGAGGTTGGCTTCAGGCCAAGCCCAGGGGCCCAGGGTGGAGGAAAGTCCATCC Gaps 3 Indels ó Pred. No. 0;
0; Mismatches st Local Similarity 99.9%; tches 1719; Conservative 361 421 601 721 165978 165799 121 181

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/product="RMPK gamma subunit"
join(1. 154,515. .918,1809. .1890,2349. .2407,2509. .2554,
2771. .2825,3027. .3153,3286. .3451,4578. .4615,4791. .4937,
5294. .5410)
                                                                                                                                                                                         join(<1. .154,515. .918,1809. .1890,2349. .2407,2509. .2554,
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GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
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Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC Box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1979 CAGGCTICAACCAAGGGGCCTGGCCTGGAG--AGGGGGGGGGGATTGACCCCGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACTGTCCTGTTCCCACAGTCCCCCACTGTGTCTCAGCACAAGGACACTGGCAGGGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 GGAGCAAATGGGGGGAGGCAGGAGAGAAAAAGAGCCCCACTTCTCAGGCCTGGGGGGGTGCC
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Pred. No. 1.9e-140;
0; Mismatches 484;
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/protein_id="AAF/3989.1"
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                                                                                       organism-"Sus scrofa"
                                                                                                   /db_xref="taxon:9823"
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                                                Location/Qualifiers
1. .5888
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                                                                                                                                                                                                                                                                                                                                       165200
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gailland,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
                                                                                                         1141 CAGACAAGGGAGCCTTGGTGCCCTGCCCTCTTTTAGGGGCCTGGGATGGAGGTTGTCT
                                                                                                                          CTCCCTAGGCTGCCCCGAGGCTCACTGCTCCCATCTCTGCAGCTGTTTGAAGCTGTCTA
                                                                                                                                                                                                                                                  CACCCTCATCAAGAACCGGATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGT
                                                                                                                                                                                                                                                                                                                       1321 ACTCCACATCCTCACACACACAAAGGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa AMPK gamma subunit (PRKAG3) gene, complete cds.
AF214521
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
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Rattus norvegicus clone CH230-262H11, *** SEQUENCING IN PROGRESS
***, 5 unordered pieces.
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                                                                                                                                                                                                                                 1399 GGAGACCTGGGCAGGTGATCAGAGGGCCTGAGGAGTCTTCAGCCCTAGCAGTCGTGGGGA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .----- 5585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1519 CCAGGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCAT 1578
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Chordata, Craniata; Vertebrata, Buteleostomi;
Rodentia, Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5415 CATCTTTGTGGACCGACGTGTCTGCACTGCCTGTGGTCAATGTAAATCTGGTA 5363
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Rattus norvegicus
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 65 conling. The true order of the places

* is not known and their order in this sequence record is
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scheer, S., Scott, G., Shen, H., Shosohtari, N., Sisson, I., Scott, G., Shen, H., Shosohtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Varay, V., Villalon, D., Vinson, R., Wang, Q., Walliams, G., Walliamson, A., Waeczyk, R., Wooden, S., Worley, K., Weisch, Wu, Y., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19.70L-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 77248 bases at least Q40
Consensus quality: 76114 bases at least Q30
Consensus quality: 79522 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project Information
Center clone name: GZRR
Center clone name: CH330-362H11
Sequencing vector: Plasmid:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1363 CATCTTTGTAAGCCTGGGCCCAGGTGGGAGGAGGGGGGAGACCTGGGCAGGTGATCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1423 GGCCTGAGGAGTCTTCAGCCCTAGCAGTCGTGGGGAAGAGCTGGGAGCCCCTCTTGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113624 -----TAGATCCAGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1543 CTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGT
                                                                                                                                                                                                        68; Gaps
                                                                                                                                                                             Score 196.2; DB 2; Length 146577;
Pred. No. 8.3e-38;
0; Mismatches 123; Indels 68; (
                      f uknown length
g of 3438 bp in length
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111897: 0
111997: 9
            94843:
94943:
98381:
                                                98481:
102086:
102186:
104593:
104693:
                                                                                                                                                                              11.4%;
68.1%;
                                                                                                                                                                                                        Matches 408; Conservative
                                                                                                                                                                                             Similarity
92316
92416
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98382
102087
102187
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107539
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LOCUS
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Muzny, D. Marie., Metzker, M. Lee., Abranzon, S., Adams, C., Alder, J., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagia, A., Agogiano, D., Anyalebechi, V., Aoyagia, A., Agogiano, D., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baras, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barca, E., Baden, H., Baldwin, C., Bandar, S., Erre, R., Cardenas, V., Carter, K., Cavazos, I.; Ceasar, H., Center, A., Clacken, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Clacken, J., Charter, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davis, C., Davis, C., Dederich, D., Delgado, O., Denson, S., Dermon, A., Durbin, K., Duval, B., Eaves, K., Bands, C., Erans, C., Ernle, W., Hang, W., Durbin, K., Duval, B., Eaves, K., Ernandez, S., Finle, W., Hagg, M., Prasor, C., Hamilton, C., Hamilton, K., Duval, B., Geer, K., Gali, R., Garcia, A., Garnar, R., Garca, M., Gubrarato, Franser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garnar, R., Guevara, M., Gubrarato, C., Manilton, K., Hannadez, R., Hines, S., Hladun, S.L., Haddun, S.L., Haddun, S.L., Haddun, S.L., Haddson, M., Hamilton, C., Hamilton, K., Houlis, B., Howells, S., Hladun, S.L., Haddson, A., Houles, M., Hannadez, R., Hines, S., Hladun, S.L., Haddson, M., Hannadez, R., Johnson, B., Johnson, B., Johnson, B., Mapue, P., Martin, K., Reute
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Direct Submission
Submission
Submission
Wolceular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24.40G-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 3, 2002 this sequence version replaced gi:22038439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warder, R., Wei, X., White, F., Williams, G., Willson, R., Walczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A. Smith, D.R., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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------- Project Information
Center project name: GBEC
center clone name: CH230-917
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Rat Genome Sequencing Consortium.
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NOTE: Estimated insert size may differ from sequence length (see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working darft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 141109 bases at least Q40 Consensus quality: 148891 bases at least Q30 Consensus quality: 155675 bases at least Q20
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COMMENT

PAT 02-NOV-2001

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GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQV
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43288 TCATCTGATGAGATCACTACCGTGTCCCATCCC - AACAGGGTGCCCTGTTGCCCCGGCC 43231
                                                                                                                 1603 GGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTC 1662
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                      same, and uses thereof
Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
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Sequence 3 from Patent W00120003.
AX099776.1 GI:13538810
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Location/Qualifiers
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RFWGEHTCYDAMATSSKLVIFDTWLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLGGCFKPLVSISPNDSLFRAYYTLI
KNRIHRLPVLDPVSGNVLHILTHKRLIKFLHIFGSLLPRPSFLYRIIQDLGIGTFRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVVLETAP ILTALDIFVDRRVSALPVVNECGQVVGLYSRFDV IHLAAQQTYNHLDMSV
GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDBTQHLLGVVSLSDILQ
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EPPGQGGGGPRSRPTAESTGLEATFPKTTPLAQADPAGVGTPFTGWDCLPSDCTASAAG
                                                                                                                                                                                                                                                                                                                                                                                                             SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
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1 (bases 1 to 2115)

Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    foases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
                  same, and uses thereof
Patent: WO 0120003-A 22-WAR-2001;
INSTITUT WATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1570 TITGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
gamma chain of ampk, dna sequences encoding
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2115;
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                                                                                                                                                                                                                                                       /note="unnamed protein product"
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Science 288 (5469), 1248-1251 (2000)
                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                  /protein_id="CAC35801.1"
/db_xref="G1:13538837"
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                                                                                                                                                                                                                                                                                     /codon_start=1
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Variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Homo sapiens
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Best Local Similarity
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Rattus norvegicus clone CH230-206Al3, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSPQAPFPRIGWDDELRKPGAOIYMRFIEBHTCYDAMATSSKLVIFDTMLEIKKAFFA
LLYANGYRAAPUMSKKOSPGALTITDFILVLHRYRRSPLYOIYEEDGRIFTERWEIT
LQGCKPLYSISSPNGLIFANTDFILVLHRYRRSPLYOIYEEDGRIFTERWEIT
CGCKPLYSISSPNGLIFARDTWILKRRIHRLPVLDPYSGWYLHILTHKRLKEKTHIF
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGOV
VGLYSRDYHLAAQOTYNHLDMSVGRALRKRTLCLEGVLSCQPHESIGEVIDRIARE
VOHRUYLWDETQHLLGVVSLSDLIAAVLATARAGIDPSGPEKI"

A 949 t
498 t
498 t
                                                                                                                                                                                                                                                                                                                                                                                                                                /product="AMP-activated protein kinase gamma 3 subunit"
/protein_id="CAB65117.1"
/db_xref="G1:6688201"
/translation="MEPGIEHALRRTPSWSSIGGSEHQEMSFLEQENSSSWPSPAVTS
SSERIRGKRRARALMYTROKSVEGEPPGGGEGPRSRPARSTGLEATFPRTTPPLAQA
DPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWACLEGILEBERPALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1131 FGCACTGGACATCTTTGTGGACCGGCGTGTGTGTGTGCTGCTGTGGTGGTCGACGAATGTGG 1190
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Boate, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1570 TITGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC
2 (bases 1 to 2290)
Carling,D
Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 ON, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         /function="AMP-activated protein kinase regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 168.2; DB 9; Length 2290; 95.6%; Pred. No. 1e-30;
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                                                                                                                                                                    1. .2290
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=experimental
                                                                                                                                                                                                                                                           /gene="AMPK gamma 3"
22. .1500
                                                                                                                                                                                                                                                                                                             /gene="AMPK gamma 3"
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HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                               Subunit"
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AC127107/c
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    REFERENCE
AUTHORS
                                                                          JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                /product="AMP-activated protein kinase gamma subunit"
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SSTDDVELATEFPATERMECELECILEBRRAKICLSPQAPPPKIGWDDELKRPGAQIYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLI
KNRTHRLPVLDPYLDPYSGNYLHILTHKRLLKFLHIFGSLLPRESFLYRTIQDLGIGTFRDL
AVVLETAPLITALDIFVDRNVSALPVVNECGQVVGLYSRFDYIHLAAQQTYNHLDMSV
GEALRQRYLCLEGYLSCQPHESLGEVIDRIAREQVHRLULDFTQHLLGVVSLSDILQ
ALVLSPAGIDALGA
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Kalm.E., Le Roy.P., Chardon.P. and Andersson.L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2290)

Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
Biochem. J. 346 pt 3, 659-669 (2000)

10698692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 168.2; DB 9; Length 2115; 95.6%; Pred. No. 1e-30;
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8
                                                                                                                                                                                                                                                                   /tissue_type="skeletal muscle"
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                                                                                                             Location/Qualifiers
1. 2115
Cycganism="Homo sapiens"
Ab xref="taxon:9606"
Chromosome="2"
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                                                                                                                                                                                                                                                                                                             /gene="PRKAG3"
                                                                                                                                                                                                                                                                                                                                                                                   /note="AMPKG3"
                                                                                                                                                                                                                                                                                                                                                            /gene="PRKAG3"
                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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AJ249977.1 GI:6688200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622 c
                                                                                                                                                                                                                                               /map="2p"
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ORGANISM
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HSA249977
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AUTHORS
                                                 JOURNAL
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KEYWORDS
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                                                                                                                     FEATURES
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Carron T.F., Carter.M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Clealand, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delgado, D., Elago, M. Erota, S. Durbin, K.J., Earnbart.C., Edgar, D., Elago, N., Ford, J., Escetco, M., Falls, T., Ferraguto, D., Elago, N., Ford, J., Eoster, P., Frantz, P., Gabisi, A., Sao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratue, P., Hames, A., Hennandez, O., Hodgeson, A., Hogues, M., Holloway, C., Holling, B., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Haber, J., Holloway, C., Tolling, B., Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kartovic, J., Kally, S., Khan, U., King, L., Koryan, J., Kovar, C., Kratovic, J., Kureshi, A., Ludry, M., Loul, J., Liu, M., Loulseged, H., Li, J., Li, Z., Lu, R., Ludar, M., Lucier, R., Luna, R., Mar, J., Martinez, E., Marten, B., Martinez, E., Martin, R., Martindale, A., Martinez, E., Marken, M., Mapua, P., Martin, R., Martindale, A., Mayen, M., Mahney, E., Michell, T., Mohabbat, K., Morgan, M., Mosa, D., Machan, M., Mayen, M., Mosa, D., Martin, R., Martindale, A., Mayen, M., Mosa, D., Martin, R., Martindale, M., Ren, Y., Rodan, R., Nayen, M., Nickerson, E., Nwokens, R., Payton, B., Peerry, J., Perez, L., Peters, J., Pakers, M., Palor, P., Tamerisa, M., Tang, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, M., Tang, H., Sutton, A., Yasquez, L., Pathus, E., Sonaike, T., Sparks, A., Stanley, H., Tamerisa, M., Tang, S., Ward-Moore, S., Ward-Mo
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NOTE: This is a 'working draft' sequence. It currently
consists of 74 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length
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contig of 1170 bp in length
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TITLE JOURNAL REFERENCE AUTHORS

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COMMENT

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Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3) mRNA, complete cds.
AF214520.1 GI:8215683
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ISPNDSLFRAVYALIKNRIHRLPVLDPVSGAYLHILTHKRLIKFLHIFGTLLRRRSFL
YRTIQDIGGTSRDLAVVLETAPLITALDIFVDRNVSALPVVNETGQVGLYSRPDVI
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/translation="MHFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAP
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Milan, Jeon, J. T. Looft, C., Amarger, V., Robic, A., Thelander, M.,
Rogel-Gaillard, C., Faull, S., Iannuccelli, N., Rask, L., Ronne, H.,
Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Milan, J., Jeon, J.T., Looft, C., Amarger, V., Robic, R.,
Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Rain, E., Le Roy, P., Chardon, P. and Andersson, L.
Direct Submission
             Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
Patent: WO 0120003-A 1.2-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Pred. No. 1e-25;
0; Mismatches 20; Indels
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Science 288 (5469), 1248-1251 (2000)
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/db_xref="taxon:9823"
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  Chardon, P.
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
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GPALRORTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDFTQHLIGVVSLSDILQ
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88.9%; Pred. No. 1e-25;
ative 0; Mismatches 20; Indels (
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1. 1873
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Search completed: June 14, 2003, 16:15:58
Job time : 4498 secs

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Human AMPK gamma s Human AMPK gamma s

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Mammalian AMPK gam Drosophila melanng Drosophila melanng Human breast cell Human foetal liver Probe #13292 for g

Total number

Database

Result

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Searched:

Sequence:

Human bone marrow Probe #1565 for g Probe #16674 used Probe #8345 used t Human genome-deriv Disease associated DNA encoding novel

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Human, AMP-activated protein kinase gamma 3 subunit, PRKAG3, variant, metabolic disease; diabetes, obesity; substitution, ds.
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/number = "Intron 4"
/note= "3' portion of intron 4"
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AAC98774
ABL39755
AAT85927
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AA147988
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/number= "Exon 5"
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/number= "Intron
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9167.709 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variants of human AMP-activated protein kinase gamma3 subunit poiated with a metabolic disease e.g. diabetes or obesity and method determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occul in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 1722;
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                "Exon
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useful for measuring gene expression in sample derived from human
          breast, comprises number of single exon nucleic acid probes
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                                                                                                                                                                                                                                                                           0; Mismatches
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          CCCAGGTGGGAGGAAGGGGGAGACCTGGGCAGGTGATCAGAGGGCCTGAGGAGTCTTCAG 1440
 CTCCCTAGGCTGCCCCGAGGCTCACTGCTCCCATCTGCAGCCTGTTTGAAGCTGTCTA 1260
                                                 ACTCCACATCTTCACACACACACACGCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG
                                                                                                                                                         CCCTAGCAGTCGTGGGGAAGAGCTGGAAGCCTCTTGAAGCTGCTGGATCCCTGATCTCC
                                        CACCCTCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New spatially-addressable set of single exon nucleic acid probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                              CGAATGTGGTACCCACCCCCAGGATGAGAGGCTCGGGCTGGA 1722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human breast cell single exon nucleic acid probe #3401
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2000US-0207456.
2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease; cancer; ss.
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27-SEP-2000;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verlighing the expression of regions of genomic DNA predicted for encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical expression analysis to measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence data for this patent did not form part of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly 120 180 240 243 183 123 GGAGICIGCAIGGCCAGCIGGGAGACCCTGGGGCCICAATTICCCCCAICIGTGGAGCCGCI 300 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360 SS. 63 121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT GGAGATGGAGGTGAGGGGGGAGATCTTGTACGTTGTTCTCGGGGCTGATCTCTCTGATAT GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 61 CCCTCTATGGGACAGCAAGAAGCAGACTTTGTGGGTGAGGAGAGGCTGGGGAGGTGAAG 181 ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAGTCCATCC Human; foetal liver; gene expression; single exon nucleic acid probe; 1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC Gaps ä 20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83; Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English 0; Indels Human foetal liver single exon nucleic acid probe #3467.

09-AUG-2001

Penn SG,

E STANDER STAN

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predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCCTGATCTCTGATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                 Probe #3373 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 378;
                                                                                                                                       Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                              congenital heart disease; ss.
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 GGAGATGGAGGTGAGGGGGAGATCTTGTACGTTGTTCTGGGGCCTGATCTCTGATAT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGAGATGGAGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGGATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGCAGGGCCAGGGTGGAGGAAGTCCATCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGTCTGCATGGCCAGCTGGGAACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGTCTGCATGCCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGTGAGGAGGAGGCTGGGGAGGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                       DR;
                                                                                                                                                                                                                                                                                                                       Rank
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1D ABA24907 standard; DNA; 378 BP.
                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                            2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                      2000GB-0024263.
                                                                                                                                     2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                      2000US-0236359
                                                                          2001WO-US00669
                                                                                                                    2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 99.7 ies 362; Conservative
                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483447/52.
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WO200157277-A2
                                                                                                                                   26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                        CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGAGAGGAGGCTGGGGAGGGTGAAG 243
                                                                                                                                               241 GGAGTCTGCATGGCCAGCTGGGAGCCCTGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT 300
                                                   GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT
                                                                                           ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC
                                                                                                                                                                                                                 62 ATGACCAGCTGACACTTTCACCTCCGCTACTGCATGCCCCTGTG-CATAGGTGCTAGGG
                                                                                                                                                              GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT
                                                                                                                                                                                                   ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG
The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
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                                                                                                                                                                                                                                                                                                                                                                                                                                Human bone marrow expressed single exon probe SEQ ID NO: 3431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR;
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                                                                                                                                                                                                                                                                                                                                 AGC 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGGCCCCTCAGATCAAGAAGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CCCTCTATGGGACAGCAAGAAGCAGCTTTGTGGGTGAGGAGGAGGCTGGGGGAGGTGAAG 120
GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT 300
                                                  301 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCCAGC 60
                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                 62 ATGACCAGCTGACACTTTCACCTCCGCTACTGCATGGCCCTGTG-CATAGGTCTAGGG
             Gaps
                                                                                                                                                                                                                                                                                                          Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in brains .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO: 3414; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                 expressed single exon probe SEQ ID NO: 3414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0207456.
2000US-0608408.
2000US-0632366.
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0180312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483446/52.
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                                                                                                        AGC 363
                                                                                                                        AGC 1
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                                                                                                                                                                                                                                                                                                                                                                                          WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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30-JUN-2000;
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                                                                                                                                                                                                                                                       05-NOV-2001
                                                                                                                                                                                                                                                                                 Human brain
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                                                                                                                                                                         RESULT
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CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC 303
                                                                                                                                                                                                                                                    ACCACAAGCTTGGGCTTCAGGCCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC 240
                                                                                                                                                                                                                                                                                                                                                             241 GGAGICTGCATGGCCAGCTGGGAGACCCTGGGGCTCAAITTCCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AIGACCAGCIGACACCITICACCICCGCIACIGCAIGGCCCIGIGCCAIAGGIGCIAGGG 360
                                                                                                                                                                                                                                                                                                  GGAGATGGAGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGCCTGATCTCTGATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed at fit.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTG-CATAGGTGCTAGGG-4
                                                                                                                                                                                                    1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to measure gene expression in human placenta sample.
                                                                                                                                                         Length 378;
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microarray; human; placenta; antenatal diagnosis;
                                                                                                                                Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                      22;
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                                                                                                                                                      Score 351; DB 23
Pred. No. 9e-83;
                                                                                                                                                                              0; Mismatches
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2000US-0207456.
2000US-0608408.
2000US-0532366.
2000US-0234687.
                                                                                                                                                      20.4%;
99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                Local Similarity 99.7 nes 362; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGC 1
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                      Query Match
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                                                                                                                                           GCAGATGGAGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT 180
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                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                     301 ATGACCAGCTGACACCTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360
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                                                                                                         142 GGAGATGGAGGAGGGGGGGGGGAGATCTTGTACGCTTGTTCTGGGGCTGATAT
                                                                                                                                                                                                                                                    GGAGTCTGCATGCCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT
                                               1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                                                                                                                                                                                         ACCACAAAGCTTGGCTTCAGGCCAAGCCCAGGGGGCCAGGGGTGGAGGAAAGTCCATCC
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for gene expression analysis in human cervical cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; microarray; gene expression; cervical epithelial
                        1;
                        Indels
 Length
                       ;
 DB 22;
Score 351; DB 22
Pred. No. 9e-83;
                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
20.4%;
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                        362; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488901/53
             Similarity
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26-MAY-2000; 2
30-JUN-2000; 2
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27-SEP-2000;
04-OCT-2000;
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Best Local
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29-JAN-2001; 2001WO-US00661
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Matches 36
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                                                                                                                                                                                                                                                                                                        362 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCCCCTGTGCCCATAGGTGCTAGGG 360
                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                    / Match 20.4%; Score 351; DB 22; Length 378; Local Similarity 99.7%; Pred. No. 9e-83; les 362; Conservative 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                          Claim 25; SEQ ID No 3507; 654pp; English.
                                            Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 378 BP.
                      (MOLE-) MOLECULAR DYNAMICS INC
04-OCT-2000; 2000GB-0024263.
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                                           Hanzel DK,
                                                                  WPI; 2001-488897/53
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel single exon nucleic acid probe used to measuring gene expression in a human breast \mbox{\, --}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID No 3335; 322pp; English.
                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
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                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0633366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                          2000GB-0024263.
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362; Conservative
                                                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK,
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ID ABS034
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haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at
fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of
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                                                                                                                                                                                                                   Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; chanilial idopathic pulmonary fibrosis; neurofibromatosis; tubercus sclerosis; datecher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary hastlocytosis; lymphangioleiomyomicosis; Karagener syndrome; pulmonary alvoelar proteinosis; fibrocystic pulmonary alvoelar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
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                                                                                                                                                                  Human genome-derived single exon probe from lung SEQ ID No 3398
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2000US-236359P.
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2000US-0608408.
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                                                                                                  (first entry)
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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181 ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGTCTGCATGGCCAGCTGGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 ATGACCAGCTGACACTTTCACCTCCGCTACTGCATGGCCCTGTG-CATAGGTGCTAGGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 GGAGATGGAGGAGGAGGGGGGAGATCTTGTACGTTGTTCTGGGGCTGATCTTGAAT
                                                                                                                                                                                                                                                                                                       1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCCTCAATTTCCCCATCTGTGGAGCCGCT
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferation; metastasis; cancer; tumour; haematopolétic disorder; myeloid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue regeneration; wound healing; infection; immune disorder;
                                                                                                                                             Length 378;
                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bone disorder; osteoporosis; vascular growth disorder;
                                                                          Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                             20.4%; Score 351; DB 24;
99.7%; Pred. No. 9e-83;
Live 0; Mismatches 0;
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA08485 standard; cDNA; 547 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-2002 (first entry)
                                                                                                                                                                                                                        Matches 362; Conservative
                                                                                                                                                                                         Best Local Similarity
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1630 TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGACGAATGTGG 1689
                                                     New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution PJIA; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the full length cDNA encoding the human
                                                                                                                       1690 TACCCACCCCAGGATGAGAGGCTCGGGCTGG 1721
                                                                                                                                                   452 TACCCACCCCCAAGAGAGCTCGGGCTGG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Silent variation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= "C1037T"
/note= "Causes R340W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/label= "C230G"
/note= "Causes P71A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
20..1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product- "PRKAG3"
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                                                                                                                                                                                                                                                                                               AAH43685 standard; cDNA; 1647 BP.
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"T559C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRKAG3 CDNA.
                                                                                                                                                                                                                                                                                                                                                AAH43685;
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                                                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                        AAH43685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences ABAG0822-ABAG09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nuclectide of the invention, methods of producing the noveb polypeptides, cantibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemacomistatic, thrombolic or chemokinetic activities; and may be involved in oncogenesis, cancer cell proliferation or metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, eq., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferative retinopathy, atherosclerosis, coronary heart disease, arterial isothemaia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypepides involved with lissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in call cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        illness,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that can be used to augment or replace cells damaged by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT;
                                                                                                05-FEB-2001; 2001WO-US03800.
                                                                                                                                              2000US-0496914.
2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 429; 1963pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                 2001-457740/49.
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                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABB11241
WO200157188-A2.
                                                                                                                                              03-FEB-2000;
27-APR-2000;
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Best Local S
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Homo sapiens.
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                                                                                                                                                                      1630 TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGG 1689
                                                                                                                                                                                                                                                                                                                                                      PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rogel-Gaillard C;
                                                                                                           1069 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC
                                                                                                                                    1570 TTTGGGCATCGCCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC
                                                                                                 gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                 Gaps
resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on
                                                             Score 168.2; DB 22; Length 1647;
Pred. No. 3.3e-34;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                            Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                        cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                             Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
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/product= "Human Prkag3 protein"
1390..2109
/*tag= c
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(ANDE/) ANDERSSON L.
                            position 1 of the open reading frame
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                                                              9.8%;
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472..1389
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                                                                      cal Similarity 95.6
173; Conservative
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Iannuccelli N,
                                                                                                                                                                                                         T 1690
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5'UTR
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The present sequence is a convenion indical actions to the present in the present is present that the present is a convenion to the present is a convenion to the present is a convenion to the present it is the present in the present is a convenion to the diagnostic and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prophosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able for modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain con present in a prkaG3 and is useful in gene therapy.
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New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA
                                                                                                                                                                                                                                                                                                                                               The present sequence is a cDNA encoding human adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.8%; Score 168.2; DB 22; Length 2109; Best Local Similarity 95.6%; Pred. No. 3.6e-34; Matches 173; Conservative 0; Mismatches 8; Indels 0;
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1..1395
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AAD03295 standard; cDNA; 1867 BP.

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AAD03295
                                    The present sequence is a cDNA encoding human adenosine monophosphate

(AMP)-activated kinase (AMRK) gamma subunit muscle-specific isoform,
complete PRKAG3. Mutation in Prkag3 results in an altered regulation of
carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
useful as therapeutic for treating carbohydrate metabolism disorders such
as diabetes, obesity, and disorders associated with muscle metabolism
cutivity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
cativity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
catalation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3 or
transgenic animal and host cell transformed with PRKAG3 or are
neterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 suseful for detecting mutations in a Prkag3 gene, or
concoding PRKAG3 and is useful in gene therapy.
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Le Roy P, Chardon P;
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Pred. No. 3.6e-34;
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                                                           11-SEP-2000; 2000WO-EP09896.
                                                                                    99EP-0402236
                                                                                              18-MAY-2000; 2000EP-0401388
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, Gellin J,
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Best Local Similarity 95.6'
Matches 173; Conservative
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P-PSDB; AAE00223.
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           WO200120003-A2.
                                                                                                                        (INRG ) INRA
(ANDE/) ANDER
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                                  22-MAR-2001
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3: PrkAg3 gene is located in the RN locus of chromosome IS.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as cubates, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic polymorphic and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a general prognosity of a sequence encoding PRKAG3, are
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Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                                                                                                                                        Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRK63; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbobydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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J, Le Roy P, Chardon P;
                                                                                                                                              Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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472..1389
/*tag= b
/product= "Sus scrofa PRKAG3 protein"
1390..1867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                              chromosome 15; ss.
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AAD03295;
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                                 Query Match 8.6%; Score 148; DB 22; Length 1867; Best Local Similarity 88.9%; Pred. No. 7.5e-29; Matches 160; Conservative 0; Mismatches 20; Indels 0;
                 Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
of PRKAG3 and is useful in gene therapy.
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BH833269 603087149
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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El to 572,
Stantaug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
Unpublished (2000)
Contact: Smith PPL
CORDACAC: Smith PPL
CORDACAC: Smith PPL
CORDA ARS. US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Frax, 402 762 Palmers
Franch Primarch 12 options.
FORWARD: AGGAAACAGCTATGACCAT
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Copyright (c) 1993 - 2003 Compugen Ltd.
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BG609812 323791 MA AW410226 hn09c01.x BE146626 hn09c01.x BE146626 hn09c01.x BE140148 60263047 BG708895 602669396 BM782063 K EST0058 BM782063 K EST0046 BM782132306 602943249 BM78383 K EST0061 BI223706 602943249 BM78383 K EST0061 BI223706 602943249 BM78383 K EST0061 BI223706 602943249 BM78383 K GST0961 BI223706 60294288 BI85947 603386088 BI85947 603386088 BI819312 603037761 BISS1389 601448767 BG21538 603038457

EST 30-JUL-2001

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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS03KJ0 1042 bp DNA linear GSS 17-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 033Ll3 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                    1543 CTCCTTCCTCACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGT 1602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGTGCTGGAGACA-NNCCAATCCTGACTGCACTGGACATCTTTGTGGACGGGGGTGTGTC 119
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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/note="Genoscope sequence ID : COBG033CF07LP1-end : T7"
'not = "Genoscope sequence ID : COBG033CF07LP1-end : T7"
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                                                                                                                                                                                                                                                       1; Gaps
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(bases 1 to 1042)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fishe
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                           Length 413;
                                                                                                                                                                                                                                      Score 132.4; DB 9; Length Pred. No. 5e-21; 3; Indels 0; Mismatches 3; Indels
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/db_xref-"taxon:99883"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Best Local Similarity 97.3%;
Matches 144; Conservative (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 413)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Wolse,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,

White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project
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                                                                                                                                                                                                                                    /note="Vector: pcMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from test1s, ovary, endometrium, hypothalamus, pituitary, and placenta."

190 c 151 g 124 l lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information, Insert Length. 1280 Std Error: 0.00 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA178898 413 bp mRNA linear EST 09-MAR-
258640.L.1 Stratagene musche 937209 Homo sapiens cDNA clone
IMAGE:611731 5' similar to SW.AAKG.RAT PRO385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                             Score 148; DB 13; Length 572;
Pred. No. 1.1e-24;
0; Mismatches 20; Indels
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/tissue_type="muscle"
/dev_stage="adult"
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                                                                                                         /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="WARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9606"
  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG.
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                                                                    Location/Qualifiers
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AA178898.1 GI:1760259
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Contact: Wilson RK
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Best Local Similarity 88.9
Matches 160; Conservative
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Fax: 314 286 1810
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Confect: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata: Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
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                                                                                                                                   1228 CTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCG 1287
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1 others
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                                                      Score 88.8; DB 13;
Pred. No. 1.5e-10;
0; Mismatches 42;
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11 Similarity 77.9%; Pred. No. 1.6e-09;
102; Conservative 0; Mismatches 29;
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/sex="mixture of female and
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/dev_stage="fry stage 40"
161 c 174 g 210 t
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Location/Qualifiers
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BJ504184
BJ504184.1 GI:22156146
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236 CAACTGTTTAT 226
177
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Matches 10
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                                                                                                                                                                                                                                                       1358 CTGCACATCTTTGTAAG------CCTGGGCCCCAGGTGGGAGGGGGGAGACCTGG 1408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1521 AGGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCG 1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BJ495978 100-2002 591 bp mRNA linear EST 08-AUG-2002 BJ495978 MF01FSA CDNA Oryzias latipes cDNA clone MF01FSA040J15 5',
                                                                                                                                                                        1469 GCCCTCTTGAAGCTGCTG-----GATCCCTGATCTCCACCTGGTCCCCATCCTAACC 1520
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostei; Buteleostei; Neoteleostei;
Acarthomorpha; Acarthopterygli; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                               436 CCCTCCTGTTTGCGGCCGTGAACACACCCCTGTCTTACTTTGCGCGTTTGCCTCGTTTCC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 AGATGTGTGAGAAGCCCAAAGCCCGCTTTCATGAAGCAGACCTGAGGGAGCTGGGCATTG 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    556 GTACATACCGGGACATTGCTTTCATTCACCCGGACACGCCCATCATCAAGCGCTCAACA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. Medka BST Project in Takeda's lab
Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              673
                                                                                           376 CCCACCCTGGTGGGGGCAGATCTTCGCCCATCTGCTTCCCCCTAGTGGCCCAAAGCCCAGA
                                                      17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTTGTGGAGAGGCGGGTGTCGCCCTGCCGGTGGTGGACGACTCCGGTAGGAACCC
                DB 17; Length 1042;
                                                      Indels
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tat: 81-559-81-6856
Fax: 81-559-81-6855
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/clone_lib="MF01FSA cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="fry stage 40"
              Score 116.8; DB 17;
Pred. No. 3.9e-17;
0; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryzias latipes"
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/db_xref="taxon:8090"
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Location/Qualifiers
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              6.8%;
          Query Match
Best Local Similarity 56.3'
Matches 269; Conservative
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TITLE
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BJ495978
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us-09-826-581-3.rst

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1599 CTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTG 1658
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                                                                                                                                                                                                                                                                                                  EST 11-DEC-2001
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//dev_stage_25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute).

a 162 c 148 g 179 t
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                                                                      1 (bases 1 to 633)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                             BJ072114 633 bp mRNA linear EST 11-DEC-2
BJ072114 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL096jl6 5', mRNA sequence.
BJ072114
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Center For Genetic Resource Information
National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed genes in X. laevis embryo Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                    1659 TGTCTGCACTGCCTGTGGTCAACGA 1683
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                                                                                                                                                           426 TCTCCGCCTTACCTGTAGTGGATGA 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 ACTCAAGTTCCTTCACCTCTTG 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                 African clawed frog.
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BJ072114
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                                                                                       BG919314 101_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4946661 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-*Organ: mammary; Vector: pcMv-SPORT6; Site_1: Sall; Site_2: Notl; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 ACCCAGAGTCAGGCAACACCTTGTACATCCTTACTCACAAGCGGATCCTCAAGTTCCTCA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 AGAGCGGTTGGGGACAGAGGAGGGGTGTTGGTGTTGATGATTGAGCGTAGCACCTCCATG 246
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                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 933)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0895 row: d column: 22
                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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ilarity 52.1%, Pred. No. 5.5e-09;
Conservative 0; Mismatches 209; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
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/clone="IMAGE:4946661"
/clone_lib="NCI_CGAP_Mam6"
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Location/Qualifiers
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/lab_host="DH10B"
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                                                                                                                                                                              BG919314.1 GI:14299790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . . . 933
                                                                                                                               mRNA sequence.
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Best Local Simi
Matches 232;
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ORIGIN
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JOURNAL
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                                                                                                                                                                              VERSION
KEYWORDS
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                                          RESULT 6
BG919314
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/dev.stage="Breast,leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks):growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli EmbiloB"
/note="Vector: pcMvSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth flom 5'-end"
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/clone_lib-"Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/tissue_type="Breast muscle, leg muscle and epiphyseal
growth plate"
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Pred. No. 1.7e-08;
0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cogburn@udel.edu, www.chickest.udel.edu.
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/strain="Commercial broiler and
Strains 90 & 21"
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                                                                                                                                                                                                                                                                                                                             Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                      1 (bases 1 to 595)
Cogburn, L.A. and Monsonego-Ornan, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9031"
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                          GI:18608720
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al Similarity 69.4%;
109; Conservative (
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BG713637
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Matches 109; Conserv
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BG713637
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/lab_host="E. coll EmbHlost
/note="Vector: pCWYSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue (embryonic
muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
plate 33.3% of the final RNA pool). Single pass sequencing
from 5'-end"
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pgm2n.pk008.g21 Normalized Chicken Breast Muscle, Leg Muscle, and Bpiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk008.g21 5' similar to gb|AAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                             Cogburn, L.A. and Monsonego-Ornan, E. ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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/clone-lb-"Normalized Chicken Breast Muscle, Le
and Epiphyseal Growth Plate cDNA library (pgm2n)
/sex-"Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 81.8; DB 13; Length 536; Pred. No. 6.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
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Strains 90 & 21"
/db_xref="taxon:9031"
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Contact: Larry A. Cogburn
University of Delaware
                                                                                                                                        BM488662.1 GI:18609593
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Matches 110; Conservative
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Fax: 302-831-2822
                                                                                           mRNA sequence.
                                                                                                                                                                                                              Gallus gallus
                                                                                             ], mRNA se
BM488662
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BM487789
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KEYWORDS
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/clone_lpb="Normalized Chicken Reproductive Tract cDNA Library (pgrln)"
/sex="Male and Female" /tissue_type="Tests, ovary and oviduct" /tissue_type="Tests, ovary and oviduct" /dev stage="Various stages;embryonic, post-hatch, immature and sexually-mature" and sexually-mature and sexually-mature fool: EMDH10B" /lab_host="R. coli EMDH10B" /note="Vector: pcNVSPORT6; Library made from three total RNA pools from each tissue (testis 25%, ovary 25%, and oviduct 50% of final RNA pool); Single pass sequencing from 5'-end"
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A large database of chicken bursal ESTs as a resource for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 CTCCCCCAATGCCAGCCTTTTTGATGCCGTCTCCTCCTGATCCGCAATAAGATCCACCG 452
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (bases 1 to 649)
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Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Indels
                             /organism="Gallus gallus"
/strain="Commercial broiler and layer"
/db_xref="taxon:9031"
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/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
227 c 155 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                            Score 80.2; DB 13;
Pred. No. 1.7e-08;
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Genome Res. 10 (12), 2062-2069 (2000)
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  Location/Qualifiers
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BM440762

BM4602.19 Normalized Chicken Reproductive Tract CDNA Library CPGLIN Gallus gallus CDNA clone pgrin.pk002.19 5' similar to gil4506061 ref!NP_002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit, AMPR gamma 1; Protein kinase, AMP-activated, noncatalytic, gemma-1 (Homo sapiens) gil12737489 ref!XP_006778.2| protein kinase, AMP-activated, gamma 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archiosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 636)
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1 (bases 1 to 641)
Cogburn, L. A. and Nys, Y.
University of Delaware and INRA, Tours-Poultry Unit Project Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.7%; Score 80.2; DB 12; Length 636;
59.4%; Pred. No. 1.7e-08;
lve 0; Mismatches 48; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 others
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                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9011"
/clone="pg11n.pk008.c13"
/clone_lib="Normalized Liver Library"
                                                                                             Burnside, J., Morgan, R.W. and Cogburn, L.A. Chicken ESTs from a normalized liver library upublished (2001)
Contact: Joan Burnside
Molecular Endocrinology
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                                                                                                                                                                                                                                                                                     Email: joan@UDel.Edu, www.chickest.udel.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Delaware*
40 Townsend Hall, Newark, DE 19717, USA
Fax: 302-831-3411
                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="liver"
/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6"
215 c 167 g 119 t
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Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                 /organism-"Gallus qallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male and Female"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .636
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University of Delaware
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Gallus gallus
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chicken.

SM Gallus gallus

Galvaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

I (basea I to 758)

SA Abdrakhmanovi... Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.

A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function

L Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV603335 Sos taurus kidney fetus Bos taurus cDNA clone E1KI015F02 5/, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Cetartiodactyla: Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 576)
Takasuga.A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H., and Sugimoto,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1228 CTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCG 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                             Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks 01d"
238 c 186 g 166 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.6%; Score 78.6; DB 9;
68.8%; Pred. No. 4.5e-08;
tive 0; Mismatches 49;
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Shirakawa Institute of Animal Genetics
                                                                                                                                                                                                                                                                                                                                                                         1. .758
/organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="25f16r1"
/clone_lib="dkfz426"
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                                                                                                                                                                                                                                                                Contact: Buerstedde JM
AJ396118.1 GI:7127728
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                                                                                                                                                                                                                                                                                                                                                                                                             /strain="CB"
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                                                                                                                              46 CTCCCCCAATGCCAGCCTTTTTGATGCCGTCTCCTCCTGATCCGCAATAAGATCCACCG 105
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                         AJ451523 FIXEN1 Gallus gallus cDNA clone 29a6r1, mRNA sequence. AJ451523
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                   Length 649;
                                                      Indels
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                                                                                                                                                                                                                                                                                 166 CCTCAAGTTCCTCAAACTCTTTATTGCAGAGGTCCCA 202
               Score 80.2; DB 9; I
Pred. No. 1.8e-08;
0; Mismatches 48;
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/dev_stage="2-3 weeks old"
/note-"CB inbred strain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus bursal lymphocyte EST pupublished (2002)
Contact: Buerstedde JM cellular Immunology
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/db_xref="taxon:9031"
/clone="29a6r1"
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                 4.78;
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Buerstedde, J.M.
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                                  al Similarity 69.4
109; Conservative
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Best Local Si
Matches 109;
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AJ451523
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                                                                                                                                          Query Match 4.4%; Score 76.4; DB 10; Length 576; Best Local Similarity 70.1%; Pred. No. 1.3e-07; Matches 101; Conservative 0; Mismatches 43; Indels 0;
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ORIGIN
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Sequence 1 Sequence 2 Sequence 7

Sequence Seq

Sequence 1 Sequence 8

Sequence Sequence Sequence

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Sequence 63, Application US/09101146
Patent No. 6124125
GENERAL INFORMATION:
APPLICANT: Darknouth College, St. Vincents Institute of
APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
NUMBER OF SECUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.0%; Score 68.8; DB 3; Length 1576; 67.4%; Pred. No. 4.9e-09;
Live 0; Mismatches 47; Indels 0
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: IBM PC
                                                              US-09-155-768-1
US-08-456-2008-11
US-08-455-543-8
US-08-193-078B-8
US-08-194-097D-8
US-08-4450-562-8
US-08-4450-562-8
US-08-450-562-8
US-09-268-163-7
US-09-268-163-7
US-09-268-163-7
US-09-268-163-7
US-08-713-118-1
US-08-713-118-1
US-08-713-118-1
US-08-713-118-1
US-08-713-118-1
US-08-455-5433-7
US-08-193-078B-7
                     PCT-US93-06160-3
US-08-687-080-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORDPERFECT 6.0 FOR WINDOW CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,146
FILING DATE: October 7, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PN7450
FILING DATE: 8 JAN 1996
ATTORNEY/AGBRI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jane Massey Licata, Esq. STREET: 66 E. Main Street CITY: Marlton STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DC-0050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
TELERAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Nucleic acid
STRANDEDNESS: Single
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Matches 97; Conserv
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US-09-101-146-63
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Sequence 2
Sequence 3
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                                                                                                                                                               June 14, 2003, 11:14:12; Search time 90 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-23-463-14
US-08-23-463-14
US-09-272-796-14
US-09-272-796-14
US-09-272-796-14
US-09-24-796-17
US-09-07-005-17
US-09-05-24-796-17
US-09-165-264-14
US-09-165-264-14
US-09-165-264-13
US-09-165-266-21
US-09-165-268-165-268-28
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Maximum Match 1008
Listing first 45 summaries
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Match
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67.6
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39.4
39.4
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37.4
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                                                                                                                                                                                                             1206 TAGGCTGCCCCGAGGCTCACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCC 1265
                                                                                                                                                                                                                                     1266 TCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCC 1305
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jonnifer L. APPLICANT: Corley, Neil C. APPLICANT: Guegler, Karl G. APPLICANT: Lal, Preeti APPLICANT: Goli, Surya K. APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 14, Application US/08878989; Patent No. 5885803; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LIBRARY: PENITU
; CLONE: 1452972
US-08-878-989-14
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US-08-878-989-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1026 TCTCTCCTAATGATAGGTGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCTCCACAGT 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1018 CTCACAGAATTAATTCCGAGCTTGGCTGCAGGTCGAGGGAGCTTGCGATYYYYYYYY 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1300 TGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAAACGCCTGCTCAAGTTCCT 1359
                                                            CAGCTTGTTTGATGCTGTCTTCATTAATTCGCAACAAGATCCACAGGCTGCCAGTTAT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             906 CTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTGACCGGCTCCCCTGGCC
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5.2%; Pred. No. 1.9e-08;
ive 223; Mismatches 152; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29,768
ER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Foley & Lardner
: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                 1360 GCACATCTTTGTAAGCCTGGGCCC 1383
                                                                                                                                                    621 CAAATTGTTTATCACTGAGTTCCC 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.9%; Scc
Best Local Similarity 6.2%; Prec
Matches 25; Conservative 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERA: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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(703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463
Patent No. 5670367
Patent No. 5670367
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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Best Local Similarity
Watches 13; Conserv
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ZIP: 22313-0299
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                                                                        509 AGCCTCTTCGATGCTGTATACTCCTTGATCAAAATAAAATCCACAGATTGCCCGTTATT 568
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tive 0; Mismatches 42; Indels 0
Score 63.8; DB 2; Length 1435;
Pred. No. 1e-07;
0; Mismatches 42; Indels 0
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CORRESPONDENCE ADDRESS:
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SOFTWARE: FactSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF-0321 US
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APPLICATION NUMBER: 08/878,989
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Hillman, Jennifer L.
Corley, Neil C.
Guegler, Karl G.
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NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 14:
 Query Match 3.7%;
Best Local Similarity 67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 67.9
Matches 89; Conservative
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                                     89; Conservative
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CLONE: 1452972
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                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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STATE:
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Sequence 17, Application US/09244796 Patent No. 6281344
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Best Local Similarity
Matches 6; Conserva
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US-08-658-136-2/c
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US-09-244-796-17
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                                                                                                              791 GGAGAGGAACCCGGAAAGGGGCTGTTGGTGGTGGTGGGCCCAGGGCTTAAGGTGGAGGATG 850
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APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: FUSIONS
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h Similarity 2.7%; Score 39.4; DB 4; Length 26 Similarity 2.7%; Pred. No. 0.19; 6; Conservative 107; Mismatches 110; Indels
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CURRENT FILING DATE: 1998-01.14
EARLIER FILING DATE: 1998-01.14
EARLIER FILING DATE: 1997-01.27
EARLIER FILING DATE: 1997-01.27
EARLIER FILING DATE: 1997-11-06
NUMBER: FOS SE ID NOS: 33
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Translation template
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Patent No. 6258558
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; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
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ORGANISM: Artificial Sequence
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US-09-244-796-17
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US-09-007-005-17
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LENGTH: 289
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Best Local S:
Matches 6,
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787 GIGGGGAGAGGAACCCGGAAAGGGGCTGITGGTGATGGTGGGCCCAGGGCTTAAGGTGGAG 846
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TITLE OF INVENTION: PUSIONS
FILE REPERENCE: 00/786/35.0007
CURRENT PILING DAME: 1999-02-05
CURRENT FILING DAME: 1999-01-27
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER PILING DAME: 1997-01-27
EARLIER PILING DAME: 1997-01-27
EARLIER PLING DAME: 1997-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASLED NOS: 33
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative 107; Mismatches 110;
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2.7%; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Translation template
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ONE MOUNTAIN ROAD
GENERAL INFORMATION:
APPLICANT: SZOSTAK, JACK W.
APPLICANT: ROBERTS, Richard W.
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CITY: FRAMINGHAM
STATE: MASSACHUSETTS
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ZIP: 01701
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95; Conservative
                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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Matches 9
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APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: LANDOTHY C
APPLICANT: DOUNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: GIAN, FENC

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                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80;
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                                                                                                                                                                                                                                                                                                                                                                                           GEN4-17.8
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APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
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ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFRENCE/DOCKET NUMBER: GEN4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08658136 Patent No. 6071717
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.3
Best Local Similarity 52.1
Matches 87; Conservative
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                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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                                                                                                                                                                                                                               FILING DATE
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US-08-658-136-1/c
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CITY: FR
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777 GGAGGGGTGAGTGGGGAGGAACCCGGAAAGGGGCTGTTGGTGGTGGTGGCCAGGGCT 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2%; Score 38.6; DB 4; Length 320; 50.3%; Pred. No. 0.33;
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; Sequence 7, Application US/09165264
; Patent No. 6197510
; GRNERAL INFORMATION:
; APPLICANT: Vinayagamoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFRENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 320
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NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8415
TELEFAX: 508-872-8415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
STAT77 base pairs
                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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GENERAL INFORMATION:
APPLICANT: Vinayage
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LENGTH: 320
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                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-14
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                                                                                                                                                                                                                                                                                                                                 2.2%; Score 38.6; DB 4; Length 320; 48.8%; Pred. No. 0.33; tive 0; Mismatches 109; Indels
                          Sequence 14, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TILLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOHN TO THE OF INVESTIGATION THOUSING AND TITLE OF INVESTIGATIONS. Multi-Loci Genomic Analysis FILE REFERENCE: 4477 COURTENT APPLICATION NUMBER: US/09/165,264 CURRENT FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     957 CCCCTGGCCTGACTCTGGCTCTTTCTGCAGA 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 GGGGGGGGGGTGTGCATCTACAGCAGAGA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 48.8
Matches 104; Conservative
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Matches 92; Conserv
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RESULT 11
US-09-165-264-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-165-264-8
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SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 36.2; DB 4; Length 320; Best Local Similarity 50.3%; Pred. No. 1.4; Matches 89; Conservative 0; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 4; Length 320;
Pred. No. 1.6;
0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                           APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 13
LENGTH: 320
                                                                                                                                                                                                                                                    ; Sequence 13, Application US/09165264
; Patent No. 6197510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
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671 TCCTGGAGCCTGGTGCCCTAGAAGCCCACGTCTTTCTGACTTCTGGAGTCCTGTCGATGT 730
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0; Gaps
                                                                         897 CTCGGGTGCCTGACGGAAGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGT 948
                                                                                              2.1%; Score 36; DB 1; Length 227%; 51.9%; Pred. No. 3.6; tive 0; Mismatches 75; Indels
                                                                                                                                                                RESULT 15
US-07-959-943-6/C
; Sequence 6, Application US/07959943
; Patent No. 5418162
; GENERAL INFORMATION:
APPLICANT: Blakely, Randy D.
APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Garon, Marc G.
TITLE OF INVENTION: Section Transporter cDNA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMEBR: US/07/959,943
FILING DATE: 19921014
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1:
Best Local Similarity 51.9
Matches 81; Conservative
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MOLECULE TYPE: CDNA
POSITION IN GENOME:
UNITS: 2278 basepairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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US-07-959-943-6
                                                                                                                                                                                                                                                                                                                                                                                                                       Gibson
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ADDRESSEE:
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Db 1823 ITCAGGAGTGAIACTITAATAATGGGCTCCTTAAG 1788
Search completed: June 14, 2003, 16:24:53
Job time: 93 secs
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8658.197 Million cell updates/sec
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1722
1 cctggcccctcagatcaaga.....gatgagaggctcgggctgga 1722
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// cgn2_6/ptodata1/pubpna/USO6_NEW_UB.Seq:*
// cgn2_6/ptodata1/pubpna/USO6_PUBCOMB.Seq:*
// cgn2_6/ptodata1/pubpna/USO8_NEW_PUB.Seq:*
// cgn2_6/ptodata1/pubpna/USO8_NEW_PUB.Seq:*
// cgn2_6/ptodata1/pubpna/USO8_NEW_PUB.Seq:*
// cgn2_6/ptodata1/pubpna/USO9_PUBCOMB.Seq:*
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// cgn2_6/ptodata1/pubpna/USO0_NEW_PUB.Seq:*
// cgn2_6/ptodata1/pubpna/USO0_NEW_PUB.Seq:*
                                                                                                                                                       June 14, 2003, 16:16:05; Search time 288 Seconds
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                            1029858 segs, 724030393 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 3, Appli Sequence 5, Appli Sequence 7, Appli Sequence 70, Appli Sequence 20146, A Sequence 29, Appli Sequence 316, Appl Sequence 346, Appl Sequence 347, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 15, Appli Sequence 2, Appli Description 0 03-09-864-761-20146 0 05-09-864-761-20146 0 05-09-804-612 05-10-184-644-346 05-10-184-644-346 05-10-184-644-346 05-10-184-634-346 05-10-184-634-346 05-10-184-634-346 05-10-032-393-47 05-10-032-393-8 0 05-09-827-998-15 0 05-09-827-998-16 US-09-826-581-3 US-09-864-761-3373 US-09-826-581-5 US-09-925-297-2 US-10-108-605-70 110 110 110 110 110 Query Match Length DB 1722 378 1647 11527 1064 910 671 1512 671 671 1184 12733 12739 4158 5313 442.4 442.4 440.6 440.6 40.0 40.2 40.3 399.8 399.8 Score 1722 351 168.2 70.4 68 44.2 ٠ ي ပပ 000

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GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT

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20 39.8 2.3 5461 10 US-09-827-999-1 Sequence 8, Appli 2 21 39.2 2.3 6719 10 US-09-827-999-1 Sequence 10, Appli 2 22 39.2 2.3 5719 10 US-09-827-991-1 Sequence 10, Appli 2 23 39.2 2.3 5759 2.9 US-10-136-104-3 24 39.2 2.3 5750 2.9 US-10-134-644-574 Sequence 71, Appli 2 25 38.8 2.3 5552 9 US-10-134-644-574 Sequence 71, Appli 2 26 38.8 2.3 5552 9 US-10-134-644-574 Sequence 71, Appli 2 27 38.4 2.2 2 27 1 28 2 2.2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	722 Homo sapiens -3 100.0%; Score 1722	1722; Conservative 0; Mismatches 0; Indels 0; Gaps	1 CCTGGCCCCTCAGATCAAGAAGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGCGAGC 60	61 CCCTCTATGGGACAGCAGAGACAGATTGTGGGTGAGAGAGA
C 2212 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	S-0	Yuery m Best Lo	Qy	Qy Db

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1629
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                                                                                                                                                                                                                                                                                                                            9.8%; Score 168.2; DB 10; Length 1647; 95.6%; Pred. No. 2.7e-39; tive 0; Mismatches 8; Indels 0;
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APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILLE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILLING DATE: 2000-03-08
PRIOR FILLING DATE: 2000-03-08
PRIOR FILLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
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Best Local Similarity 68.1%; Pred. No. 1.3e-10;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-2
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; Patent No. US20020081659A1
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                                                                                                                                                                                                                                                                                                                                Query Match 9.8'
Best Local Similarity 95.6'
Matches 173; Conservative
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                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
TITLE OF INVENTION: VARIANTS OF SECURE OF SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                       N: EXPRESED IN HELA, SIGNAL = 4

N: EXPRESED IN HELAT, GIGNAL = 4.1

N: EXPRESED IN PLACENTA, SIGNAL = 3.9

N: EXPRESED IN HALIOO, SIGNAL = 3.9

N: EXPRESED IN ADUT LIVER, SIGNAL = 3.8

N: EXPRESED IN BT44, SIGNAL = 3.8

N: EXPRESED IN PETAL LIVER, SIGNAL = 5.3

N: EXPRESED IN BOWE MARROW, SIGNAL = 4.8

N: EXPRESED IN LUNG, SIGNAL = 4.2

N: EXPRESED IN BRAIN, SIGNAL = 4.2
PRIOR FILING DATE: 2000-09-21
PRIOR APLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NOS: 49117
SEQ ID NO 3373
LENGTH: 378
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Patent No. US20020142310A1
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ORGANISM: Homo sapiens
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OTHER INFORMATION: ED
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APPLICANT: Kinders, Robert
APPLICANT: Corey, Michael J.
TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: ENCOING THE SAME AND METHODS FOR SCREENING FOR OR
TITLE OF INVENTION: MODULATING THE SAME
FILE REPRENDE: 130001.406
CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT APPLICATION NUMBER: US/09/804.682
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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NH. EXPRESSED IN HEART, SIGNAL = 4.1

NH. EXPRESSED IN PLACENTA, SIGNAL = 4

NH. EXPRESSED IN BLIOO, SIGNAL = 3.9

NH. EXPRESSED IN ADULT LIVER, SIGNAL = 5.8

NH. EXPRESSED IN FUTAL LIVER, SIGNAL = 5.3

NH. EXPRESSED IN FUTAL LIVER, SIGNAL = 5.3

NH. EXPRESSED IN POTE MARROW, SIGNAL = 4.8

NH. EXPRESSED IN BAIN, SIGNAL = 4.2

NH. EXPRESSED IN BRAIN, SIGNAL = 4.2

NH. EXPRESSED IN BRAIN, SIGNAL = 4.2

NH. EXPRESSED IN BRAIN, SIGNAL = 4.3

NH. HITH GII11430152, EVALUE 2.00e-22

NH. EST_HUMAN HITH SP$4619, EVALUE 3.00e-06
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100.0%; Pred. No. 2.6e-09;
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00665
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Conservative
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Best Local Similarity
Matches 65; Conserva
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; OTHER INFORMATION:
US-09-864-761-20146
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US-09-804-682-29/c
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APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENDE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Accomica-X-1

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2010-05-23

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2001-10-33

PRIOR FILING DATE: 2001-10-34

PRIOR FILING DATE: 2001-10-34

PRIOR FILING DATE: 2001-10-34

PRIOR FILING DATE: 2001-10-34

PRIOR FILING DATE: 2001-01-37

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                    APPLICANT: Broadus, Julie
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lyun
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
TITLE OF INVENTION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 70
LENGTH: 11527
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                                                                          US-10-108-605-70; Sequence 70, Application US/10108605; Patent No. US20020160934A1; GBMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA CORGANISM: Drosophila melanogaster US-10-108-605-70
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US-09-864-761-20146/c
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                                                                                                                                                                                                                                     | :: : : | : | : | : | : | : | : : | | : | : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                          131 GAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATATACCACAAGCT 190
                                                                                                                                                                                                                                                                                                                                                                                       596 LRGPQPRRRLLSSGPDLTLQFQAPPGPPNPGLGQGFVLHFKEVPRNDTCPELPPEWGWR 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 TGGCTTCAGGCCAAGCCCAGCCAGGGGCCAGGGGGAAGGTCCATCCGGAGTCTGCA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           836 PSRQLEGGNLALAILLPLGLVIVLGSGVYIYYTKLQGKSLFGFSGSHSYSPITVESDFSN 895
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APPLICANT: Watanabe, Colin K.
APPLICANT: Abnowy Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R.C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.5%; Score 42.4; DB 9; Length 671; Best Local Similarity 5.3%; Pred. No. 0.018; Matches 20; Conservative 151; Mismatches 206; Indels
                                                         ch 2.5%; Score 43; DB 9; Length 910; l Similarity 13.2%; Pred. No. 0.013; 48; Conservative 93; Mismatches 224; Indels
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-184-644-346/c

Sequence 346, Application US/10184644

; Publication No. US20030044930Al

; GENERAL INFORMATION:
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Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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ORGANISM: Homo Sapien
                                                            Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 TCCCA 435
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us-10-123-155-112
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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: LOCATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948,

: LOCATION: 957, 961, 965, 981, 991, 993, 1001, 1002, 1005, 1011, 1018,

: LOCATION: 1043, 1047, 1049, 1051, 1054, 1056

: OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                           72, 110, 209, 214, 231, 232, 256, 282, 292, 297, 306, 319, 354, 355, 363, 372, 376, 378, 457, 458, 459, 468, 470
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47.8%; Pred. No. 0.0058;
tive 0; Mismatches 93; Indels 0;
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654,
                                                                                                                                                                                                                                                                                                                                                        511,
652,
725,
803,
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                                                                                                                                                                                                                                                                                                                                                 LOCATION: 485, 487, 488, 494, 496, 499, LOCATION: 583, 600, 611, 613, 623, 624, LOCATION: 694, 701, 713, 716, 720, 721, LOCATION: 744, 781, 782, 785, 789, 799, OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                        LOCATION: 5, 6, 16, 21, 24, 25, 33, 39, LOCATION: 235, 237, 238, 244, 245, 246, LOCATION: 321, 323, 330, 344, 340, 349, LOCATION: 397, 405, 432, 437, 454, 455,
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Publication No. US20030068794A1
                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
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Gerritsen,Mary E.
Goddard,Audrey
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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Best Local Similarity 47.8%
Matches 85; Conservative
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                                                                                                                             NAME/KEY: misc_feature
                                                            ORGANISM: Homo sapiens
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US-10-123-155-112
LENGTH: 1064
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Gaps

1164 TGCCCTCCTTTTTAGGGGCCTGGGATGGAGGTTGTCTCTCCCTAGGCTGCCCCGAGGCTC 1223

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1226 GAGGGGGAAGGGCTAGGAAACTCCAGCAGAGGGAGGGGGTTKGGACCCACTATGGACAGT 1167
                                                                                        1224 ACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCC 1283
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49.1%; Pred. No. 0.062;
tive 1; Mismatches 108; Indels
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                                                                                                                                                                                                                                                                                                              US-09-984-271-18/C
Sequence 18, Application US/09984271
Publication No. US20030040088A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REPERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT FILING DATE: 2001-10-29
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 1999-07-14
PRIOR PLICATION NUMBER: 09/482,273
PRIOR PLIING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR PILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR PILING DATE: 1998-07-15
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OTHER INFORMATION: n equals a,t,g, or c
09-984-271-18
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Matches 105; Conservative
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455 .SYMYAY. BMB.MT..M...YBYM.M.C.MYT..ASSS..MMTSMMT.Y...T...SHSS 396
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CURRENT FILLING DATE: 2002-06-28
BYFIOT APPLICATION FEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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; Publication No. US20030068684A1
; GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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US-10-184-634-346/c
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US-10-184-634-346
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                Query Match 2.4%; Score 40.6; DB 9; Best Local Similarity 7.5%; Pred. No. 0.059; Matches 25; Conservative 135; Mismatches 173;
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FILE REPERENCE: 93330R1030
CURRENT APPLICATION NUMBER: U5/10/123,155
CURRENT FILING DATE: 2002-04-15
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Goddard, Audrey
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DeForge, Laura
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Gurney, Austin L.
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Filvaroff, Ellen
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 394
LENGTH: 1184
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US-10-184-634-346
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                    Sequence 346, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Wood, William I.
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Gurney, Austin L.
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Gurney, Austin L.
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Goddard, Audrey
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                                                                                        APPLICANT: Baker, Kevin P.
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  US-10-184-644-346
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                                                                  Length 1184;
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TITLE OF INVENTION: BACTERIAL PROMOTEKS AND METHODS OF USE
TILE REFERENCE: ELITRA.010A
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTERQ for Windows Version 4.0
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                                                                  Query Match 2.3%; Score 40.2; DB 9; Length 11 Best Local Similarity 8.8%; Pred. No. 0.089; Matches 57; Conservative 175; Mismatches 412; Indels
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              ORGANISM: Homo Sapien
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                             US-10-123-155-394
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                                                                                                     Score 40; DB 9; Length 127
Pred. No. 0.18;
0; Mismatches 105; Indels
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                                         ; OTHER INFORMATION: Vector pEPEF14 US-10-032-393-47
ORGANISM: Artificial Sequence
                                                                                                     Query Match 2.3%;
Best Local Similarity 49.5%;
Matches 103; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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June 13, 2003, 01:49:14; Search time 192.613 Seconds (without alignments) 9216.782 Million cell updates/sec
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11. 9D_ba:*

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65. 9D_pb:*

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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No. S	Score	Match	Length	DB	TD CI		Description	uс
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	27.6	2.5	653		PM7F7B		AL685186	Penicilli
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19	27.6	7	214971		AC094543		AC094543	Rattus no
20	27.4	4.9	48489		AC091776		AC091776	Lamy
21		6.9	65932		AP004938		AP004938	Lotus jap
22		9.	68736		AC090435		AC090435	lamyd
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36	٠	4.6	154126		ACU10758			
37		4.6	157437		AC021669			·
38		9.	164290		AC096454		AC096454	
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					ALIGNMENTS			
RESULT 1								
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DEFINITION			3 from 1	Patent	1/22 DP nt WO0177305.	7	rw.	13 - NOV - 2001
ACCESSION		AX281580						
VERSION	AX		1 GI:16	:166088	831			
SOURCE	hun	human.						
ORGANISM		no sapiens	ens					
		Eukaryota; Mammalia; E	; Metazoa; Eutheria;	ja;	Chordata; Craniata Primates; Catarrhi	ı, i	Vertebrata; Eutel	<pre>Euteleostomi; Homo.</pre>
REFERENCE								
AUTHORS TITLE		ည်း	‡;	Luthman,H e human a	n,H. and Marklund,S. n amp-activated protein	und,S. d protein k	kinase gamma	3 subunit
JOURNAL	Pat	Patent: W	WO 0177305-A	J5-A	m	١		

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Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 8, 2001 this sequence version replaced gi:13431203.
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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                                                                                                                                            100.0%; Score 61; DB 6; Length 1722; 100.0%; Pred. No. 3.8e-09; tve 0; Mismatches 0; Indels
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
Upublished (2001)
3 (bases 1 to 206854)
Waterston,R.H.
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
104 c 534 g 363
                 Location/Qualifiers
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Waterston, R.H.
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Waterston, R.H.
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libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38993. Am unresolved tandem in the HERV SVA exists between 18430-185163. PCR suggests that approximately 1700 bps are missing.
                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
                         clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The RPCI-11 human BAC library was made from the blood of one male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4. .37
/note="match to EST A1670836 (NID:g4850567) wa04g10.x1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mapping information for this clone was provided by Dr. John D. Warbherson. Department of Genetics, Washington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Data from AC079810 and AC073128 was used to finish this clone,

    .37
    /note="match to EST BF304755 (NID:911251653)"

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/note="match to EST BG477625 (NID:913409904)"
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/note="match to EST BE908408 (NID:910402954)"
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/note-"match to EST BE314060
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/db_xref="taxon:9606"
/chromosome="2"
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NEIGHBORING SEQUENCE INFORMATION:
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/clone_lib="RPCI-11"
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/note="match to EST AA043371 (NID:g1521226) zk53el0.rl"
588. .929
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Anote-"match to EST AI656812 (NID:94740791) tt54b06.x1"

967. 1091

Anote-"match to EST AA043371 (NID:91521226) zk53e10.r1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317. 1084

'hote="match to EST AA481361 (NID:92210913) zv44e01.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match to EST AA043371 (NID:g1521226) zk53e10.rl"
594. .763
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                                                                                                                                                                                            note="match to EST BE047599 (NID:98364652) tz39c01.y1"
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                                                                                     to EST A1670836 (NID:94850567) wa04g10.x1"
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281. .344
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/note="match to EST BI059713 (NID:914467240)"
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594, .763
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594, .763
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'note="match to EST AL567345 (NID:g12920610)"
                                                    to EST BG470047 (NID:913402322)"
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281. .344
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                                                                                                                                                                                                                                                                'note="match to EST BE908408 (NID:g10402954)"
                                                                                                                                                                                                                                                                                                                                 'note="match to EST BF304755 (NID:g11251653)"
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594. .763
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                                                                                                                                                          to EST AW880850 (NID:98042860)"
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/note="similar to Homo sapiens EST BI114348
(NID:g14565249)"
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2 (bases I to 122129)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Buguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,

Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,

Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Gopette,M., Graham,L.,

Grand,Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

Klein,J., LaRocque,K., Lanazares,R., Landerers,T., Lehockzky,J.,

Levine,R., Lieu,C., Liu,G., Locke,K., MacGonald,P., Marquis,N.,

McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

Murphy,T., Marjot,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

Pisanl,C., Pollata,Y., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Theodore,J., Thrrell,A., Travers,M., Trigilio,J.,

Young,G., Zainoun,J., Zimmer,A. and Zody,M., Trigilio,J.,

Polymission
                                                                                                                                                                                                                                                                                                                                      ACUZ/416 152129 bp DNA linear HTG 07-JUN-2000
Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
unordered pleces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 152129)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
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                                                                                                                                                                        Length 206854;
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http://ftp.genome.washington.edu/RW/RepeatMasker.html
967. .1090
/note="similar to Homo sapiens EST BI114348
(NID:91455249)"
967. .1085
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Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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Center clone name: 544_c_11
------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                    Score 61; DB 9;
Pred. No. 2e-09;
                                                                                                                                                                                                                                 0; Mismatches
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                 100.0%;
illarity 100.0%;
Conservative 0
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NOTE: This is a 'working draft' sequence. It currently consists of 32 conligs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 135376 bases at least Q40 Consensus quality: 143546 bases at least Q20 Consensus quality: 145503 bases at least Q20 Insert size: 161000; agarose-fp Insert size: 161009; sum-of-contig Quality coverage: 3.1 in Q20 bases; sum-of-contigs Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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60595: contig of 4624 bp in length
60595: gap of 100 bp
66595: contig of 5900 bp in length
66695: gap of 100 bp
73218: contig of 6523 bp in length
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77115: contig of 3797 bp in length
77215: gap of 100 bp
85022: contig of 7807 bp in length
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f 1097 bp in length
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f 1041 bp in length
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f 1286 bp in length
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6161: contig of
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46466 51285: conti
51286 51385: gap of
51386 55871: conti
55872 55971: gap of
55972 60595: conti
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3924 5020: cont
5021 5120: gap of
5121 6161: cont
6162 6261: gap of
6262 7547: cont
7548 7647: cont
7648 9983: con
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42467 46365: cont
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101294 113090: contig of 11797 bp in length
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17224. .19466
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27160. .30170
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                                                                                                                                                                                                         ACLU6624 91247 bp DNA linear HTG 13-JUL-2002
Rattus norvegicus clone CH230-22513, *** SEQUENCING IN PROGRESS
***, 52 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                        0; Gaps
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                                                          97.4%;
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                     Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence Version replaced gi:18139148.
Direct Submission
Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 91247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 46677 bases at least Q40 Consensus quality: 50328 bases at least Q20 Consensus quality: 53862 bases at least Q20
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1138: gap of unknown length
2413: contig of 1175 bp in length
2413: gap of unknown length
3595: contig of 1182 bp in length
4800: contig of 1182 bp in length
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642: contig of 1142 bp in length
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7321: contig of 1179 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Length 91247;

DB 2;

49.8%; Score 30.4;

Query Match

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MURLY,D. M., Adams, C., Atlo-Oduola, B., Ali-osman, F.R., Allen, C., Atlorocks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bilmage, K., Blankenburg, K., Bontin, D., Boutck, J., Boute, S., Blankenburg, K., Bontin, D., Boudck, J., Boute, S., Briewa, M., Brown, M., Bryant, N.P., Boudck, J., Boute, S., Briewa, M., Brown, M., Bryant, N.P., Boudck, J., Charles, B.K., David, N.C., Carron, T.E., Dardan, C.D., Carron, T.E., Dardan, C.D., Cox. Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., David, R., Davila, M.L., Davis, C., Edyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Edyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Dayer, H.C., Ding, Y., Dinh, H.H., Davila, K. J., Dagar, D., Edyle, M.D., Ding, Y., Dinh, H.H., Davila, M.L., Ding, Y., Dinh, H.H., Davila, K. J., Edyle, M.D., Escotto, M., Falls, C., Edyle, M.D., Edyle, M.D., Foster, P., Frantz, P., Fanls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Gabrisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Hernandez, C., Harris, K., Harr, M., Haves, A., Hernandez, C., Harris, K., Harr, M., Havis, P., Hane, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Ollivet, S., Joudah, S., Karly, S., Khan, U., King, L., Korvah, J., Jackson, L., Li, J., J., Li, X., Lucier, R., Lucier, R., Lucier, R., Martin, R., Ma, J., Luna, R., Mayen, R., Martin, R., Martin, R., Ma, J., Luna, R., Mayen, R., Martin, R., Martin, R., Martin, R., Martin, R., Mayen, R., Mayen, R., Martin, R., Mayen, R., Mangers, R., Pangez, L., Weres, M., Pally, S., Warren, S., Wallilanon, D., Wallilanon, S., Wallilanon, S., Wallianon, S., Wallianon, S.,
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Rattus norvegicus clone CH230-150G18, *** SEQUENCING IN PROGRESS
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Direct Submission
Submitted (17-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
(variey, K.C.
Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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NOTE: This is a 'working draft' sequence. It currently consists of 56 conligs. The true order of the pieces is not known and their order in this sequence record is
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:20162777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                Sequencing vector: Plasmid; Carlstos Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 1003 of reads Chemistry: Dye-terminator Big Dye: 1003 of reads Consensus quality: 65762 bases at least Q40 Consensus quality: 77462 bases at least Q30 Consensus quality: 77155 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
                                                                                                   Center: Baylor College of Medicine
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TWTMELGGKYNIECERNTAGAELDFKKRFFFGSSANNOLSGKTNSGEFTLAKTGHW
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AETQDHSRKTNEGSGDLLDSPGGPWGTTYVPSQYQEELGELDFTSQYDTYSEERKSLM
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LRWYLSGFYKKPKGIKKPYNPILGETPRCRMHPQTNSHTPYIABQYSHHPDYSBAFY
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Gars gene; Cdknlc gene; cyclin-dependent kinase inhibitor 1C;
cars gene; Cdknlc gene; cyclin-dependent kinase inhibitor 1C;
cysteinyl-tRNA-synthetase; PLE gene; trug gene; Name of the cysteinyl-trend synthetase; plugene; trug the companient of the comp
                                                                                                       ROD 06-MAR-2002
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Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY
Revised by author 22-MAY-2000
3 (bases 1 to 281000)
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Submitted (24-JAN-2001) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
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Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
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1906. .8110,9688. .9772,11978. .12149,12416. .12608,
13783. .13967,14347. .14428,15828. .15926,16308. .16404,
17790. .17888,21514. .21610,21996. .22086,22181. .22317,
22743. .22928,23228. .23334,24142. .24268,25136. .25238,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Engemann, S., Strodicke, M., Paulsen, M., Franck, O., Reinhardt, R., Lane, N., Reik, W. and Walter, J. Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended
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On Jan 27, 2001 this sequence version replaced gi:11191799.
related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.
Location/Qualifiers
1. 281000
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/strain="129 SV"
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/chromosome="7"
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                                                                              MMU276505 281000 bp DNA linear R
Mus musculus genomic fragment, 281000 bp, chromosome
AJ276505
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11063728
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Direct Submission
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In (Dases 1 to 117082)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Botten, S., Bireva, M., Brown, M., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burcell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Deladado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan Rocha, S., Dinh, H.H., Earnhart, C., Edgar, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC126076 117082 bp DNA linear HTG 24-JUL-2002
Rattus norvegicus clone CH230-143P6, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                    Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 140819)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-7012-2002) Genome Sequencing Center, 4444 Forest Park
Submitted (16-7012-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jul 16, 2002 this sequence version replaced gi:21040003.
                                       Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 140819) McPherson, J.D. and Waterston, R.H. The sequence of Mus musculus clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/organism~"Mus musculus"
/db_xref~"taxon:10090"
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McPherson, J.D. and Waterston, R.H.
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AC126076.2 GI:2169
HTG; HTGS_PHASE1.
Rattus norvegicus.
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Best Local Similarity 77.8%
Watches 35; Conservative
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                                                                                                                                                                                                                                  Direct Submission
                      house mouse.
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47068, .47141,48531, .48627)</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                      join(31277. .31342,35572. .35662,37049. .37176,46179. .46291,
47068. .47141,48531. .48627)
/gene="Tnfrhl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     jóin(35584. 3562,37049. 37176,46179. 46291,47068. 47141,48631. 48580)
/gene="Tnfrhl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="tumor necrosis factor receptor p60 homologue"
/protein_id="Cac7352.1"
/db_xref="g1:12583597"
/db_xref="g1:12583597"
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/KCHPCTTTGKDNGI.HDCELCSTCDKDQNMYADCSATSDRKCEQQIGIYYYDPKFPESC
RPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI"
/gene="Tnfrh1"
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                                                                                                                                                                                      join(30593. 130688,131306. 131403,132305. 132456, 140377. 140517. 1411097. 141184,142488. 142590, 145511. 145524,146438. 146565,146958. 147085, 147169. 147274,147610. 147707,147985. 148174, 148124. 148792,152041. 152121,154098. 155258, 155968. 159408]
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AC121886.2 GI:21844658
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47068. .47141
/gene="Tnfrh1"
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48531. .48580
/gene="Infrhl"
                                                                                                                                                                                                                                                                                                                                                              30593. .130688
/gene="Cars"
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/gene="Tnfrh1"
                                                           25136. .25238
/gene="Obph1"
                                                                                                                          27169. .27307
/gene="Obph1"
               /gene="Obph1"
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30593. .13068
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25136. .25
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Matches 40; Conservative
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g of 1656 bp in length
f unknown length
g of 1043 bp in length
f unknown length
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contig of 1250
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Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Henrandez,J.,
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Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L., C., Lewis,L.,
Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Mardod,R., Morris,S.,
Miner,G., Mitchell,T., Wohabbat,R., Morris,S.,
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Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M. Okwuon,G.,
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Pickerson,E., Nwokenkwo,S., Oguh,M. Okwuon,G.,
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Sodergren,E., Socti,G., Shen,H., Shooshtari,N., Sisson,I.,
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Tansey,J., Taylor,C., Taylor,T., Telficod,B., Thomas,N., Ward-Moore,S., Warren,R., Washington,C., Watliamson,A., Wileford, Williams,G., Wullamson,A., Wileford, Williams,G., Wullamson,A., Wileford, Williams,G., Wallamson,A., Wileford,B., Nocken, S., Warren,R., Washington,D., Winson,R., Wull, C., Wul,Y., Wul,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Hannel,Shed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgs.bcm.tmc.edu/docs/denbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 63 contings. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary agas between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                  Unpublished

(bases 1 to 117082)

(bases 1 to 117082)

(briect Submission

Submitted (03-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

(bases 1 to 117082)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 5, 2002 this sequence version replaced gi:21686820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 55139 bases at least 040 consensus quality: 61060 bases at least 030 consensus quality: 64630 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1055: contig of 1055 bp in length
1155: gap of unknown length
2165: contig of 1010 bp in length
2265: gap of unknown length
3314: contig of 1049 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Context: hgsc.heip@bcm.tmc.edu
Center project Information
Center project name: 6276
Center clone name: CH230-143P6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as ... be preserved.
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kovar, C., Kovar, C., Liu, J., Liu, J., Liu, Y., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhawa, L., Lu, Y., London, P., Longacre, S., Ma, J., Maheshwari, M., Mahlindartne, M., Mahlindar, M., Mahlindartne, M., Mahlindar, C., Martinez, E., Mangum, B., Mapua, R., Martinez, E., Mangum, R., Mapua, M., Morris, S., Morgan, M., Morris, S., Morgan, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokelemeh, O., Okwuonu, G., Olarpunagaodo, A., Pal, S., Parker, F., Pasternea, S., Pal, H., Perez, A., Perez, L., Ffankoch, C., Plopper, F., Poindexter, A., Perez, L., Ffankoch, C., Plopper, F., Poindexter, A., Reugh, M., Regier, M., Richards, S., Murphy, M., Quiroz, J., Rachin, E., Reuter, M., Richards, S., Margh, R., Relly, M., Really, M., Renter, M., Richards, S., Shen, H., Shetky, S., Shetsman, S., Shen, H., Shetky, S., Shetsman, S., Shen, H., Shetky, J., Shetsman, S., Shetsman, S., Shetsman, R., Steimle, M., Strong, R., Sutton, R., Syatk, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Stetmen, R., Walsk, M., Thomas, S., Walsk, M., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Warten, R., Walsk, M., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Warten, R., Walsk, M., Walsk, M., Walsk, M., Tabor, W., Walsk, M., Wight, D., Walsk, M., Walsk, M., Tabor, W., Walsk, M., Wight, D., Walsk, M., Walsk, M., Tabor, W., Walsk, M., Wight, R., Walsk, M., Walsk, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 79 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baylor Plaza, Houston, TX 77030, USA
On Aug 23, 2002 this sequence version replaced gi:21716685.
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Sequencing vector: plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality: 96145 bases at least Q40
Consensus quality: 105750 bases at least Q30
consensus quality: 11678 bases at least Q30
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1171: gap of unknown length
2289: contig of 1118 bp in length
2389: gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
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Rattus norvegicus clone CH230-6L21, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.
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G/5185
MARC 11245-11246:999628105:1 Sheep WBC Ovis aries STS genomic, sequence tagged site.
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Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 899)
Freking, B.A., Leymaster, K.A., Keele, J.W. and Smith, T.P.L. Identification of a mutation apparently causing the polar Overdominance callipyge phenotype in sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 155645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50-200 ng genomic DNA
each 20 pmoles
each 88 uM
0.25 units (Qiagen Hotstar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28.8; DB 2; Length 1:
Pred. No. 26;
0; Mismatches 17; Indels
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Commercially supplied Qiagen HotStar buffer
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bp in length
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length
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gap of unknown length
                          in length
                                                                                                                                                                              in length
                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                  in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
USDA 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
Email: freking@email.marc.usda.gov
Primer B: AGTGTCACCCTTCCTGGAC
Primer B: TGGAGACCCACTGGAAACTT
                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                  gap of unknown Lescontig of 2022 bl. gap of unknown Lescontig of 1327 bg. gap of unknown Lescontig of unknown Lesc
                          contig of 2195 by
gap of unknown Locontig of 1208 by
gap of unknown Locontig of 1181 by
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contig of 2099 by
gap of unknown l
contig of 1308 by
gap of unknown l
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unknown l
of 1489 h
                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 1277
gap of unknown
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gap of
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G75185.1 GI:20563988
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59337:
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60618:
62717:
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70740:
71803:
71903:
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69.68;
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67836:
67936:
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Cycles:
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dNTPs:
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Ovis aries
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Best Local Similarity
Matches 39; Conserv
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AUTHORS
TITLE
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COMMENT
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G75185/c
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KEYWORDS
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sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G74939 945 bp DNA linear STS 14-MAY-2002
MARC 11247-11248:1020442896:1 Sheep WBC Ovis aries STS genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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1 (bases 1 to 945)
Freking, B. A., Leymaster, K. A., Keele, J. W. and Smith, T. D. L. Identification of a mutation apparently causing the polar
                                                                                                                                                                                                   /strain="Dorset, Romanov, and Dorset-Romanov crossbreds"
/db xref="taxon:9940"
/clone_lib="sheep WBC"
/dev_stage="adult"
/note="Organ: blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The
The STS is derived from PCR amplicons generated from genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                2 others
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95 degrees for 30 seconds
54 - 60 degrees for 30 seconds
68 degrees for 2 minutes
32 to 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
NO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overdominance callipyge phenotype in sheep
                                                                                                                                                                                                                                                                                                                                                                                            DB 11;
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Pred. No. 59;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: freking@email.marc.usda.gov
Primer A: ATCTGGCAGGTCCTCTTA
Primer B: GAACTTGCCCTTGGAAGTGA
PCR Profile:
                                                                                                                                                             1. 899
/organism="Ovis aries"
                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              263 g
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                                                                                                                                                                                                                                                                                                                                                                                            46.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tagged site
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336 c
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nes 40; Conservative
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ORIGIN
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Matches
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G74939/c
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SOURCE
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                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of
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Submitted (22-FBB-2001) Department of Genetics, B43, University of Liege, 20, Bd de Colonster, Liege 4000, Belgium
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF354168 215046 bp DNA linear HTG 16-MAY-2001
Ovis aries chromosome 18 clone 229G11; 359E3, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human-ovine comparative sequencing of a 250-kb imprinted domain encompassing the callippyee (clpg) locus and identification of six imprinted transcripts: DLK1, DRT, GTL2, PEG11, antiPEG11, and MEG8 Genome Res. 11 (5), 850-862 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Romanov, and Dorset-Romanov crossbreds'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charlier, C., Segers, K., Wagenaar, D., Karim, L., Berghmans, S., Jalllon, O., Shay, T., Weissenbach, J., Cockett, N., Gyapay, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charlier, C., Segers, K., Wagenaar, D., Karim, L., Berghmans, S., Jaillon, O., Shay, T., Weissenbach, J., Cockett, N., Gyapay, G. and
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* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 12055 27921: contig of 12054 bp in length
* 12075 27921: contig of 18847 bp in length
* 27922 27941: gap of unknown length
* 27942 29846: contig of 1905 bp in length
* 29867 33482: contig of 1905 bp in length
* 29867 33482: contig of 3616 bp in length
* 33483 33502: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 46.9%; Score 28.6; il Similarity 67.8%; Pred. No. 59; 40; Conservative 0; Mismatches
                                                                                                                                                                             /organism="Ovis aries"
/strain="Dorset, Romanov
/db_xref="taxon:9940"
/clone_lib="Sheep WBC"
/dev_staqe="adult"
/note="Organ: blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE2; HTGS_DRAFT.
Ovis aries.
                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       236 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, 30 ordered pieces.
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                                                                                                                                                            . 945
                                                                                                           20 or greater.
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Matches 40; Conserv
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JOURNAL
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KEYWORDS
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L (Dases 1 to 18444)

Butary, D. M., Adams, C., Atlo-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Babrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Babrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Bonnin, D., Boudck, J., Bowle, S., Barkew, M., Brown, E., Brown, M., Bryant, N.P., Boudck, J., Bowle, S., Barkew, M., Brown, E., Brown, M., Bryant, N.P., Boudck, J., Charley, D., Dathorne, S.R., David, R., Davila, M.L., Dayar, Carroll, L., Dederich, D.A., Dathorne, S.R., David, R., Davila, M.L., Dayar, Davila, M.L., Dayar, Carroll, L., Dederich, D.A., Davila, M., Davis, C., Davy-Carroll, L., Dederich, D.A., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Barcht, G., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Barcht, C., Harley, M., Canrer, T., Garcia, W., Gunrarte, P., Frantz, P., Frantz, P., Gorrell, J.H., Guevard, W., Gunrarte, P., Hale, S., Hamilton, K., Harnandez, C., Harrisk, K., Hart, M., Havlak, P., Hawes, A., Harnandez, J., Harrisk, Harth, Havlak, P., Hawes, J., Jackson, J.E., Jacobson, B., Hogues, M., Hulyk, S., Hume, J., Jackson, J.E., Jacobson, B., Hollys, S., Hume, J., Jackson, J., Gordo, R., Hogues, M., Hulyk, S., Hume, J., Jackson, J., Jackson, B., Kallyk, S., Khan, U., King, J., Kovrah, J., Kovrah, J., Karlsson, B., Kallyk, M., Mapua, P., Martin, R., Marcin, R., Marcin, R., Martin, R., Marcin, R., Marcin, R., Martin, R., Martin, R., Marcin, R., Martin, R., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Rattus norvegicus clone CH230-326J5, *** SEQUENCING IN PROGRESS ***, 70 unordered pleces.
                                                                                                                                                                                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 136726 bases at least Q40
Consensus quality: 144728 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                     Rattus norvegicus.
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Unpublished
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Direct Submission
                                                                                                                                          Rattus norvegicus
                                              AC128911
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  DEFINITION
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Rattus norvegicus clone CH230-195D20, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.
AC113756
AC113756.3 G1:21744532
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                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and thehal order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Margo, D.B., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbbrooks, S.L., Barton, D.B., Blankenburg, K., Bonnin, D., Bunch, P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Charez, D., Chen, R., Ched, C., Chedle, C., Chen, C., Coyle, M.D., Dathore, S.R., David, R., Davis, C., Day, Carroll, L., Dedercith, D. A., Davis, C., Day, Carroll, L., Dedercith, D. Davis, C., Day, Carroll, L., Dedercith, D. Davis, C., Day, Carroll, L., Dedercith, D. Davis, C., Day, Carroll, L., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Pan, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Pan, A.L., Garrer, T., Garza, N., Gill, R., Garrell, J. H., Guevara, W., Gunarathe, P., Hale, S., Hamiton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Haniton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Haniton, K., Honsen, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Joudah, S., Kratovic, J., Kureshi, A., Landry, W., Leal, B., Lewis, L.C., Lewis, L., Li, J., Liz, Lidharge, D., Martin, R., Martindale, A., Martina, R., Martina, E., Martina, R., Waller, S., Savery, G., Scherr, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Ruber, S., Wallen, R., Wall, M., Rayuez, L., Park, M., Papar, S., Wallen, S., Wallen,
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Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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On Jul 13, 2002 this sequence version replaced gi:19525921.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 79 contigs. The true order of the pieces is not known and thehri order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, P., Carter, M., Caracos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, G., Chon, C., Choydry, I., Christopoulos, C., Chen, G., Chen, G., Choydry, I., Christopoulos, C., Chen, G., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davis, C., Dayland, E., Ding, Y., Dinh, H.H., Delaney, K.R., Davis, C., Dayland, C., Elbaj, C., Escotto, M., Earnhatt, C., Edgar, D., Edwards, C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C., Elbaj, C., Escotto, M., Garis, M., Garis, M., Garza, N., Gill, R., Gaois, J., Garcia, A., Garner, T., Garza, N., Gill, R., Garis, C., Harris, K., Hart, M., Hale, S., Hamel, Lon, K., Harris, C., Harris, K., Hart, M., Halley, S., Hamel, S., Hamilton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jacobson, B., Kallson, A., Hodgson, M., Holloway, C., Hollins, B., Jacobson, B., Kallyk, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kallyk, S., Khan, U., King, L., Korvah, J., Kovar, C., Lid, J., Li, J., Liu, Y., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, J., Liu, R., Marlin, R., Martin, R., Martin,
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NOTE: This is a 'working draft' sequence. It currently consists of 94 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 170476) Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2002 this sequence version replaced g1:18701729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990139 Consensus quality: 103990 bases at least Q40 Consensus quality: 112822 bases at least Q30 Consensus quality: 1118677 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
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Rattus norvegicus clone CH230-26L15, *** SEQUENCING IN PROGRESS
***, 94 unordered pieces.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Copyright (c) 1993 - 2003 Compugen Ltd
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Sequence 143899 BP; 36346 A; 35277 C; 35318 G; 35657 T; 1301 other;
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                          AAL38336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a ffor a C at nucleotide 550; and in exon 10 variation may be a substitution of a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide variation may be a mino acid substitution with the amino acid substitution Way Nation of the protein of a protein way also be nucleotide variation
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The invention relates to a Nogo receptor homologue polypeptide, NgR2 or NgR3, comprising a 50 amino acid LRRCT sequence, a 384 amino acid NTLRRCT sequence, or a 420, 461 or 392 amino acid sequence, all given in the sequence, or a 420, 461 or 392 amino acid sequence, all given in the specification. The NgR3 protein or its binding antibody is useful for decreasing inhibition of axonal growth of a central nervous system (CNS) neuron, by contacting the neuron NgR3 or its antibody, and for treating CNS disease, disorder or injury, NgR3 or a vector comprising NgR3 is useful for treating cerebral injury, spinal cord injury, stroke, demyelinating diseases, e.g. multiple sclerosis, monophasic cemyelinating diseases, e.g. multiple sclerosis, monophasic cemyelination, encephalomyelitis, multiple sclerosis, monophasic cemyelitis, Marchiafava-Bignami disease, Spongy degeneration, Alexander's disease. Organizate Strabbe's disease. NgR3 is useful for inducing an immune response in a mammal against NgR3, as a bait protein in a two-hybrid or three-hybrid cor three-hybrid sussay, and sa a research tool for identification, characterisation and purification of interacting, requiatory proteins. The nucleotide sequences of the invention are useful for screening for RFLP associated
                                                                                                                                                                                                                                                                                                                                                          NgR2; NgR3; axonal growth; central nervous system; CNR5; cerebral injury; spinal cord injury; stroke; demyelianting diseases; multiple solenosis; monophasic demyeliantion; encephalomyelitis; Marchidava-Bignami disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; canavan's disease; metachromatic leukodystrophy; Krabbe's disease; immune, bait protein; genetic mapping; gene therapy; krabbe's disease; immune, bait protein; genetic mapping; gene therapy; transgenic animal; urregulated cellular growth; cancer; tumour; human;
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                                                                                                                                                                                                                                                                                                               Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for
ing central nervous system disorder, cerebral injury, spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NgR3, for localisation and/or quantitation of NgR3, and for diagnostic and therapeutic purposes. The sequences of the invention, vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies are useful for treating or preventing unregulated cellular growth such as cancer and tumour growth. This polynucleotide sequence represents the genomic sequence encoding a human NgR2 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with certain disorders, for genetic mapping, and for gene therapy. T
vector containing NGR3 is useful for producing non-human transgenic
animals. The NGR3 binding antibody is useful for isolating and purif
                                                                                                                                                                                                  Genomic sequence encoding a human NgR2 protein.
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                                                                                                 (first entry)
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(BIOJ ) BIOGEN INC.
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AAL38336;
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20000S-0235836.
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20000S-0236367.
20000S-0236368.
20000S-0236369.
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2000US-0246613.
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2000US-0233401
2000US-0233063
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2000US-0234223
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2000US-0231413.
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2000US-0234998
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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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20-CCT-2000;
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                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                       Gaps
                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34227
           Length 143899;
                                      Indels
              DB 24;
                                     18;
           Score 27.2; DB Pred. No. 25; 0; Mismatches
                                                                                                                                                     AAK79415 standard; DNA; 17761 BP.
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20000S-0216847.
20000S-0217487.
20000S-0217480.
20000S-0217496.
20000S-0220964.
2000US-0220964.
2000US-0224518.
          44.6%;
milarity 67.9%;
Conservative 0
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2000US-0225214.
2000US-0225266.
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2000US-0214886.
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2000US-0190076.
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2000US-0205515.
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           Ouery Match
Best Local Similarity
Matches 38; Conserv
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24-FEB-2000;

26-MAR-2000;

16-MAR-2000;

18-MAR-2000;

18-MAR-2000;

18-MAR-2000;

19-MAY-2000;

28-JUN-2000;

28-JUN-2000;

29-JUL-2000;

11-JUL-2000;

26-JUL-2000;

27-MG-2000;

27-MG-2000;

27-MG-2000;

22-AUG-2000;

22-AUG-2000;
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05-SEP-2000;
05-SEP-2000;
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                                                                                                                           RESULT 3
AAK79415
ID AAK79
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Human; connective tissue related disorder; cancer; gene therapy; cytostatic; gene; ds.
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2000US-0229345
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2000US-0205515
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01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
                                                                                                                                                                                        04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
17-MAR-2000;
17-MAR-2000;
18-APR-2000;
                                                   Homo sapiens.
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28-JUN-2000;
30-JUN-2000;
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14-AUG-2000;
14-AUG-2000;
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08-SEP-2000;
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12-SEP-2000;
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05-SEP-2000;
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14-AUG-2000;
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23-AUG-2000;
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07-JUL-2000;
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26-JUL-2000;
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    AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
trearment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expension by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally. (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to provent,
cancers and cancer metastases of haematopoietic antigen genomic
concers and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK64942 to AAK64960 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence #608 encoding novel human connective tissue polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 34227; 3071pp + Sequence Listing; English
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                           17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249300.
10-DEC-2000; 2000US-0249300.
01-DEC-2000; 2000US-025198.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251988.
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17-NOV-2000;
17-NOV-2000;
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08-DEC-2000;
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ABK42709
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XEXEXEX

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27-SEP-2000; 2000US-023534,
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20-ocr-2000; 2000US-0241785.
20-ocr-2000; 2000US-0241786.
20-ocr-2000; 2000US-0241786.
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2000US-0249216.
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2000US-0237039.
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2000US-0241826.
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2000US-0246523.
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2000US-0254097
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2000US-0246474
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08-NOV-2000; 2
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17-NOV-2000; 2
17-NOV-2000; 3
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01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
                                                                                                        02-0CT-2000; 2
02-0CT-2000; 2
02-0CT-2000; 2
02-0CT-2000; 2
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17-NOV-2000;
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08-DEC-2000;
11-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide (DDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides.

Wote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1563 GTGAGGTGTGGGGTATTGTCTGGGGTTCCAGAAAGCCTGTGCCGTGCTGGGGGTC 1620
                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel human connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection prevention of Chrysophrys major iridovirus. The protein encoded by the DNA is useful as an antigen for preventing infection of Chrysophrys major iridovirus. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes proteins related to neutralisation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of Ehime-1 strain of Red sea bream iridoviris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding a protein related to neutralization and infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neutralisation; Chrysophrys major iridovirus; antigen; RSIV; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17761 BP; 3197 A; 5132 C; 5595 G; 3837 T; 0 other;
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                                                                                                                                                                                                                               Disclosure; SEQ ID No 1596; 673pp; English.
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(KURI/) KURITA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 13-51; 65pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL59091 standard; DNA; 112414 BP
                                                                             Ruben SM;
                                     (HUMA-) HUMAN GENOME SCI INC.
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05-JAN-2001; 2001US-0259678.
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                                                                           Rosen CA, Barash SC,
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                                                                                                               WPI; 2001-565190/63.
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ABL59091/c
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2000US-0232401.
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2000US-0235499
2000US-0235494.
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2000US-0235370.
2000US-02358970.
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2000US-023142.
2000US-0231242.
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2000US-0246524.
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2000US-0231413.
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nucleotide sequence of the Ehime-1 strain of Red sea bream iridoviris (RSIV).
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                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25277
                                                                                                 Query Match 42.3%; Score 25.8; DB 24; Length 112414; Best Local Similarity 73.3%; Pred. No. 67; Matches 33; Conservative 0; Mismatches 12; Indels 0;
                                                                Sequence 112414 BP; 26205 A; 29684 C; 30351 G; 26174 T; 0 other;
                                                                                                                                                                                              18391 GGGGTGGCGATCTGATGGGTGATGGGGGGTGTAGCGCGAGGG 18347
                                                                                                                                                                         AAK70465 standard; DNA; 14070 BP
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2000US-0225757.
2000US-0225758.
2000US-0225759.
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2000US-0186350.
2000US-0189874.
2000US-0190076.
2000US-0198123.
2000US-0205515.
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2000US-0216880.
2000US-0217487.
2000US-0218290.
2000US-0220963.
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2000US-0224519.
2000US-022513.
200US-0225214.
200US-022526.
200US-0225267.
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2000US-0214886.
2000US-0215135.
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2000US-0229287.
2000US-0229343.
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2000US-0226681.
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01-SEP-2000;
01-SEP-2000;
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The present invention describes primer sets for synthesising 5602 full-length CDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of ignouncleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence where the compination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, certain and/or diagnosis of the abnormality of the proteins encoded by the full-length convar. The primers allow obtaining of the full-length convariant any specialised methods. AMH3632 to AMH3632 to AMH3632 represent human amino cid sequences; and AMH3632 to AMH3632 represent human amino call sequences; and AMH3632 to AMH3632 represent human amino call sequences; and the exemplification of the protein convergence.
                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0; Mismatches 18; Indels
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, Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T, Nishikawa T, Hayashi K, S
, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                  Human cDNA clone (5'-primer) SEQ ID NO:5249.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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26-JUN-2001 (first entry)
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Best Local Similarity 66.7
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (I) poplynuclectides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metatases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK874912 to AAK874950 and AAM82169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5618 GIGGGGGTGGGGCTGGTGTGAGAACCCTGGGGGTGGGGGTGGGGGTG 5673
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0; Mismatches
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ID AAH08414 standard; CDNA; 686 BP.
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AC AAH08414;
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66.1%;
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2000US-0256719
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Best Local Similarity 66.1
Matches 37; Conservative
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08-DEC-2000;
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01-DEC-2000;
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17-NOV-2000;
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δλ g (first entry)

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Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor and the CREB/ATF transcription factors in the presence of a test
                                                                                                                                                                                                   Human; ATFx; gamma aminobutyric acid B receptor; GABA B receptor; transcription factor; ss.
                                                                                                                                                      Human ATFx coding sequence with 5' extension.
AAF77880 standard; cDNA; 1105 BP.
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                                                                                                   30-MAY-2001
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                                                     AAF77880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      include: Ortostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antisthmatic; antirheumatic; antianthritic; antidiabetic; antisthmatic; antirheumatic; antianthritic; antidiabetic; antisthmatic; antirheumatic; antianthritic; antinflammatory; antithroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; hrombolytic; coaqulant; cootropic; vasotropic; antipsoriatic and antianglogenic. The nootropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. CC polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of inhibiting the proliferation, differentiation or mobilisation of cdisorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate for effection, modulate haemostatic or thrombolytic activity, modulate haemostatic or thrombolytic activity, modulate and antagonists may be also be used in drug screens. AAC78449 to AAC78450 and AAB4440 represent sequences used in the exemplification of
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                                                                                                                                              diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antilnflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acids comprising sequences encoding peptides
                                                                                                                              cancer associated gene; cancer antigen; detection; cancer;
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                                                                        Human cancer associated gene sequence SEQ ID NO:334
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Pred. No. 72;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM;
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es 36; Conserv
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P-PSDB; AAB43731
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                     08-FEB-2001
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Matches
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99GB-0020569

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The present invention relates to a method for identifying a modulator of gamma aninobutyric acid_B (GABA_B) receptor_mediated activity, by monitoring the interaction between a CREBATF transcription factor capable of binding to GABA_B receptor. The present sequence is the coding sequence for human ATFX, which was used in the method of the present invention. ATFX is a member of the CREBATF family of transcription factors. ATFX contains a bZIP domain, by which it interacts with the coiled coil domain of GABA_B receptor. Modulators of GABA_B receptor activity are useful for traeting central nervous system or peripheral nervous system disorders. The present sequence encodes an ATFX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                       with a N-terminal extension (compared to AAB80892).
                                                                                                                                                                                                                                                                                                                                      DB 22;
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                                                                                                                                                                                                                                                                                                                                 Score 25.2;
Pred. No. 72;
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66.7%;
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Les 36; Conservative
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RESULT 9 AAF77880/c

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2000US-0180628 2000US-0184664

2000US-0186350

2000US-0189874 2000US-0190076 2000US-0205515 2000US-0214886 2000US-0215135. 2000US-0216647. 2000US-0216880 2000US-0217487 2000US-0217496 2000US-0218290. 2000US-0220963 2000US-0220964

2000US-0198123

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17-JAN-2001; 2001WO-US01322
                                        WO200155343-A1.
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01-SEP-2000,
01-SEP-2000,
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05-SEP-2000,
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08-SEP-2000,
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12-SEP-2000;
14-SEP-2000;
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11-JUL-2000;
11-JUL-2000;
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14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;
22-AUG-2000;
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25-SEP-2000;
26-SEP-2000;
  Homo sapiens.
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18-APR-2000;
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                                                                                     02-AUG-2001
The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dr primer and an oligonucleotide complementary

to the complementary strand of a polymucleotide which comprises one of

the 5602 nucleotide sequences defined in the specification, where the

coligonucleotide comprises at least 15 nucleotides, or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polymucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to the

complementary strand of a polymucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polymucleotide which comprises a 13'-end sequence, where the

oligonucleotide which comprises at 15 nucleotides and the combination of

the 5'-end sequence/3'-end sequence is selected from those defined in

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primer sets can be used in antisense therapy and

particularly full-length cDMAs. The primers are also useful for the defined and a particularly full-length cDMAs. The primers are also useful for the defined and a particularly full-length cDMAs. The primers are also useful for the defined and a particularly full-length and a particularly full-length and a particularly for a particular of the specification and a particular of the specification are useful and a particular of the primer sets can be used in antisense therapy and

particularly full-length cDMAs. The primers are also useful for the defined and a particular of the primer sets can be useful and a particular of the primer sets can be useful and a particular of the primer and useful and a particular of the primer sets can be useful and a particular of the primer and useful and a particular of the primer and a particular of the primer are useful and a particular of the primer and a particular of the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection and/or discusses of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH031628 and AAH13633 to AAH0342 represent human cold sequences; AAB92446 to AAH36893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs -
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                                                                                                                                                                                                                                                                                                           Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; connective tissue related disorder; cancer; gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25.2; DB 22; Length 1374;
Pred. No. 73;
0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                         Saito K, Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1374 BP; 225 A; 516 C; 365 C; 268 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 18921; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                       hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                    Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK42266 standard; DNA; 5938 BP
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                                                                                                                                                  27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                     28-JUL-2000; 2000EP-0116126.
                                                                                                                                  99JP-0248036
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les 36; Conservative
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                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-318749/34.
  EP1074617-A2
                                                                                                                                  29-JUL-1999;
                                               07-FEB-2001
                                                                                                                                                                                                                                                                                                                           Ishii S,
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                                                                                                                                                                                                                                                                                                           ota T,
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Matches
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2000US-0226681. 2000US-0226868. 20000S-0227182

2000US-0227009 2000US-0229287

2000US-0226279

2000US-0225268 2000US-0225447 2000US-0229343 2000US-0229344 2000US-0229513 2000US-0230437 2000US-0230438 2000US-0231242 2000US-0231243

2000US-0229345 2000US-0229509 2000US-0231414

2000US-0231413 2000US-0232080 2000US-0232081 2000US-0231968

2000US-0232397 2000US-0232398 2000US-0232400 2000US-0232401 2000US-0233063 2000US-0233064

2000US-0232399

2000US-0234997. 2000US-0234998. 2000US-0235484.

2000US-0233065

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27-SEP-2000; 2000US-0235834.
27-SEP-2000; 2000US-0235836.
29-SEP-2000; 2000US-0235836.
29-SEP-2000; 2000US-0235836.
29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236802.
29-SEP-2000; 2000US-0236802.
02-0CT-2000; 2000US-0237039.
02-0CT-2000; 2000US-0237039.
02-0CT-2000; 2000US-0237039.
03-0CT-2000; 2000US-0237039.
03-0CT-2000; 2000US-0237039.
03-0CT-2000; 2000US-024108.
03-0CT-2000; 2000US-0241186.
03-0CT-2000; 2000US-0241186.
03-0CT-2000; 2000US-0241186.
03-0CT-2000; 2000US-0241186.
03-0CT-2000; 2000US-0241186.
03-0CT-2000; 2000US-0241186.
03-0CT-2000; 2000US-024186.
03-0CT-2000; 2000US-02418.

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2000US-0249207.
2000US-0249208.
2000US-0249209.
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01-DEC-2000; 2000US-0250160.
01-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0251030.
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2000US-0249245.
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20000S-0249265.
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17-NOV-2000; 2
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17-NOV-2000;
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05-DEC-2000;
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17-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC

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tissue related polypeptides (AAU86435-AAU86923) and the polypucleotide (CDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK41102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                             The present invention relates to the isolation of novel human connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p53-dependent apoptosis-associated protein and its encoding gene p53AIPI, used for screening apoptosis mediated remedies for cancer and as controllers of apoptosis induction
                                                                             Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human p53-dependent apoptosis-associated protein, P53AIPI comprising fully defined 806, 777, 2659 nucleotide sequences (ABL54631-ABL54633 respectively) given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; p53; p53AIPI; p53-dependent apoptosis-associated; apoptosis;
cytostatic; cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 5938;
                                                                                                                                                                                                                                                                                                                                                                        Sequence 5938 BP; 1295 A; 1601 C; 1751 G; 1291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                             Disclosure; SEQ ID No 1153; 673pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human p53AIPI associated DNA SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                        41.3%; Score 25.2; 66.7%; Pred. No. 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 92-104; 121pp; Japanese.
                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL54634 standard; DNA; 9305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYTY ) UNIV TOKYO.
(ONCO-) ONCOTHERAPY SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity 66.7 Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura Y, Arakawa H;
                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-217192/27.
                                               WPI; 2001-565190/63.
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               Rosen CA,
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ABL54634/c
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AAA14998;
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and the three respectively encoded human p53-dependent apoptoxisis-associated proteins having fully defined 124, 86 and 108 amino acid sequences (ABB08837-ABB08839 respectively) given in the specification. The protein and encoded gene have cytostatic activity, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression of two or more genes represented in ABM93503-ABM97455 in a tissue sample. The method of the invention has hepatotropic, and tissue sample. The method of the invention has hepatotropic, and tissue sample. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                         useful in screening for regulators of apoptosis for subsequent use as cancer treatments. The present sequence is that of the Human p53AIPI associated DNA, useful to the invention.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a
                                                                                                                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                       Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
                                                                                                                                                                                                                                 0;
                                                                                                                                                                                           DB 24; Length 9305;
                                                                                                                                                     Sequence 9305 BP; 2133 A; 2438 C; 2570 G; 2164 T; 0 other;
                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                             85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene #2926 used to diagnose liver cancer.
                                                                                                                                                                                         41.3%; Score 25.2;
66.7%; Pred. No. 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alvares C, Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2926; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2001; 2001WO-US30589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-2000; 2000US-237054P.
                                                                                                                                                                                                                                                                                                                                                                                                         ABN96428 standard; DNA; 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                               36; Conservative
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                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN96428;
                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human proliferation and apoptosis related protein polypeptides used for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; proliferation and apoptosis related protein; PROAP; psoriasis; cell proliferative disorder; immunological disorder; hepatitis; reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma; acquired immune defloiency syndrome; AIDS; allergy; anaemia; asthma; diabetes mellitus; osteoarthritis; endometriosis; uterine fibroid; menstrual cycle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "proliferation and apoptosis related protein"
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                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA encoding a human proliferation and apoptosis related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human proliferation and apoptosis
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      DB 24; Length 275;
                                                         10; Indels
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                                                                                                                      17 GAATCTTATGGGCACCCAGAGGGGGGGGGGGGGGGAGT
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Shih LL;
                              Pred. No. 75;
0; Mismatches
         Score 25;
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   41.08;
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Matches 31; Conservative
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11-FEB-1999,
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                                                                                                                                                                                                                                                                                                      gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS; Alzheimer's disease, cognitive disorder; schizophrenia; osteoporosis; arthritis; psoriasis; digestive; endocrine; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polynucleotides. Specific uses are
                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                           secreted protein; prevention; treatment; protein therapy;
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Lafleur DW;
Shi Y, Soppet DR;
                                     41.0%; Score 25; DB 21; Length 303;
64.9%; Pred. No. 75;
                                                               20; Indels
                                                                                                                                                                                                                                                                  Human secreted protein cDNA fragment containing gene 15.
            Sequence 303 BP; 67 A; 85 C; 110 G; 41 T; 0 other;
                                                               0; Mismatches
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Florence KA, Komatsoulis GA,
sen HS, Rosen CA, Ruben SM,
                                                   Pred. No.
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                                                                                                                                                                                    AAX37383 standard; cDNA; 541 BP
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P-PSDB; AAY07758.
                                                  Sest Local Similarity
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Florence C,
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Young PE;
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Cc described for each of the 70 polynucleotides, based on which tissues cc they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, leukemisas, diseases of the immune system, autoimmune cd sorders, leukemisas, diseases of the immune system, autoimmune cd disorders, leukemisas, diseases of the immune system, autoimmune cd disorders, hepatic and renal disease, lymphomas, inflammation, allergies, cathma, sepsis, diabetes, Alzheimer's and cognitive disorders, schizophrenia, osteoporosis, arthritis, psoriasis, diseative/endocrine cd invention are represented in AAV07744-Y07850 and the encoding nucleic caids are represented in AAV37369-X37441.

Query Match

Query Mat
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SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 354)
NCI/MINDS-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NCI/MINDS-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NAtional Cancer institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
U Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW026388 354 bp mRNA linear EST 09-MAR-2000 wvl2f05.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529345 3' similar to contains element MSR1 repetitive element ; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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Copyright (c) 1993 - 2003 Compugen Ltd.
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BF272027 GA_Eb001 BF93428 HYSKEM001 BG191779 RS713025 BE890765 601431204 BM601525 AGENCOURT BM601525 AGENCOURT BM64195 AGENCOURT BM764195 AGENCOURT BM764195 AGENCOURT BM764195 AGENCOURT BM764195 AGENCOURT BM764195 AGENCOURT BM764195 AGENCOURT BM72225 OAT1D02.8 BM72225 OAT1D02.8 BM72225 OAT1D02.8 BM72225 OAT1D02.8 BM764657 601577506 BM78476 AGENCOURT BM938470 AGENCOURT BM938470 AGENCOURT BM938470 AGENCOURT BM938470 AGENCOURT BM91866 XA56623 AW081866 XA56605.X

B1489045 603021030 B1489015 603021030 B1495192 BB195192 B1430892 0G05G06T3 B195582 HVSNEM02 ALZO0974 82_005_A BES63498 601657281 AU256222 AU256222

score:

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Scoring table:

Total number

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AG180340 Pan trog1 AZ527770 ENTDA48TF BF272027 GA_ED001 B1953428 HVSMEm001

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1056 bp mRNA linear EST 05-MAR-2002 AGENCOURT_6419113 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534991 BM800472
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/lab.host="DH10B (phage-resistant)"
/nab.host="DH10B (thage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "
a 334 c 277 g 207 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1056)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1222 row: column: 16
High quality sequence stop: 635.
Location/Qualiflers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                               DB 14; Length 1208;
                                                                                     Indels
                                                                                   16;
                                           ; Score 30.4; DB
; Pred. No. 69;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/clone="IMAGE:5534991"
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                                               49.88;
                                                               Best_Local Similarity 71.4%;
Matches 40; Conservative
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//lab_host="DH10B (phage-resistant)"
//note="Organ: skin, Vector: pcMv-SPORT6; Site_1: Not!;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life
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1 (bases 1 to 1208)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: ArCC/DCTU/JUPP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://fmage.lill.gov
Plate: LLAM13333 row: d column: 18
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                                                                                                                                                        /clone="IMAGE:2529345"
/clone_lb="MCI_GGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH108"
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1245 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 338.
Location/Qualifiers
1. 354
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/db_xref="taxon:9606"
/clone="IMAGE:6062177"
/clone_lib="NIH_MGC_72"
                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
1. ,1208
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Best Local Similarity
Matches 40; Conserv
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/Accimination for the control of the
                            /lab_host="DHi00" (phage-resistant)"
/lab_host="Organ: spleen; Vector: pOTB7; Site_1: Xho1; Site_2:
ECRI: CDNA made by oligo-dr priming. Directionally cloned
into EcoRI/Anol Sites using the following 5' adaptor:
GGCACAGG(6). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MCC Library.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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1.4 W.B., Grüber.C., Jessee,J. and Polayes,D.

Full-length cDMs libraries and normalization

Onpublished (2001)
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55.2%; Pred. No. 2.4e+02;
iive 10; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 28.8; DB 14
Pred. No. 1.9e+02;
0; Mismatches 17
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/db_xref="taxon:9606"
/clone="CSODD007Y022"
      /clone_lib="NIH_MGC_113"
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 47.2%;
Best Local Similarity 69.6%;
Matches 39; Conservative (
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/clone="CLUBBOOGCOCO"
/clone="CLUBBOOGCOCO"
/clone="CLUBBOOGCOCO"
/clone="Lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pcWVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcWYSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Pax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
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AGENCOURT_8292191 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280902
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: Mgc clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2472 row: n column: 07
High quality sequence stop: 415.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrbini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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1 (bases 1 to 688)
Liw, B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
/clone="IMAGE:6280902"
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                                                                                                                       Contact: Genoscope
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Best Local Similarity 55.7
Matches 34; Conservative
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/tissue_type="1,ymphona, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph, Vector: poTBF; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dr priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                        BM909483 1729 bp mRNA linear EST 12-MAR-2002 AGENCOURT_6640847 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5434071
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MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                        27
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Best Local Similarity 68.4%; Pred. No. 2.9e+02;
Matches 39; Conservative 0; Mismatches 18;
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Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-rémail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:5434071"
/clone_lib="NIH_MGC_99"
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                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
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                                              EST 22-OCT-2001
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Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library Unpublished (2001)
On Feb 22, 2001 this sequence version replaced gi:13109940.
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                        HUSMEC0002B16f Hordeum volgare seedling shoot EST library HVCDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEC0002B16f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Hordeum vulgare seedling shoot EST library
HVcDNA0003 (Etiolated and unstressed)"
/tissue_type="Seedling shoot"
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(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
156 c 264 g 116 t 10 others
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68.4%; Pred. No. 2.7e+02;
tive 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Hordeum vulgare"
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/db_xref="taxon:4513"
/clone="HVSMEc0002B16f"
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Seg primer: AATTAACCCTCACTAAAGGG
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BG309093.2 GI:16313793
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Matches 39; Conservat
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RESULT 7
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BQ038856
BQ038856.2 GI:20383618
                                                                                                                                                   Email: cgapbs-rémail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/ILNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NJSC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="tailbud"
/dev_stage="embryo, stages 20-27"
/lab_host="DH10B (phage=resistant).
/note="Vector: pCMV-SPORI6.ccdb; Site_1: NotI; Site_2:
EcoRV: Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
                                                     NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
National Institute of Child Health and Human Development, National
Cancer Insitute, Xenopus Gene Collection
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Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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S Morgan,R.W. and Burnside,J.
Chicken lymphoid ESTS
L Unpublished (201)
On Mar 27, 2002 this sequence version replaced gi:19772396.
Contact: Joan Burnside
Molecular Endoarinology
University of Delaware
Molecular Endoarinology
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-341
Exx: 302-831-341
Email: joan@Upel.Edu, www.chickest.udel.edu.
Location/Qualifiers
ree
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Local Similarity 66.7%; Pred. No. 2.9e+02;
nes 40; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                   Plate: LiAM11853 row: F column: 1
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="IMAGE:5336064"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 t
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NICHD_XGC_Emb7"
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/db_xref="taxon:9031"
                                                                                                               Unpublished (2002)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 9
                   Kenopodinae; Silurana.
                                                                                                                                                                                                                                                                                         info@image.llnl.gov
Plate: LLAM11853 rc
                                     (bases 1 to 403)
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Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-132E07.R.
Pan troglodytes
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-132E07.R, genomic survey sequence.
AG122806
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                         /tissue_type="thymus, bursa, spleen, PBL, bone marrow"
/lab_host="E.coli EMDH10B"
                                                                                                                                                                                                                                                                                                                               /clone="pgnlc.pk010.k15"
/clone_lib="normalized chicken lymphoid cDNA library"
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 653)
Fuliyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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258 c 82 g 173 t
                                                                                                                                                                                                                                 Length 530;
                                                                                                                                                        33 others
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Pred. No. 3.4e+02;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                            Query Match 45.9%; Score 28; DB 14; Best Local Similarity 66.7%; Pred. No. 2.9e+02; Matches 40; Conservative 0; Mismatches 20
                                                                                                                             9
                                                                                                                                                     126 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                           /note="Vector: pCMVSPORT
149 c 142 g 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="PTB-132E07.R"
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R.Site 2 : SacI
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Similarity 69.1%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
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/clone_lib**NIFE_NGC_100*
/tissue_type**Nepatocellular carcinoma, cell line*
/tissue_type**Nepatocellular carcinoma, cell line*
/lab_host**Datio8 (phage-resistant)*
/note**Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRIX/AhoI sites using the following 5: adaptor:
GGCAGCAG(G). Size-selected >500Dp for average insert size
1 8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and superscript
INT (Life Technologies). Note: this is a NIH_MGC
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A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 493)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH756447 493 bp DNA linear GSS 01-MAF SALK_053697.52.05.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_053697.52.05.n, DNA
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2444 row: j column: 15
High quality sequence stop: 438.
Location/Qualifiers
   Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Indels
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Pred. No. 3.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:6270062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH756447.1 GI:19038842
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69.18;
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Arabidopsis thallana
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Matches 38; Conservative
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                                                                                                                                                                                                      troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
                                                             GSS 03-NOV-2001
                                    AG090162 712 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-089K05.R, genomic survey sequence.
AG090162
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MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Pred. No. 3.5e+02;
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/db_xref="taxon:9598"
/clone="PTB-089K05.R"
/sex="male"
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/clone_lib="PTB Chimpanze
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                                                                                                                                                                                                                                  BAC Library clone:PTB-089K05.R.
Pan troglodytes
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full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NHB-MGC Library." 2 others
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/db_xref="taxon:3702"
/clone="SALK_053697.52.05.n"
/clone="lb="Arabidopsis thaliana TDNA insertion lines*
/otoe_lb="spc was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html*
a 160 c 112 g 106 t 12 others
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WHF-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Phitp://mage.llnl.gov
Plate: LLAM11479 row: k column: 08
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/lab_host="DH108"
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/clone~"IMAGE:5191807"
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/cgn2_6/ptodata/l/ina/5B_COMB.seq:*
/cgn2_6/ptodata/l/ina/6A_COMB.seq:*
/cgn2_6/ptodata/l/ina/6B_COMB.seq:*
/cgn2_6/ptodata/l/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/l/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                     441362 segs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 13, Appli Sequence 140, App Sequence 140, Appl Sequence 17, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 218, Appli Description Sequence 3 Sequence 3 Sequence 3 Sequence US-08-459-568-3 US-08-39-411-3 US-08-516-472-3 US-09-586-472-3 US-09-586-472-3 US-08-290-665A-139 US-08-290-665A-140 US-08-290-665A-140 US-08-10398-139 PCT-US95-10398-139 PCT-US95-10398-139 PCT-US95-10398-130 US-09-103-840A-1 US-09-103-840A-1 US-09-103-840A-1 US-09-133-136-1 US-08-588-136-1 US-08-943-731-136 US-09-188-930-26 US-09-316-536-74 US-09-316-536-74 US-09-316-536-1 US-09-316-536-1 US-09-188-930-30 SUMMARIES Length DB 601 728 1001 1015 1338 1347 2543 2543 Query Score Result Ño. 0 0 0 0 0 0 0 0 0 0 000000000000

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US-08-336-408B-1 PCT-US31-00399-1 US-08-290-665A-136 US-08-290-665A-138 US-08-290-665A-138 US-08-290-665A-138 US-08-290-665A-138 US-08-290-665A-138 US-08-290-665A-138 US-08-1039B-138 PCT-US95-1039B-138 PCT-US95-1039B-138 US-08-157-235-3 US-08-171-389-85 US-08-475-228A-85 US-08-475-228A-85 US-08-475-228A-85	ALIGNMENT	ma Pro 0, 0, 126	Score 24.8; Pred. No. 12;); Mismatches
US.	·	us/08459568 Retinoblastom Palar Finger P 93 Siland Flores bla and	_
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1866 1866 573 573 573 573 573 573 803 803 466 466 466 466		action US, Shi 170N: Shi 1	za t
38.0 38.0 337.7 37.7 37.7 37.7 37.7 37.7 37.7 3		Application US/ 1811301 1811301 1811301 1 INVENTION: Ent. INVENTION: Ent. INVENTION: Ent. 1 Expures: 93 INTERNION: 210 INTERNION: 210 INTERNION: 210 INTERNION: 93 INTERNION: 9	ch 1 Similarity 35; Conserv
23.7 23.7 25.7 25.7 25.7 25.7 25.7 25.7 25.7 25		ULT 1 08-459-568-3/C equence 3, Application US/08459568 general No. 581304 APPLICANT: Huang, Shi TITLE OF INVENTION: Retinoblasto TITLE OF INVENTION: Zinc Finger CORRESPONDENCE ADDRESS: ADDRESSE: Campbell and Flores STREET: 4370 La Jolla Village CITY: San Diego STATE: California COUNTRY: USA ZIP: SAL Diego STATE: California COUNTRY: USA ZIP: SAL DIEGO STATE: California COUNTRY: USA ZIP: POLOZ COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE APPLICATION NUMBER: US/08/459, FILING DATE: 06-MAR-1995 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 31,815 SEQUENCE CHARACTERISTICS: LENGTH: 5183 base pairs TYPE: nucleic acid STRANDEDNESS: double TOCATION: 1.5158 NAME/KEY: CDS LUCATION: 1.5158 NAME/KEY: CDS	cat
00000000000000000000000000000000000000		TESULT 1 US-08-459-568-3/C Sequence 3, Application U Sequence 3, Application U Sequence 3, Application U GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS CORRESPONDENCE ADDRESS CORRESPONDENCE ADDRESS CORRESPONDENCE ADDRESS CORRESPONDENCE ADDRESS COUNTRY: STREET: 4370 La JOI COUNTRY: COMPUTER: ENDABLE FORM MEDIUM TYPE: Floppy COMPUTER: TBM FC COMPUTER: FLING DATE: OC-UN COMPUTER: PAPLICATION DATA APPLICATION NUMBER: FLING DATE: OC-UN CLASSIFICATION NUMBER: FLING DATE: OC-UN CLASSIFICATION NUMBER: FILING DATE: OC-UN TELEFONDENCE CHARACTERIST TELEFONDENCE CHARACTERIS	Ouery Match Best Local Matches 3
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Score 24.8; DB 3; Length 5868; Pred. No. 13;
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APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
Zinc Finger Proteins
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CORRESPONDENCE ADDRESS:
CAMPBELL & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/516,859A
FILING DATE: 18 AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
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                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-MG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; Sequence 3. Application US/09586472
Patent No. 6323335
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 67.3%;
Matches 35; Conservative
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5868 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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; LOCATION:
US-08-516-859A-3
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| Sequence 3, Application US/08399411 |
| Sequence 3, Application US/08399411 |
| Seneral No. 5831008 |
| GENERAL INFORMATION: |
| TITLE OF INVENTION: Retinoblastoma Protein - Interacting |
| TITLE OF INVENTION: Zinc Finger Proteins |
| NUMBER OF SEQUENCES: 93 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Campbell and Flores |
| STREET: 4370 La Jolla Village Drive, Suite 700 |
| CITY: San Diego |
| CITY: California |
| Convention |
| Co
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APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Retinoblastoma Proteins
INFURBATION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4470 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
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67.3%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08516859A Patent No. 6069231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ 1D NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 5183 base pairs TYPE: nucleic acid syranDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 67.3
Matches 35; Conservative
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US-08-516-859A-3/c
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US-08-399-411-3
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                       Query Match 40.7%; Score 24.8; DB 4; Length 5868; Best Local Similarity 67.3%; Pred. No. 13; Matches 35; Conservative 0; Mismatches 17; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Pred. No. 11
                                                                                                                                                                                                                                                                                                                Sequence 139, Application US/08290665A; Sequence 139, Application US/08290665A; Patent No. 5823852
APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/290,665A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 758-4800
TELERA: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: Z4
US-08-290-665A-139
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCL
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: CORE
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQUENCES: 263
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 573 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                          CDS
121..5278
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Best Local Similarity
Matches 33; Conserv
                         linear
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     STRANDEDNESS:
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                       TOPOLOGY:
FEATURE:
                                                                         ; LOCATION:
US-09-528-706-3
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                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                   NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAN: (619) 535-9001
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               Score 24.8; DB
Pred. No. 13;
0; Mismatches
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-1J 1776
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APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/528,706
                                                                                                                                                                                                                     LENGTH: 5868 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09528706
Patent No. 6468985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/POCKET NUMBER: P-1.J.
TELECOMMUNICATION INFORMATION:
TELEPRAN: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5868 base pairs
TYPE: nucleic acid
                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                       121..5278
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.7%;
Best Local Similarity 67.3%;
Matches 35; Conservative (
                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 92122
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLARES OF HEPATTIS C VIRUS AND THE USE OF REAGENING DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BUKH, J., MILLER, .....
APPLICANT: PURCELL, R.H.
TAYBUTION: NUCLECTIDE AND DEDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMOUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDERFEET 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398 FILING DATE: 15-AUG-1995
                                                                                                                                                                            NUMBER: PCT/US95/10398
15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 140, Application PC/TUS9510398 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NOMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                             MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM; PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MORGAN & FINNEGAN
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                                                                                                                                                                                                                                                                                                                                                                                                      NAME: RICHARD W. BORK REGISTRATION NUMBER: 36,459
                                                                                                                                             SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US FILING DATE: 15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEK: 421792,
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
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NEW YORK
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COMPUTER READABLE FORM:
                                                         COMPUTER READABLE FORM:
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Best Local Similarity
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NEW YORK
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CITY: NE
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                 COUNTRY:
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                                                                                                                                       NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-405-1994
CLASSIFICATION: 435
ATPORNEY/AGEWT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
RECISTRATION NUMBER: 36,459
REPRENCE/DOCKET NUMBER: 2026-4116
TELEPHONE: (212) 756-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                             APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 139, Application PC/TUS9510398 GENERAL INFORMATION:
                                 Sequence 140, Application US/08290665A Patent No. 5882852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERA: (212) ...
TELEX: 421792
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                           ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MORGAN & FINNEGAN
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STREET: 345 PARK AVENUE
CITY: NEW YORK
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TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQU
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
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Matches 33; Conservative
                                                                                                                                       TITLE OF INVENTION: NUCT
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: CORE
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQUENTIALS OF SEQUENCES: 263
CORRESPONDENCE ADDRESS: 265
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                         STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                   NEW YORK
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               US-08-290-665A-140/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-10398-139/c
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Gaps

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3958304 GAAGGGTGGTCGACGACGAGGAGTTGTGGGCGCCCAGATCGGTGCGGCGGACGCGATGGACGCTCG 3958247
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GENERAL INFORMATION:
APPLICANT: FLEISCHAAN, Robert D.
APPLICANT: FLEISCHAAN, Robert D.
APPLICANT: FLEISCHAAN, Robert D.
APPLICANT: FRESER, Claire M.
APPLICANT: FRESER, Claire M.
APPLICANT: FRESER, Claire M.
APPLICANT: FOR SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-220007-00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATEURIN VET: 2.1
SEQ ID NO 2
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OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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APPLICANT: FRISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRAZE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2.
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                      Gaps
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40.0%; Score 24.4; Di
Best Local Similarity 63.8%; Pred. No. 30;
Matches 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                  40.0%; Score 24.4; D
68.0%; Pred. No. 14;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09103840A; Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09103840A; Patent No. 6294328
                         17:
REFERENCE/DOCKET NUMBER: I
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 957 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 68.0°
Matches 34; Conservative
                                                                                                                                    linear
                                                                                                                                                                                                      ; ANTI-SENSE: NO
US-08-836-075A-17
                                                                                                                                    TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4403765
                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-103-840A-2/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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US-003-836-075A-17/C
Sequence 17, Application US/08836075A
Sequence 17, Application US/08836075A
Sequence 17, Application US/08836075A
Sequence 17, Application US/08836075A
Sequence 17, Application:
APPLICANT: WARRTION:
APPLICANT: STUTYER, LIEVER, LIEVER
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
TITLE OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 GCCGGGGATCATTTGGCCCCCAAGACGTCGAGAGGCCGCGGGGGGAC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Word 6.0 / ASCII text output CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24.6; DB Pred. No. 11; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/836,075A FILING DATE: 21 Apr 1997
RIOR APPLICATION DATE: APPLICATION NUMBER: PCT/EP95/04155 FILING DATE: 23 Oct 1995
RIOR APPLICATION NUMBER: EP 94870166.9 FILING DATE: 21 Oct 1994
RIOR APPLICATION NUMBER: EP 95870076.7 FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 36,459
ER: 2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
CITY: HOUSTON
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 30,459
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
21P: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     TELEX: 421792
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KAMMERER, PATRICIA A. REGISTRATION NUMBER: 29,775
                                                                                                                                                                                                                                                                  TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: Z8
PCT-US95-10398-140
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                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
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LENGTH: 4411529

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39.7%; Score 24.2; DB 3; Length 53526; 62.3%; Pred. No. 26;
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                                                                                                                                                                                        APPLICANT: KIINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: GINN, FED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELEPROMINICATION INFORMATION:
TELEPROMINICATION SOR-872-5415
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08658136; Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE WAPPLICANT: LANDES, GREGORY MAPPLICANT: BURN, TIMOTHY C
                                                                                                                                     ; Sequence 2, Application US/08658136; Patent No. 6071717; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                            ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.3
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: FRAMINGHAM
STATE: MASSACHUSE:
COUNTRY: USA
ZIP: 01701
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                                             16496 C 16496
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           61 C 61
                                                                                                  RESULT 14
US-08-658-136-2
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US-08-658-136-1
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Pred. No. 30;
0; Mismatches 21; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.7%; Score 24.2; DB 1; Length 31571; 62.3%; Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYCYSTIC KIDNEY DISEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ludwig, S. Peter
REGISTRAITON NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372/0A462
TELECOMMUNICATION INFORMATION:
TYPE: DATA CREANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CONNORS, TINCTHY D. APPLICANT: DACKOWSKI, WILLIAM R. APPLICANT: GERMINO, GREGORY APPLICANT: GIAN, FENG TITLE OF INVENTION: POLYCYSTIC KID NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08323443B Patent No. 5654170
                                                                                                                                                                                                                                                                                                                                                       KLINGER, KATHERINE W.
LANDES, GREGORY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 31571 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                40.0%;
                                                                                                                                                                                                                                                                                                                                                                                            BURN, TIMOTHY C.
                                                                                           Query Match
Best Local Similarity 63.88
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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CLONE: PKD1 GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 38; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: 1
STATE:
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Gaps

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APPLICANT: CONNORS, TIMOTHY D

APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GRAN, FRECORY
TITLE OF INVENTION. POLYCYSTIC KIDNEY DISEASE GENE
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
CORRESPONDENCE SEGRENATION
STREET: ONE OUNDATIN ROAD
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
TITLE OF COMPANIES CONTRY:
COUNTRY: USA
COUNTRY
C
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(without alignments)
4579.068 Million cell updates/sec
                                                                                                                                                                               June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
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2. (cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
3. (cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4. (cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
5. (cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
5. (cgn2_6/ptodata/1/pubpna/NSO7_NEW_PUB.seq:*
6. (cgn2_6/ptodata/1/pubpna/NSO8_NEW_PUB.seq:*
7. (cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7. (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
7. (cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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7. (cgn2_6/ptodata/1/pubpna/USO1_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1029858 seqs, 724030393 residues
                                                                                                                                                                                                                                                                        US-09-826-581-3_COPY_612_672
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

c 20 24.4 40.0 3367 9 US-10-223-085- c 21 24.4 40.0 3367 9 US-10-223-086- c 22 24.4 40.0 3367 9 US-10-223-086- c 23 24.4 40.0 3367 9 US-10-223-086- c 24 24.4 40.0 3889 9 US-10-223-089- c 25 24.4 40.0 1368 9 US-10-223-089- c 26 24.2 39.7 1862 9 US-10-221-141- c 28 24.3 99.3 1882 9 US-10-020-141- c 28 23.8 99.0 606 9 US-09-764-891- c 39 23.8 99.0 1606 9 US-09-764-891- c 31 23.8 99.0 1606 9 US-09-764-891- c 32 23.6 38.7 421 9 US-09-764-866- 33 23.6 38.7 421 9 US-09-764-866- 34 23.6 38.7 421 9 US-09-764-866- 35 23.6 38.7 421 9 US-09-764-866- 36 23.6 38.7 22452 9 US-09-764-866- 37 23.6 38.7 22452 9 US-09-764-866- 38 23.6 38.7 22452 9 US-09-764-866- 39 23.4 38.4 39.4 1001 9 US-09-866-0504- c 42 23.4 38.4 1001 9 US-01-152-661- c 43 23.4 38.4 1001 9 US-01-152-661- c 44 23.4 38.4 1001 9 US-09-866-0504- c 44 23.4 38.4 1001 9 US-09-866-0504- c 44 23.4 38.4 1001 9 US-01-152-661- c 45 23.4 38.4 1001 9 US-01-152-661- c 45 23.4 38.4 1001 9 US-01-152-661- c 47 23.4 38.4 1001 9 US-01-152-661- c 48 23.4 38.4 1001 9 US-01-152-661- c 49 23.4 38.4 1001 9 US-01-152-661- c 40 DS-09-826-581-3 c CURRENT PILIMO DATE: 2001-04-05 c DREMENT PILIMO DATE: 2001-04-05 c DREMENT FILING DATE: 2001-04-05 c DREMENT PILING DATE: 2001-04-05 c DREMEN	US-10-223-085-33 US-10-223-086-33 US-10-223-084-33 US-10-223-089-33 US-10-223-090-33 US-10-223-090-33 US-10-223-090-33 US-10-223-090-33 US-10-223-090-33 US-10-223-090-33 US-10-223-090-33 US-10-204-968A-1 US-09-764-891-5477 US-09-764-891-5477 US-09-764-891-10204 US-09-738-626-1796 US-09-867-701-10278 US-09-867-701-10278 US-09-868-1487 US-09-868-1487 US-09-868-1489 US-09-866-1538 US-09-869-1538 US-09-86	ALIGNMENTS 26581 PETHE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUI 059/826,581 60/195,665 Version 4.0	100.0%; Score 61; DB 10; Length 1722; imilarity 100.0%; Pred. No. 1.8e-12; Conservative 0; Mismatches 0; Indels 0; Gaps 0; GTGAGGAGTGGGCTGGGAATCTTATGGCACACAGGGGCGGGGGGGG	1 1 1 1 1 1 1 1 1 1
C 20 24.4 40.0 C 23 24.4 40.0 C 23 24.4 40.0 C 24 24.4 40.0 C 25 24.2 39.3 C 26 24.2 39.3 C 27 24 39.3 C 28 23.8 39.0 C 30 23.8 39.0 C 31 23.8 39.0 C 31 23.8 39.0 C 31 23.8 39.0 C 31 23.8 39.0 C 32 23.6 38.7 C 34 23.6 38.7 C 35 23.6 38.7 C 36 23.6 38.7 C 37 23.6 38.7 C 38 23.6 C 3	33367 33367 33367 33367 33367 33367 3367 3367 3367 3462 3689	ton US/09; 2310A1), Leif 1, Lefald, 2, Lefald, 3, VARIANTS 1, STANTS 1, SO01-0, 10, SO01-	100.00 rvative rcccrede.	cation US 0300543755 al.
C 20 24.4 C 23 24.4 C 23 24.4 C 24 24.4 C 25 24.2 C 27 24.4 C 28 24.2 C 29 23.8 C 39 23.8 C 31 23.8 C 31 23.8 C 31 23.8 C 33 23.6 C 33 23.6 C 34 23.4 C 41 23.4 C 41 23.4 C 42 23.4 C 42 23.4 C 43 23.4 C 44 23.4 C 44 23.4 C 44 23.4 C 45 23.4 C 48 23.4 C 49 23.4 C 48 23.4 C 49 23.4 C 48 23.4 C 48 23.4 C 48 23.4 C 48 23.4 C 49 23.4 C 49 23.4 C 49 23.4 C 40 23.4 C 41 23.4 C 42 23.4 C 43 23.4 C 44 23.4 C 45 23.4 C 46 23.4 C 47 23.4 C 48 23.4 C 48 23.4 C 48 23.4 C 49 23.4 C 49 23.4 C 40 23.4 C 40 20.6 C 60 20.6 C 70 2	44444444444444444444444444444444444444	3 Applicati S2020143 RMATION: Anderssor Luthman, Marklunan, Marklunan, MCE: 111 ING DATE CATION N G DATE: EQ ID NOG astSEQ f astSEQ f	imilarit; ; Consee GTGAGGAGG GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	1596 6, Applic No. US201 RMATION: ROSEN EL
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		RESULT US-09-1 Sequents Sequen	Quer Best Matc Qy Db Qy	RESULT US-10- ; Sequ ; Publ ; GENE

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tive 0; Mismatches 18; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                         Score 25.2; DB 10; Length
Pred. No. 5.3;
0; Mismatches 18; Indels
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PCOORS.
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0
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                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (1023)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-922-301-334
                                          or
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; Patent No. US20020132767A1
                                     OTHER INFORMATION: n equals a,t,g,
                                                                                           OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                    41.3%;
66.7%;
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Best Local Similarity 66.7%;
Matches 36; Conservative
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Best Local Similarity 66.73
Matches 36; Conservative
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Best Local Similarity 66.73
Matches 36; Conservative
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   NAME/KEY: misc_feature
LOCATION: (989)
                                                        NAME/KEY: misc_feature
LOCATION: (1005)
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; ORGANISM: Homo sapiens
US-10-092-154-1153
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; ORGANISM: Homo sapiens
US-09-764-847-1153
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US-09-764-847-1153/c
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Pred. No. 2.3;
0; Mismatches 20; Indels (
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE REFERENCE: PA106
CURRENT PELICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 334
LENGTH: 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATE SOCIAL AND STATEMENT OF THE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC009
FILE REPERENCE: PC009
CURRENT APPLICATION UNBER: US/09/764,847
CURRENT APPLIAG DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SEQ ID NO 1596
LENGTH: 17761
              CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER: OS SEO ID NOS: 2003
Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1596
LENCTH: 17761
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LOCATION: (59)
OTHER INFORMATION: n equals a,t,g, or c
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Patent No. US20020132767A1
GENERAL INFORMATION:
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Patent No. US20020052308A1
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nes 38; Conservative
                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1596
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US-09-764-847-1596
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FILE REFERENCE: PC009C1
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APPLICANT: Olga Bandman
TITLE OF INVENTION GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REPERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DAFE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                               Sequence 30, Application US/09964899
Fatent No. US2020174446A1
FEBERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4.31612 A
CURRENT APPLICATION NUMBER: US/09/964,899
CURRENT APPLICATION NUMBER: US/09/964,899
FRIOR FILING DATE: 2001-09-27
FRIOR PEDILOGATION NUMBER: 60/236,893
FRIOR FILING DATE: 2000-09-29
FRIOR FILING DATE: 2000-09-20
FRIOR FILING 
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                                                                                                         ch 41.0%; Score 25; DB 12; Length 1847; 1 Similarity 64.9%; Pred. No. 6; 37; Conservative 0; Mismatches 20; Indels
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OTHER INFORMATION: Incyte ID No. US20020137081A1 344297.3
                                               15;
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; Pred. No. 6.2;
0; Mismatches
            69.4%; Pred. No. 6.6;
tive 0; Mismatches
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Best Local Similarity 64.9%;
Matches 37; Conservative (
Best Local Similarity 69.4
Matches 34; Conservative
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ORGANISM: Homo sapiens
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US-09-964-899-30
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US-09-864-761-4800
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US-09-964-899-30
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LENGTH: 1351
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LENGTH: 1847
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      1855 GAGGGGACAGAGCTAGGAGAAGGGAGGCCAGCAAGGGCAGGGGTGCAGGGG 1802
                                                                                                                                                                                                                                        APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer; FILE REFERENCE: 44921-5028-60
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR PILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-14
SHOR RILING DATE: 2000-06-10-02
NUMBER OF SCI ID NOS: 3560
SOFTWARE: Patentin Ver. 2.1
LENGTH: 275
TYPE: DNA
ORGANIZM: Homo sapiens
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NAME/KEY: unsure
LOCATION: (1)..(275)
CTHER INFORMATION: n = a or c or g or t
US-09-880-107-2925
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TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2014P1
CURRENT APPLICATION NUMBER: US/10/144,929
CURRENT APPLICATION NUMBER: US/09/251,329
PRIOR APPLICATION NUMBER: US/09/251,329
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: PCT/US98/17044
PRIOR FILING DATE: 1999-08-18
NUMBER OF SEC ID NOS: 257
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or
US-10-144-929-25
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OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                            Sequence 2925, Application US/09880107
Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-144-929-25/c
; Sequence 25, Application US/10144929
; Publication No. US20030069405al
; GENERAL INFORMATION:
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                                                                                                                                                                                                                            GENERAL INFORMATION:
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NAME/KEY: SITE
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NAME/KEY: SITE
                                                                                                                         US-09-880-107-2925
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LENGTH: 541
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Best Local S
Matches 31
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
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N: EXPRESSED IN BT474, SIGNAL = 1.4
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
N: EXPRESSED IN LUNG, SIGNAL = 2.6
N: EXPRESSED IN PLACENTA, SIGNAL = 1.8
N: EXPRESSED IN PLACENTA, SIGNAL = 0.98
N: NT HIT: 9111423021, EVALUE 0.00e+00
N: SWISSPROT HIT: 061116, EVALUE 1.00e-09
N: EST_HUMAN HIT: BE885438.1, EVALUE 0.00e+100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00665
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PRIOR FILLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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PRIOR FILLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                       Sequence 21539, Application US/09864761 Patent No. US20020048763A1
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 35; Conserv
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; OTHER INFORMATION:
US-09-864-761-21539
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                                                                                                                                                             APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica "A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 7;
0; Mismatches 17; Indels 0;
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/09/864,761

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-06-03

PRIOR PELING DATE: 2000-06-03

PRIOR PELING DATE: 2000-06-04

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR APPLICATION NUMBER: US 60/24,687

PRIOR PELING DATE: 2000-06-30

PRIOR PELING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/608-408

PRIOR PELING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/608-408

PRIOR PELING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/608-408

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OTHER INFORMATION: EXPRESSED IN HEAR!
OTHER INFORMATION: EXPRESSED IN BT474
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Best Local Similarity 67.3%;
Matches 35; Conservative (
                                                               APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
US20020048763A1
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      Patent No.
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RESULT 12

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; LOCATION:
US-09-878-281-193
US-09-899-046-193
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                                                                    RESULT 13
US-10-024-450-3/C
| Sequence 3, Application US/10024450
| Sequence 3, Application US/10024450
| Sequence 3, Application No. US20030032606A1
| GENERAL INFORMATION:
| APPLICANT: Huang, Shi
| APPLICANT: Chadwick, Robert B.
| TITLE OF INVENTION: Mctrosatellite-Instability Positive Tumors Using RIZ
| FILE REPERENCE: P-15 5101
| CURRENT APPLICATION NUMBER: US 60/256,582
| PRIOR PILING DATE: 2000-12-17
| PRIOR PILING DATE: 2000-12-19
| NUMBER OF SEQ ID NOS: 15
| SOFTWARE: FastSEQ for Mindows Version 4.0
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TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
COMPOURER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels
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APPLICATION NUMBER: US/09/899,046
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 193, Application US/09899046
Publication No. US20030008274A1
GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 498 base pairs
TYPE: nucleic acid
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US-10-024-450-3
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ORGANISM: Homo sapien
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US-09-899-046-193/C
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TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
THILE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Query Match 40.3%; Score 24.6; DB 9; Length 498; Best Local Similarity 70.2%; Pred, No. 9.1; Matches 33; Conservative 0; Mismatches 14; Indels
                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/878,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: June 13, 2003, 09:00:37 Job time: 21.2903 secs
                                                                                                                                                                                                                                    US-09-878-281-193/c
; Sequence 193, Application US/09878281
; Publication No. US20030032005A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHRRACTERISTICS:
LENGTH: 498 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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LOCATION: 1.495
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APPLICANT:
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nuc	nucleic search, using sw model
Run on:	June 13, 2003, 01:49:14; Search time 5200.55 Seconds (Without alignments) 9216.782 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-826-581-5 1647 1 ttggtctggggctggccacaacaccagcctctagtcttc 1647
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of	hits satisfying chosen parameters: 4109280
Minimum DB seq I	length: 0 length: 2000000000
Post-processing:	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:* 9b ba:* 9b ba:* 9 ba:* 9 ba:* 9 bat:* 9b bat:* 9 bat:* 10 gb_pr:* 10 gb_pr:* 11 gb_sts:* 12 gb_sy:* 13 gb_un:* 13 gb_un:* 15 em_ba:* 16 em_lun:* 17 em_lun:* 18 em_lun:* 19 em_lun:* 19 em_lun:* 10 em_lun:* 10 em_lun:* 11 em_lun:* 12 em_lun:* 13 gb_un:* 14 em_lun:* 15 em_lun:* 16 em_lun:* 17 em_lun:* 18 em_lun:* 19 em_lun:* 10 em_lun:* 10 em_lun:* 11 em_lun:* 12 em_lun:* 13 em_lun:* 14 em_lun:* 15 em_lun:* 17 em_lun:* 18 em_lun:* 18 em_lun:* 18 em_lun:* 19 em_lun:* 10 em_lun:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2290 bp mRNA linear PRI 07-APR-2000 for AMP-activated protein kinase gamma 3 subunit
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GSLLPRPSFLYRTIQDLGTFRDLAVVLETAPILTALDIFVDRRYSALPVVNBCGQV
VGLYSRPPVHAAAQQTVHLAMAGYGRALRRRTLCLEGYLSCQPHESLGEVIDRIARE
QVHRLYLVDFTGHLLGYVSLSDILGALVLSPAGIDPSGPEKI"

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Submitted (12-0CT-1999) Carling D., Cellular Stress Group, Mi
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 UNIVIED KINGDOM
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/db_xref="taxon:9606"
22. .1500
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                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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AVVLETAFILTALDIFVDRRVSALPVVNECGQVVGIYSRFDVIHLAAQQYYNHLDMSV
GEALRQRYLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDFTQHLLGYVSLSDILQ
TCCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAATGAAGGGAACTGGAGAACTCAGC 1560
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
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Variants of the gamma chain of ampk, dna sequences encoding
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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                  Score 1453;
Pred. No. 0;
                  88.2%;
97.3%;
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Matches 1501; Conservative
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/protein_id="AaF73987.1"
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/protein_id="MaF1E60ENSSMPSPAVTSSERIRGKRRAKALRWTROKSVEEG
/translation="MSF1E60ENSSMPSPAVTSSERIRGKRRAKALRWTROKSVEEG
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Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
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                                                                   GCCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCTGCACACCTGGAAGC 1534
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1 (bases 1 to 2115)

Milan, Jeon, Tr., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.
1494 CTATGATTCAGGCTTCTTCAGCCTTCCAAAATTGCCTTTGCCT 1536
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/tissue_type="skeletal muscle"
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
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ORIGIN Query Match Query Match Best Local Similarity 97.8%; Score 1447; DB 6; Length 2109; Best Local Similarity 97.8%; Pred. No. 0; Matches 1495; Conservative 0; Mismatches 35; Indels 7; Gaps 2; OY 101 TTCCTAGAGCAAAAACAGCAGCTAGGCCATCACCAGCTGTCACCAGCTAGAA 160	121 G 281 G 181 G 181 G 341 G 241 G	TCCAGCACAGATGATGATGAGGAGCTGGGGAGTTCCCAGCCACAGAGGCCTGGGAGTGTTTTCCAGCCACAGAGGCCTGGGAGTGTTTTTTTT	QY 581 ATGCAGGACACCTGCTACGATGCCATGGCAACTAGCTCCTAGAC 640 Db 481 ATGCAGGACCACCTGCTACCTTGTTTTTTTTTTTTTTTT	OY 761 CTGGTGCTGCTACTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAACAAT 820	
QY 1115 GCACCCATCCTGACTGCACTGGACCGCGCGTGTGTCTGCACTGCCTGTG 1174 Db 1021 GCACCCATCCTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTG 1080 QY 1175 GTCAACGAATGTGGTCACTGGACATCTTTGTGGACGCGTGTGTGATCACCTGTG 1080 QY 1175 GTCAACGAATGTGGTCAGGTCGTGGCCTCTATTCCCGCTTTGATGTGATCACCTGGCT 1234 Db 1081 GTCAACGAATGTGGTCAGGTCGTGGCCTTATTCCCGCTTTGATGTGATTCACCTGGCT 1140 QY 1235 GCCCAGCAAACCTACAGGTCGGCCTCTATTCCCGCTTGATGTGATTCACCTGGCAGAGACA 1204 Db 1141 GCCAGCAACCTACACACCACTGGACATGAGTGGGAGAAGCCCTGAGGCAGAGAGCA 1200 QY 1295 CTATGTTGAACCTTTCCTCCCCAGCCCCAGGAGAGCTTGGGGGAAGTGATCGAC 1354 Db 1141 GCCAGCAACCTTTCTTCCTCCCCAGCCCCAGGAGAGCTTGGGGGAAGTGATCGAC 1354 DD 11201 CTATGTTGTGGAGGCTTTCCTCCCCAGCCCCACGAGAGCTTGGGGGAAGTGATCGAC 1260 DD 1201 CTATGTTGTGGAGGGCTTTCCTCCCAGCCCCACGAGAGCTTGGGGGAAGTGATCGAC 1260	09 1355 AGGATTGCTCGGGAGCAGGTTGCTGGTGGAGCGAGACCCAGCATCTTG 1414 1 1 1 1 1 1 1 1	QY 1535 CAATGAAGGGAACTGGGGTAACTTCTCCCCCACCCCATTTGCTGGTTCAG 1594 Db 1440 CAATGAAGGAATTGAGAACAGCTTCATTTCCCCAATTTGCTGGTTCAG 1493 QY 1595 CTATGATTCAGGTAGGCTCTGCCTGGCCATGACCAGCCT 1637 Db 1494 CTATGATTCAGGTAGGCTCTGCCTTCCAAAATTGCTTTGCCT 1536 RESULT 5 111111111111111111111111111111111111	AX099776 LOCUS AX099776 AX099777 AX099776 AX09777 AX099776 AX099776 AX099776 AX099777 AX099777 AX09977 AX09977 AX09977 AX09977 AX0977 AX0977 AX0977 AX0977 AX0	g,	44 88 8

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95 ATGAGCTTCCTAGAGAAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 154	GCGGGGGGGGCACTCCACCACAGGGGGCACTCCCTCTGACCCTGTGGCGGCCCCTCTGGGGGGCGCTCCTGGCGGGGGG	TGGGCTGGTGGAAGAAGCCAGCCCGTGCCCA 	92 CGGGCAGCCCCTATGGGACAGCAGAAGCAGACTTTGTGGGGATGCTGACCATCACT 751	872 GTCTCCATCTCCTAATGATAGCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGG 931	1052 TACCGCACTATCCAAGAITTGGCATCGCCACATTCCGAGACTTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG
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1246 CAGGTAGTGGGCCTTTGATGTGTGCCCTGGCTGCCCAACAACATC 1305 1250 AACCACTGGCCTTAGTTGGTGTGGTGTGTGTGTGTGTGTG	1436 CCGGGGCTCTCCCCCCCCCCCCTGCTGGAACCTCGGGGCCTGAACCTCGGGGCCTGAACCTTCGGGGCTCTGGTGCCTCGGGGCCTGAACCTTGGAGGCCTGGAGGCCTGGAACCTTGGGGCCTGAACCTTGGTGCTCCTGGGAGCCTGGAAGGGGACCTGGAACCTTGGTCCTCGAGGCCACCTGGAAGCCATGGAAGCCATGGAACCTTGGTCCTCCAGGCCACCTGGCACCTGGAAGCCAGTGAAGGGAGCCTGGAACCTTGGTTCCTCCCCACCTGGCACCTGGAAGCAGTGAAGGGAGCCTGGAACCTTGCTTCCTCCCCACCTGGCACCTGGAAGCAGTAAGATCAAGGAACCTTGCTTCCCCCCCC	QY 1609 GGCTCTGCCCTGGGCC 1624	ORGANISM Sus scrota Dikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE AUTHORS TITLE Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits JOURNAL TOWN State University Research Foundation, Inc. (US) FRATURES LOCATION STATE LOCATION STA		AVVLETARILIZATOR SALPYVNETGOVGLYSKPDY HLAARQUIYHHLUMNV GEALRQPISCHSCOVGLYSKPDY HLAARQUIYHHLUMNV GEALRQPISCHSCOVGPHETLGEVIDRIVNETQHRLGGVVSLSDILQ ALVLSPAGIDALGA" BASE COUNT 381 a 581 c 535 g 376 t ORIGIN Query Match 69.3%; Score 1142; DB 6; Length 1873; Best Local Similarity 85.8%; Pred. No. 1.2e-252; Matches 1316; Conservative 0; Mismatches 210; Indels 8; Gaps 4;

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KNRTHRLPVLDPVSGAVLHITHKRLLKFLHFGTLLPRPESELYRTYQDLGIGTFRDD.
AVVLETAPILTALDIFVDRYSKALPWBTGQVVGLYSRPDYHLAAQQYVHLDMN
GEALRQRTLCLEGVLSCQPHETLGEVIDNIYREQVHRLVLMDEYQHLLGVVELSDILQ
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0; Mismatches 211; Indels
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AF214520 GI:8215683
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                                                                                                                                                                                                                                                                               1412 TIGGGCGTGGICTCCCTCTCCGACAFCCTTCAGGCACTGGTGCTCAGCCCTGCTGCTGCATC 1471
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                                                                  GCTGCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGGAGAAGCCCTGAGGCAGAGG 1291
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Jannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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Mlan,D., Ocon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-daillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
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/db_xref="taxon:9823"
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DSNTPILDIGJEFGAASAGGBEGLYDERAPPGPSPSPULLPSLGADGEGAPGAVYM
HFWGPHILDIGJEFGAASAGGBEGLYDERAPPGPSPSPULLPSLGAWDGAVYM
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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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Patent: WO 0220850-A 1 14-MAR-2002;
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                          ATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAC
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HFWQEHTCYDAWATSSKLVIFDTWLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
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AVVLETAR ITALDIFVDRRYSALDVNRETGOVGGISREDVHILAAQOTVHILDHN
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reproductive and meat quality traits
Patent: WO 0220850-A 5 14-MAR-2002;
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Novel prkag3 alleles and use of the same as reproductive and meat quality traits Patent: WO 0220850-A 7 14-MAR-2002; IOWA State University Research Foundation, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Score 1138.8; DB 6;
Pred. No. 6.6e-252;
0; Mismatches 212;
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Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G. Novel prkag3 alleles and use of the same as genetic markers reproductive and meat quality traits Patent: WO 0220850-A 9 14-MAR-2002; IOWR State University Research Foundation, Inc. (US)
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REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and Chardon, P. TITLE Variants of the gamma chain of ampk, dna sequences encoding the JOURNAL Patent: Wo 0120003-A 1 22-MAR-2001; INSTITUT NATIONAL DE LA REGHERGHE GORONOMIQUE (INRA) (FR); Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE) REATURES Location/Qualifiers source /organism="Sus scrofa"	/db_xref="taxon:9823" CDS /d21389 /note="unnamed protein product" /codon_start=1 /protein_id="CAC35798.1" /db_xref="d1:13538809" /translation="wHFWDEHTOYDAWATSSKLVIFDTMLEIKKAFFALVANGVRAAP LWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVS	PNDSLFEAVYA TIQDLGIGTER RAQOTYNBLDW HLLGVYSLSDI 583 c 68.9%;	Hest Local Similarity 85.7%; Fred. No. 5.86-251; Matches 1309; Conservative 0; Mismatches 211; Indels 8; Gaps 4; Qy 101 TrCCTAGAGCAAAAACAGCAGCTAGCAGCTAGCAGCTAGCAGCTAGCAGCTAGAA 160 Db 1 TCCTAGAGCAAGAGAGAGCGGTTCATGGCCAACCTGAACCAGCTCAGAA 60	QY 161 AGAATCCGTGGGAAAGCCTAAAGCCTTGAGATGGACAAGGCAGAAGTGGGGGG 220	DD	QY 338 GTGGGCACTCCACCAACAGGTGGGACTGCCTCTGACTGTACAGGTGCA 397 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	458 TGTGAGCTAGAGAGGCCTGCCCCTGCTGCCCCCCCCCCC	DD 418 TTACCCAGGCTGGGATGATGAGCTGCAGAGCCGGGGGCCCAGGTCTACATGCAC 477
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                                                                                                                                                                                                                                                                       Carling, D.
Direct Submission
Submitted (07-FBB-1996) D. Carling, MRC Ciinical Sciences Centre, Submitted (07-FBB-1996) D. Carling, MRC Ciinical Sciences Centre, Department of Molecular Medicine, RPMS, Hammersmith Hospital, DuCane Road, London, MI2 ONN, UK
Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                             gamma
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/function="binds to alpha and beta subunits of AMPK,
forming a heterotrimer"
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                                             1 (bases 1 to 1328)
Woods,A., Cheung,P.C., Smith,F.C., Davison,M.D.,
Berl,R.K. and Carling,D.
Characterization of AWP-activated protein kinase
subunits. Assembly of the heterotrimeric complex
J. Blod. Chem. 271 (17), 10282-10290 (1996)
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APP-activated protein kinase; gamma subunit.
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Rattus norvegicus
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481 AICCACAGGCTICCAGITATIGACCCGGAGICAGGCAACACCITGTACATTCITACTCAC		AAGCGGATCCTCAAGTTCTTTATCACTGAGTTCCCCAAGCCGGAATTCATG	TACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGGTGGTGCTGGAG		ACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCT		GIGGTCAACGAATGTGGGGTCGTCGGGCCTCTATTCCCGCTTTGATGTGATTCACCTG		GCTGCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGGGGAGAAGCCCTGAGGCAGAGG		ACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCCAGAGAGCTTGGGGGAAGTGATC	TCACACTACTTCGAGGGGTTCTCAAGTGCTACTACATGAGGACTCTAGAAGCAATCATC	GACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTC	AATAGACTGGAGGAGGAGGTTCACCGTCTGGTGGTGGTGGATGAACATGACGTGGTG	TTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCA 1457	961 AAGGGATTGTTATGTTGTTGTTGTTGTTGTTGTTGTTGTGTGTGTGTGTGTG
481	992	541	1052	601	1112	661	1172	721	1232	781	1292	841	1352	901	1412	961
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Search completed: June 13, 2003, 04:39:40 Job time: 5204.55 secs

Human pancreatic c Mammalian AMPK-gam Human NS cDNA sequ Disease associated

AAC98774 AAT85927 ABL39755 AAX06882 AAH14839 ABL18857

AAH43684 AAK72740

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Pig AMPK gamma sub Human AMP-activate PRKAG3 intron 2 -Human cDNA differe

AAD03295 ABA08485 AAH43682 ABK84324 Human cDNA sequenc Drosophila melanog PRKAG3 intron 10 -Human immune/haema DNA encoding novel Bovine embryonic g Human polynucleoti Drosophila melanog CDNA sequence #559

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ABL18856
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ABL389333
ABV39323
ABV39323
ABA24907
AAX8874
AAK13463

Human immune/haema DNA encoding novel Human cDNA clone (Human colon cancer PRKAG3 intron 4 - Human secreted pro Pig PRKAG3 gene 5' Pig PRKAG3 gene 5' Human prostate exp Human prostate exp Human breast cell Human foetal liver Probe #3373 for ge

#3398 for ge #3507 used t #3335 used t

ALIGNMENTS

bone marrow

us-09-826-581-5.rng

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June 13, 2003, 01:37:39 ; Search time 598.355 Seconds (without alignments) 6198.732 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss. /*tag= c /label= "T559C" /note= "Silent variation" 1037 /*tag= b /label= "C230G" /note= "Causes P71A" 559 /*tag= d /label= "C1037T" /note= "Causes R340W" Location/Qualifiers 20..1489 /*tag= a /product= "PRKAG3" AAH43685 standard; cDNA; 1647 BP 21-JAN-2002 (first entry) Homo sapiens PRKAG3 CDNA variation variation variation AAH43685; RESULT 1 AAH43685

Sus scrofa PRKAG3
Pig PRKAG3 polymor
Pig AMPK gamma sub
Pig wild-type PRKA
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AAH43685 AAD03320 AAD03296 AAD3321 AAD36457 AAD36456 AAD36458 AAD36459

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PRKAG3 cDNA. Homo Human AMPK gamma s Human AMPK gamma s

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                                                                                                                                                                                                New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                        This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRRAG3). Detecting the presence of the PRRAG3 DNA, or a variant, is useful in determining a risk estimate of a matabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon resulting in the amino acid substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 1037, variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R40W. There may also be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1647; DB 22; Length 1647; larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                   PRKAG3; diabetes, obesity, myopathy; cardiovascular disease, anorectic, genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New variants of the gamma subunit of verlebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                   Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rogel-Gaillard C;
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                                                                                                                                                                                                                        gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                           cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                          "Human complete Prkag3 protein"
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(ANDE/) ANDERSSON L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCACCGGGCTGGAGGCCACATTCCCCAAGACCACACCTTGGCTCAAGCTGATCCTGCC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGTGGGCACTCCACCAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCAGCT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GGGGTGGGCACTCCAACAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCAGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGTGTGAGCTAGAAGGCCTGCTGCAAGAGGCCTGCCCTGTGCCTGTCCCCGCAGGCC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATTTCCCAAGCTGGGATGACGAACTGCGGAAACCCGGCGCCCCAGATCTACATG 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGGATGCTGACCATCACTGAC 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTC 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCATCTCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCCATCAAGAACCGGATC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
heterotrimentc AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGG
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                                                                                                                                                                                                                                                                                                                                                          395 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCCCAGCCACAGAGGCCTGG
                                                                                                                                                                                                                                                                                                                                    155 TCAGAAAGAATCCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCG
                                                                                                                                                                                                                                                    95 ATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC
                                                                                                                                                                                                                                                                                         1 ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                   215 GIGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGICCCCGGICCAGGCCAGCTGCTGAG
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                     Length 2115;
                                                                                                                                                                                                            Indels
                                                                                                                          Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
                                                                                                                                                                   DB 22;
                                                                                                                                                                                                            35;
                                                                                                                                                                 Score 1453; DB
Pred. No. 0;
0; Mismatches
                                                                                                                                                                 88.2%;
97.3%;
                                                                                                                                                                                       sest Local Similarity 97.3 datches 1501; Conservative
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The present sequence is a cDNA encoding human adenosine monophosphate

(MAP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
PRKAG3 whtation in Prkag3 results in an altered regulation of
carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
useful as therapeutic for treating carbohydrate metabolism disorders such
as diabetes, obesity, and disorders associated with muscle metabolism
cuschity, and for restoring a normal AMPK function. PRKAG3 sequence
activity, and for restoring a normal AMPK function. PRKAG3 sequence
condition, genetic testing and prognosis of a metabolic disorder,
cretrably a carbohydrate metabolism disorder. Primers that can detect
condition genetic testing and prognosis of a metabolism resulting
cretrably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting adysiunction of carbohydrate metabolism resulting
crown the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a
heterotrimeric AMPK consisting of PRKAG3 or a
conding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
a person conding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
a person conding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
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a person conding PRKAG3 is useful for the conding prace of the conding prace of the conding prace of the conding prace of the conding the first cystathione beta synthase (CBS) domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGGGGAGCCACCAGGTCAGGGGAAGGTCCCCGGTCCAGGCCAGCTGCTGAGTCCACC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GAAGGGAGCCACCAGGTCAGGGGAAGGTCCCCGGTCCAGGCCAACTGCTGAGTCCACC 180
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                                                                                                                                                                                                                                                                                                                                                                             New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 TTCCTAGAGCAAGAAACAGCAGCTCATGGCCCATCACCAGCTGTGACCAGCAGCTCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTCCTAGAGCAAGAAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCTCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 AGAATCCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 GGCACTCCACCAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCAGCTGCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 GGCTGGAGGCCACATTCCCCAAGACCACACCTTGGCTCAAGCTGATCCTGCCGGGGTG
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                                                                                                                                                                                                                                                  Rogel-Gaillard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
                                                                                                                                                                                                                                                Looft C, Kalm E, Milan D, Robic A, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1447; DB 22;
Pred. No. 0;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRKAG3 and is useful in gene therapy.
                                                                                                                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Fig 2; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.9%;
97.3%;
                       2000WO-EP09896
                                                                    99EP-0402236
                                                                                         18-MAY-2000; 2000EP-0401388
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                                                                                                                                                                                                      KALM E.
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                       11-SEP-2000;
                                                                    10-SEP-1999;
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Human; gamma subunit; adenosine monophosphate-activated kinase; AWPK; strKRG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbolydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                CGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACA
                                                                                                                                                         GCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTG
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diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRK4G3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting
                                                                                                                                                                                                                                                             Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; RKMG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbolydrate netabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
            The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle specific isoform, PRKAG3 splice variant DNA. PrkaG3 gene is located in the RN locus of chromosome 15. Mutation in PrkaG3 seults in an allered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rogel-Gaillard
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Le Roy P, Chardon P;
                                                                                      Treasserrerascerrecaaaarrscerrecer 1530
                                                              TTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGCCT 1637
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                                                                                                                                                                                                                                      Sus scrofa PRKAG3 splice variant DNA
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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(ANDE/) ANDERSSON
(LOOF/) LOOFT C.
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18-MAY-2000;
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from the expression of a functionally altered allele of PRKAG3.
Transpente animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy. Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other; 8 × 8 8 8 8 8 8 8 8

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172 168 228 232 288 292 ACCCCTTCCTGGAGCAGCCTTGGGGGTTCTGAGCATCAGAGATGAGCTTCCTAGAGCAA ACTCCCTCCTGGAGCAGCCTCGGGGGACCTAAGCATCAAGAGATGAGCTTCCTAGAGCAA AAACGCAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCA CCAGGTCAGGGGGAAGGTCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGGCTGCAGGCC Gaps DB 22; Length 2022; .; 8 Score 1172.8; DB 22; Lengt. Pred. No. 5.2e-296;); Mismatches 217; Indels 0; 71.2%; 85.7%; Query Match 71.2' Best Local Similarity 85.7' Matches 1351; Conservative 173 169 229 233 109 53 113

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ACATTCCCCAAGACCACACCCTTGGCTCAAGCTGATCC---TGCCGGGGTGGGCACTCCA 583 293

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TCTGACATCCTTCAGGCTCTGGTGCTCAGCCCTGGAATTGATGCCCTCGGGGCCTGA 1545 TCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCCTGA 1489 CTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAAAACGCCTGCTCAAGTTC 1310 GTCCTTTCCTGCCAGCCCCACGAGGAGCTTGGGGGAAGTGATCGACAGGATTGCTCGGGAG CAGGTACACACGCTGGTGCTAGTGGACGAGGACCCAGCATCTCTTGGGCGTGGTCTCCCTC GAAGATCTGAGTCCTCAATCCCAAGCCACCT-GCACACCTGGAAGCCAATGAAGGGAACT GGAGAACTCAGCCTTCATCTTCCCCCACCCCCATTTGCTGGTTCAGCTATGATTCAGGTA 1070 TIGGGCATCGGCACATTCCGAGACTIGGCTGTGGTGCTGGAGACAGCACCCATCCTGACT GCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGGT CAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCCAGCAAACCTAC AACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGGACACTATGTCTGGAGGGA GGCICTGCCCTGGGCC 1624 1246 1549 1006 1010 1066 1130 1186 1190 1250 1306 1366 1370 1430 1486 1490 1546 1605 1609 950

ВP AAD36457 standard; DNA; 1873 (first entry) 09-AUG-2002

GGCTCCGCCGGGGCC 1680

1665

AMP activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP; PRKAG3 polymorphic variant DNA (PRKAG3-30) Pig

ds.

dene;

Sus scrofa.

/standard_name= "Single nucleotide polymorphism (SNP)" PRKAG3 polymorphic variant (PRKAG3-30) Location/Qualifiers "Pig 1 (88) /*tag- a /product= " replace (89 1395 /*tag= variation

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                                                                                                                                                                                                                                                                                                                                                kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
                                                                                                                                                                                                         Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                   those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein.
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                                                                                                                                                                                                                                                                                        invention relates to a method for screening animals to determine
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Pred. No. 5.6e-288;
0; Mismatches 210;
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85.8%;
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2001US-260239P.
2001US-299111P.
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                                                                            08-SEP-2000;
08-JAN-2001;
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ŏ g ŏ οp οž g QΥ a Q a δ g ŏ 셤 ð 360 120 300 451 417 154 214 331 391 9 TCAGAAAGAATCCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCG GTGGAGGAAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCCAGGCCAGGTGGTGAG TCCACCGGGCTGGAGGCCACATTCCCCAAGACCACACCTTGGCTCAAGCTGATCC---T GCCGGGGTGGGCACTCCACCAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCA GCCGAGGTGGACAACCCCCCAACAGAGGGGGACATCCTCCCCTCTGACTGTGCAGCCTCA GCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCCCAGCCACAGAGGCC GCCTCCGACTCCAACACACACCATCTGGATCTGGGCATAGAGTTCTCAGCCTCGGCGCGC TCGGGGGATGAGCT - - TGGGCTGGTGGAAGAAGCCAGCCCCGTGCCCATCCCCAGAG GIGCIGITACCCAGGCTGGGCTGGGATGATGAGCTGCAGAAGCCGGGGGCCCAGGTCTAC TGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAGGCCTGCCCTGTGCCTGTCCCCGCAG GCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAAAACCCGGCCCCAGATCTAC ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC Best Local Similarity 85.8 Matches 1316; Conservative 95 512 418 452 361 155 61 215 275 181 332 241 392 301 q g à qq ò ò ò g à 엄 ŏ g οy qq ò

1017 1171 1317 1437 1590 1111 1077 1291 1197 1377 1051 1351 1352 GACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTC 1411 1412 THGGGCGHGGHCHCCCHCTCCGACAHCCTTCAGGCACHGGHGCTCAGCCCHGCTGGCATC 1471 957 691 897 751 657 811 717 871 777 837 991 931 ATCCACCGCCTGCCGGTCCTGGACCTGTCTCCGGGGCTGTGCTCCACATCCTCACACAT 1318 CIGGGGGGGGGGGGCCTCCCTCTCAACATCCTTCAGGCTCTGGGGGCGCTCAGCCCTGCTGGAATT ATGCACTTCATGCAGGAGCACACCTGCTACGATGCCATGGGGACCAGCTCCAAACTGGTC GAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG ATCCATCGCCTGCTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAC 1052 TACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGGAG GTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTG 1292 ACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGGCCCCACGAGAGGTTGGGGGAAGTGATC 1472 GAIGCCCTCGGGGCCTGAGAAGAICTGAGICCTCAATCCCAAGCCACCT-GCACCTGG ATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTG CGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGGATGCTGACCATCACT GACTICATCCIGGIGCIGCATCGCIACIACIACAGGICCCCCCCTGGICCAGAICTAIGAGAIT GTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGG GCTGCCCAGCAAACCTACAACCTGGACATGAGTGTGGGGAGAAGCCCTGAGGCAGAGG AAGCCAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCCACCCCATTTGCTGGT TCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCC 1624 CTGGCTCTTGTTCAGGTAGGCTCCGCCCGGGGCC 1438 1591 1497 1172 1232 1531

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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMFK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Perkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic eating and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                                                      Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rogel-Gaillard C;
                                                                                                        complete PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated with energy metabolism such as diabetes, obesity, and
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J, Le Roy P, Chardon P;
                                                                                                        Pig AMPK gamma subunit muscle-specific isoform,
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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                                                                                                                                                                                                                                                                                      Location/Qualifiers
AAD03319 standard; cDNA; 1873 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-2000; 2000WO-EP09896.
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18-MAY-2000; 2000EP-0401388.
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Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

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                                                                 ATGAGCTICCTAGAGCAAGGAGAGAGCCGTTCATGGCCATCCCGAGCTGTAACCACCACCACC
                                                                                                                                                   GIGGAGGAAGGGGAGCCACCAGGICAGGGGGAAGGICCCCGGICCAGGCCAGCIGCIGAG
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 Length 1873;
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 22;
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 Score 1140.4; DB 2. Pred. No. 1.5e-287;
                          0; Mismatches
69.2%;
85.7%;
             Best_Local Similarity 85.7
Matches 1315; Conservative
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                                                                                            GCTGCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAAAGG 1291
                                                                                                                       ACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGGGAAGTGATC 1351
                                                                                                                                           ACACTGTGTCTGGAAGGCGTCCTTTCCTGCCAGGCCCACGAGACCTTGGGGGAAGTCATT 1257
                                                                                                                                                                                   GACCGGATTGTCCGGGAACAGGTGCACCGCCTGGTGCTGGATGAGACCCAGCACTT 1317
ACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCT 1171
                                       GTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTG 1231
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                                                                                                                                                               GACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMP activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
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replace (89, C)
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/standard_name~ "Single nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pig wild-type PRKAG3 gene.
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                                                                                                                                                                                                                                                                                           Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for screening animals to determine
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85.7%; Pred. No. 1.5e-287;
ive 0; Mismatches 211;
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                                                                                                                                  (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Fig 1; 109pp; English.
                                     2000US-231045P.
2001US-260239P.
2001US-299111P.
                                                                                                                                                                               Rothschild MF, Ciobanu DC,
10-SEP-2001; 2001WO-US28283
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Best Local Simi
Matches 1315;
                                                                    08-JAN-2001;
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                                                  598 CGAGCGGCACCTTTGTGGGACAGCAAGAAGCAGAGCTTCGTGGGGATGCTGACCATCACA
                                                                                   GACTICATCITGGIGCIGCACCGCTATIACAGGICCCCCTGGICCAGAICTACGAGAIT
                                                                                                   GAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG
                                                                                                                                     GTCTCCATCTCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGG
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                 ATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCCCTGGTGGCCAACGGCGTC
                                  CGGGCAGCCCCTCTATGGGACAGCAGAAGCAGAGCTTTGTGGGGGATGCTGACCATCACT
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AAD36458 standard; DNA; 1873 BP

RESULT 8 AAD36458

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 ATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 TCAGAAAGAATCCGTGGGAAACGGAGGGCCCAAAGCCTTGAGATGGACAAGGCAGAAGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGAGCTTCCTAGAGCAAGGAGAGCCGTTCATGGCCATCCCGAGCTGTAACCACCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                            polymorphic variant (PRKAG3-52)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                             AMP activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP; gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
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                                                         PRKAG3 polymorphic variant DNA (PRKAG3-52)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 34; Page 93-95; 109pp; English.
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    /*tag-
/product= "Pig ...
replace (154, A)
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2001; 2001WO-US28283
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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P-PSDB; AAE22986.
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18-JUN-2001;
   09-AUG-2002
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Matches 1314;
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                                                                                                                                                                                                                                    Sus scrofa
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polymorphic variant (PRKAG3-199)"
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                                                                                                                                                             1438 AAGCCAGTGAAGGGAGC-CGTGGACTCAGCTCTCCCCTCAGCCCCAGTGATGCTGGT
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GACCGGATTGTCCGGGAACAGGTGCACCGCCTGGTGCTGGATGAGACCCCAGCACTT
                                             1378 GATGCCCTCGGGGCCTGAGAACCTTGGAACCTTTGCTCTCAGGCCACCTGGCACCTGG
                              TIGGGCGIGGICICCCICTCCGACAICCTICAGGCACIGGIGCICAGCCCIGCIGCAGCAIC
                                                                                      GATGCCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCT-GCACACCTGG
                                                                                                                                              1531 AAGCCAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCACCCCCATTTGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of generic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used
                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase regulatory gamma subunit; PRKAG3 at quality; single nucleotide polymorphism; SNP;
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                                                                                                                                                                                                      1591 TCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCC 1624
                                                                                                                                                                                                                                                                                                                                                                                                (PRKAG3-199).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..1395
                                                                                                                                                                                                                                                                                                                                                                                                PRKAG3 polymorphic variant DNA
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replace (595, A)
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2001US-260239P.
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                                                                                                                                                                                                                                                                                                           AAD36459 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          screening; meat qu
gene; variant; ds.
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18-JUN-2001;
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                                                                       GCCGAGGTGGACAACCCCCCAACAGAGGGGACATCCTCCCCTCTGACTGTGCAGCCTCA 300
                                                                                                    GCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCCCCAGCCCACAGAGGCC 451
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                                            GCCGGGGTGGGCACTCCACCAACAGGGTGGGACTGCCTCCCCTCTGACTGTACAGCCTCA
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
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                                                                                                                                                                                                                    1078 GIGGICAACGAAACIGGACAGGIAGIGGGCCICIACICCCCTITGAIGIGAICCACCIG
                                                                                                                                                                                                                                                            GCTGCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGG
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                                                                                                ACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCT
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for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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0; Mismatches 212; Indels
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CGGCCACCCCTCTATGGACAGCAAGAAGAGCTTTGTGGGGGATGCTGACCATCACT
                            598 CAAGCGGCACCTTTGTGGGACAGCAAGAAGCAGAGCTTCGTGGGGATGCTGACCATCACA
                                                      GACTTCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCCAGATCTATGAGATT
                                                                                                               GAACAACATAAGATTGAGACCTGGAGGCAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG
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                                                                                                                                                                                                                                    The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant DNA (PRRAG3-200).
                                                                                                                                        Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 ATGAGCTTCCTAGAGCAAGAAAACAGCACCTCATGGCCATCACCAGCTGTGACCAGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 1138.8; DB 24; Leus-Pred. No. 3.8e-287;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
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                                                                     Plastow
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                                                                                                                                                                                                               Disclosure; Page 102-104; 109pp; English
                                                                    Malek M,
                                         (IOWA ) UNIV IOWA STATE RES FOUND INC
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85.7%;
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evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
                                              PRÄAG3; diabetes; obesity; myopathy; cardiovascular disease, anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heterotrimeric AMPK consisting of PRARAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the kN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbobydrate metabolism, particularly in skeletal muscle. PKKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                             protein"
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muscle-specific isoform,
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           AGAATCCGTGGGAAACGCAGGGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAG
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                                                                                  GAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCCAGGCCAGCTGCTGAGTCCACC
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Gaps

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Indels

211;

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Best Local Similarity 85.7 Matches 1309; Conservative

Similarity

Query Match

68.9%; Score 1134.4; DB 22; Length 1867; 85.7%; Pred. No. 5.4e-286;

BP; 380 A; 583 C; 529 G; 375 T; 0 other;

Sequence 1867

P-PSDB; ABB11241.

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GIGGICICCCICICCGACAICCITICAGGCACIGGTGCICAGCCCIGCTGGCAICGAIGCC 1477
                                                                                                                                                                                                                                                                         CTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCT-GCACCTGGAAGCCA 1536
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                                                                               CAGCAAACCTACAACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGACACTA 1297
                                                                                                                             TGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAGGCTTGGGGGAAGTGATCGACAGG 1357
1178 AACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCC 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.
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                              1078 AACGAAACTGGACAGGTAGTGGGCCTCTACTCTCGCTTTGATGTGATCCACCTGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine; cell proliferation; cell differentiation;
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157188-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT,
                                                                1238
                                                                                                                             1298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA08485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. The polypeptides, methods of detecting the nucleotides, antibodies against the polypeptides, methods of detecting the nucleotides or to prypeptides of the invention. Although novel, many of the bind to polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell confidence activities; stem cell growth activity; hemmitopolesis receptor or ligand activities; or may be commodulatory activity; tissue growth activity; chemototic or chemokinetic activities; hasmostatic, thrombolytic activities; receptor or ligand activities; or may be conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions are useful disorders (e.g., matching or architical schemmia, bone disorders (e.g., matching are regeneration and conditions and ulcers), while those with cepanic or properties may be used in the treatment of viral, and innal protein in addition in the invention and interva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a CDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness,
                                                        Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel human polypeptide of the invention.
                                                                                                                                                                                      Claim 1; Page 429; 1963pp; English.
                                                                                                                       e.g. arthritis and cancer
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ô 978 ACATCCTCACACACACACAAAGGCCTGCTCAAGTTCCTGCACATTCTTTGGTTCCCTGCTGCCCC 1037 857 9 1 IGCTGACCATCACTGACTTCATCCTGGTGCTGTATCGCTACTACAGGTCCCCCCTGGTCC 738 TGCTGACCATCACTGACTTCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCC GCTTCAAGCCTCTGGTCTCCATCTCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCC TCATCAAGAACCGGATCCATCGCCTGCTCTTGACCCGGTGTCAGGCAACGTACTCC Gaps ö 22; Length 547; Indels .5e-107; DB 0; Mismatches Score 448.8; Pred. No. 3.5 27.2%; Conservative Similarity Matches 450; 61 828 918 Query Match Local g Š g δy g δλ ă 셤 à

Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;

1038 GGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGG 1097

ACATCCTCACACACAAAGGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCC

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G for a C at nucleotide 320, resulting in the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENE LOGIC INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                          in intron 6.
                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2002
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                         CIGIGGIGCIGGAGACACCCATCCIGACIGCACIGGACATCTTIGIGGACCGGCGIG 1157
                                 GGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                         Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
The sequences given in AAH43681-84 represents genomic fragments encoding the human AAP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk setimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of
                                                                                                                                                                                                                                                                                                                                                                          /number= "Intron 4"
/note= "5' portion of intron 4"
                                                                                                                                                                                                                                                                      intron 2"
                                                           1158 TGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1189
                                                                    /note= "3' portion of
22..177
                                                                                                                                                                                                                                                                                                               c
r= "Intron 3"
                                                                                                                                                                                                                                                             "Intron 2"
                                                                                                                                                                                                                                    .ocation/Qualifiers
                                                                                                                                                                                                                                                                                           /number="Exon 3"
178.541
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                /number= "Exon 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-2000; 2000US-195665P
                                                                                                                                                                        PRKAG3 intron 2 - intron 4.
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                                                                                                                                                                                                                                                                                                                                                         946..989
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                                                                                                                       AAH43682 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                    WO200177305-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson L,
                                                                                                                                                        21-JAN-2002
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                                                                           421
                                                                                                                                       AAH43682;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 CCTCCCCTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACGGAGTTCCCAGCCACACAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACGGAGTTCCCAGCACAGAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAG 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 GCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACCACCTGCTACGATGC 606
substitution P71A; in exon 4 variation may be a substitution of a for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                              247 AGGTCCCCGGTCCAGGCCAGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 CACACCCTTGGCTCAAGCTGATCCTGCCGGGGTGGGCACTCCAACAACAGGGTGGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTTCCCCAAGCTGGGCTGGGATGACGAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATGCCAACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA differentially expressed in granulocytic cells #895.
                                                                                                                                                                                                                                       DB 22; Length 989; 2e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                               Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                    Score 407.2; D. Fred. No. 3.2e-'0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK84324 standard; cDNA; 1578
                                                                                                                                                                                                                                       24.78;
99.38;
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Best Local Similarity 99.37
Watches 409; Conservative
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1286

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TGATCGACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGC 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGGACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGGGAAG 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATCAACAGGCTAGTGGAAGCAGAGGTTCACCGACTTGTAGTGGTGGATGAAATGATG 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTC 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCGATCACATTACTTTGAGGGTGTTCTCAAGTGCTACCTGCATGAGACTCTGGAGACCA 956
                                                                                                                                   657 TCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1227 ACCTGGCTGCCCAGCAAACCTACAACCAGCTGGACATGAGTGTGGGAGAAGCCCTGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis; identification; cytostatic; neuroprofective; noncotropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic;
                                          ACCGGATCCATCGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA
                                                                                                                                                                                                CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCCT
                                                                                                                                                                                                                                                                                                                                                                           1107 TGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                       717 GCACTACCACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC
                  CTCTGGTCTCCATCTCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCTCATCAAGA
                                                                                                                                                                                                                                          597 CCCACAAGCGCATTCTGAAGTTCCTCAAATTGTTTATCACTGAGTTCCCCAAGCCAGAGT
                                                                                                                                                                                                                                                                                      TCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1017 TGGTCAAGGGAATTGTATCACTGTCTGACATCCTGCAGGCCCTGGTGTC 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1407 ATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCA 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreatic cancer; pancreatic cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC98774 standard; cDNA; 1691
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                                                                                                                                                                                                ò
                                                                                                                                                                                                                                   The invention relates to detecting (MI) granulocyte (GC) activation

(GCA), by detecting the level of expression of gene(s) (GS) identified by

(GCA), by detecting the level of expression of gene(s) (GS) identified by

(DNA chip analysis as given in the specification, and comparing

(DNA chief analysis as given in the specification, and comparing

(CC, where differential expression level in an unactivated

(CC, where differential expression of GS is indicative of GCA.

(Also included are modulating (M2) GA by contacting GC with an agent

(CC that alters the expression of at least one gene in GS; (2) screening (M3)

(CC that capable of modulating GCA or an inflammation (especially

(CC thronic) in a tissue, an allergic response in a subject, exposure of a

(CC subject to a pathogen or sterile inflammatory disease using the

(CC subject to a pathogen or sterile inflammatory disease, by detecting the

(CC subject to a pathogen or sterile inflammatory disease, by detecting the

(A) treating (MS) an inflammatory disease, by detecting the

(A) treating (MS) an inflammatory disease, by contacting a tissue having

(CC sterile inflammatory disease, by contacting a tissue having

(CC sterile inflammatory disease, by contacting a tissue having

(CC preferably in an inflammation in a tissue; M is useful for

(CC preferably in an inflammation in a tissue; M is useful for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACTGATTTCATCAATATCCTGCACCGCTACTATAAATCAGCCTTGGTACAGATCTATG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGC 626
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                                                                                    differential expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part
                                                                                 Detecting granulocyte activation by detecting differential expressic of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
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Vockley J;
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0; Mismatches
Yamaga S,
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                                                                                                                                                                                                Claim 1; SEQ ID No 895; 114pp; English.
Weissman SM,
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65.1%;
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Matches 580; Conservative
                                            WPI; 2002-435328/46.
Beazer-Barclay Y,
                                                                                                                                                        drug toxicity
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WPI; 2000-579444/54.

DR P-PSDB; AAB54009.

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New nucleic acid that is a pancreatic cancer antigen for preventing, pertracting a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition reacting, or ameliorating a medical condition, particular pancreatic cancer antigens, given in AAB54008 to AAC99231 encode the human pancreatic cancer antigens, given in AAB54008 to proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens, given in AAB54008 to cancer antigens, and can be used consurportective, nootropic, immunomodulacry, relaxant, contraceptive, cancer cancer antigens and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating and proteins can be used for confision or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the conferce antigens can be identified. The pancreatic cancer antigens can be used to design nucleic detect, treat or prevent pancreatic cancer antigens can be used to generate antibodies cand diagnostic methods. The proteins can be used to generate antibodies and bushoost tile methods. The proteins can be used to generate antibodies cand diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including continent of the proteins can be used to prevent neces to generate antibodies continents can be used to prevent neces or prevent neural, immune system, muscular, cerproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, necessaries and in the exemplification of the present invention.
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) Sequence 1691 BP; 458 A; 382 C; 401 G; 449 T; 1 other;

Query Match 23.9%; Score 393.4; DB 21; Length 1691;

Best Local Similarity 65.1%; Pred. No. 1.6e-92;

Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps

CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCCCGGCCCTCCT 1046 1047 TCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACTTCCGAGACTTGGCTGTGGTGC 1106 123 TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 182 302 ACCEGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA 986 567 TCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGC 626 627 TAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACG 686 687 GTGTGCGGGCAGCCCTTTATGGACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCA 746 TCACTGACTICATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCCAGATCTATG 806 AGATTGAACAACATAAGATTGAGACCTGGAGGGGGAGATCTACCTGCAAGGCTGCTTCAAGC 866 363 AGCTAGAAGAACACAAGATAGAAACTTGGAGAGGGGGTGTATCTCCAGGACTCCTTTAAAC 422 CTCTGGTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCTCTCATCAAGA 926 423 CGCTTGTCTGCATTTCTCCTAATGCCAGCTTGTTTGATGCTGTCTCTTCATTAATTCGGA 482 ACAAGATCCACAGGCTGCCAGTTATTGACCCAGAATCAGGCAATACTTGTACATCCTCA 542 543 cccacaagcgccarrcreaagrrccrcaaarrgrrrarcacrgagrrccccaagccagagr 602 Gaps 580; Conservative 183 303 483 284 747 807 867 927 Matches q ŏ g òγ g ŏ g a qq à g òχ g δŻ δy δ

	963 IGGTCAAGGGAAITGTATCACTGTCTGCACGCCCTGCTGCTCTA 1013		qq
	1407 ATCICTIGGCGIGGTCTCCCTCTCCGACAICCTICAGGCACIGGTGCTCA 1457		Ωÿ
862	903 TCATCAACAGGCTAGTGGAAGCAGAGGTTCACCGACTTGTAGTGGTGGATGAAATGATG 962		đ
1406	1347 IGAICGACAGGAITGCICGGGAGCAGGTACACAGGCIGGTGCIAGTGGACGAGACCCAGC 1406	1347	ΩŽ
902	843 ATCGATCATTACTTTGAGGGTGTTCTCAAGTGCTACCTGCATGAGACTCTGGAGACCA 902	843	合
1346	1287 AGAGGACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAGGTTGGGGGAAG 1346	1287	Qy
842		783	q
1286	1227 ACCIGGCCGAGCAAACCIACAAACCACCTGGACAIGAGTGTGGGAAAGCCCIGAGGC 1286	1227	QY
782		723	đ
1226		1167	Qγ
722	663 GCACTACCACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC 722	663	qq
1166	TGGAGACAGCCATCCTGACTGCACTGGACATCTTTGTGGACGGGCGTGTCTGCAC 1166	1107	Qy
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Search completed: June 13, 2003, 02:59:53 Job time : 601.355 secs

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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-230-371A-20
US-09-165-863-45
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US-09-500-569-15
US-08-728-323A-1
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US-08-142-368A-13
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US-09-130-114-2
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28 38 2.3 2531 3 US-08-967-727-13 Sequence 13, Appl 30 38 2.3 11495 4 US-08-037-230D-13 Sequence 13, Appl 31 37.8 2.3 11495 4 US-09-056-105-9 Sequence 1, Appl 32 37.8 2.3 44135 4 US-09-103-840A-2 Sequence 1, Appl 33 37.8 2.3 44135 4 US-09-103-840A-2 Sequence 1, Appl 33 37.8 2.3 44135 4 US-09-103-840A-2 Sequence 1, Appl 33 37.8 2.2 44135 4 US-09-103-840A-2 Sequence 1, Appl 36 8 2.2 1926 4 US-09-103-840A-1 Sequence 2, Appl 36 8 2.2 2580 4 US-09-20-855A-2 Sequence 2, Appl 37 36 8 2.2 2580 4 US-09-39-081-2 Sequence 2, Appl 37 36 8 2.2 2580 4 US-09-39-081-2 Sequence 1, Appl 37 36 8 2.2 2600 4 US-09-620-95-1 Sequence 1, Appl 37 36 8 2.2 10596 1 US-08-910-647-1 Sequence 1, Appl 36 8 2.2 10596 1 US-08-081-15 Sequence 15, Appl 36 8 2.2 10596 1 US-08-081-15 Sequence 15, Appl 36 8 2.2 10596 1 US-08-081-15 Sequence 15, Appl 36 8 2.2 10596 2 US-08-194-088-15 Sequence 15, Appl 36 8 2.2 10596 2 US-08-194-088-15 Sequence 15, Appl 36 8 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2.2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2 2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2 2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2 2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2 2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2 2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2 2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2 2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2 2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9 2 2 10596 5 PCT-US93-04648-15 Sequence 15, Appl 36 9
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Gaps
Sequence 63, Application US/09101146
Patent No. 6124125
GENERAL INFORMATION:
APPLICANT: Darfmouth College, St. Vincents Institute of APPLICANT: Medical Research, Remp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: THE PROBLEM WINDOWS 95
COMPUTER: THE PROBLEM WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,146
FILING DATE: OCTODER 7, 1998
CLIASSIFICATION AND 1996
FILING DATE: B JAN 1996
FILING DATE: B JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
RESISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC-0050
TELECOMMUNICATION INFORMATION:
TELECOMMUNI
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64.9%; Pred. No. 2.1e-93;
ive 0; Mismatches 313;
                                                                                                                                                                                                                                                                                                                                                                                                      E: Jane Massey Licata, Esq.
66 E. Main Street
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 64.9°
Matches 578; Conservative
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TYPE: Nucleic acid
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No
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US-09-101-146-63
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567 TCTACATGCGCTTCATGCAGGAGCACCACCTGCTACGATGCCATGGCAACTAGCTCCAAGC

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CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCCTCCT 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%; Score 366.6; DB 362.9%; Pred. No. 3.3e-87;
                                                                                                                                                                                   SOFTWARE: FASTSEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                PF-0321
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Lucy J J
36,749
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                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1435 base pairs
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                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucres REGISTRATION NUMBER:
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LIBRARY: PENITUT01
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NUMBER OF SEQUENCES:
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                                                            Palo Alto
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                                                                                                         94304
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                                                         CITY: PA
STATE: C
COUNTRY:
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                                                                                            GIGIGCGGCCACCCCTCTAIGGACACCAGCAGAAGCAGAGCITIGIGGGGAIGCIGACCA 746
                                                                                                           TCACTGACTTCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCCAGATCTATG 806
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TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 235
                                               ACCGGATCCATCCCTGCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA
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Patent No. 5885803
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APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
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APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goll, Surya K.
APPLICANT: Shah, Purvi
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08-878-989-14
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APPLICANT: Guegler, Karl G.
APPLICANT: Gold, Surya K.
APPLICANT: Shah, Purva K.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09272796
Patent No. 6207148
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STATE:
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987 CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCCT 1046
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Pred. No. 3.3e-87;
0; Mismatches 334;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                         INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
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62.9%;
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                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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CLONE: 1452972
                                                                                                                                                                                                                  linear
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1104 TGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTG 1163
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APPLICANT: KIPPS, THOMAS J.
APPLICANT: WI, YUNG.
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT FILING DATE: 1998-04-06
EARLIER FILING DATE: 1998-04-06
MUMBER OF SEQ. ID NOS: 35
NUMBER OF SEQ. ID NOS: 35
SOFTWARE: FASTERO for Windows Version 3.0
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Pred. No. 0.3
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Patent No. 6287569
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Best Local Similarity 44.7%;
Matches 160; Conservative
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ORGANISM: Homo sapiens
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US-08-232-463-14/c
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US-09-056-105-8
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963 TCGTGGACAGAATAGTAAGAGCTGAGGTCCATCGCTGGTGGTGGTAAATGAAGCAGATA 1022
                                     1407 ATCICITGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTG 1466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHETELINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLEOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, SLEPHEN A.
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)863-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
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CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                                                              Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                          Foley & Lardner
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MEDIUM TYPE: Floppy disk
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LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ADDRESSEE: Foley & La
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FILING DATE: 26-AUG
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ZIP: 22313-0299
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TELEFAX: 6/v
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                                                                                                                                                                                                            RESULT 4
US-08-232-463-14
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; Sequence 14, Application US/08299849B; Patent No. 5612201; GENERAL INFORMATION:
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Best Local Similarity 44.4%;
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STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                   Matches 159; Conservative
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CORRESPONDENCE ADDRESS:
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STATE: New
7 10022
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                                                                                                                                                                                                                                                               LENGTH: 1022
 JS-09-056-105-18
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                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTTGAGATGGACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 GGGCTGGCCACATGGAGCCCGGGCTGGAGCACGCACTGCGCAGGACCCCTTCCTGGAGC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103; Indels
                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                             GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPAN: (703)883-4109
TELERA: 899140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.4%; Score 40.2;
4.5%; Pred. No. 0.5
                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORIEY/AGENT INFORMATION:
NAME: BENT, SLEPHEN A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 GGTCCCGGTCCAGGCCAGCTGCTG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP 91 114 300.6
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 14, Application US/08232463 Patent No. 5670367
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TELEFAX: 899149
; INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
"YPE: nucleic acid
"YPE: nucleic acid
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                                                                                                                                                                                            STATE: VA
COUNTRY: USA
21P: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-232-463-14
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479 GAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTC 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      539 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACAC 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANN: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANN: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          673 TCTGGTGGCCAACGCTGTGCGGGCAGCCCCTCTATGGGACAGCAGAAGCAGAGCTTT 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1022;
Sequence 18, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
APPLICANT: KIPES, THOMAS J.
APPLICANT: WU, YUNJ
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR;
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER PILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
COFTWARE FEASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39.6; DB 4;
Pred. No. 0.38;
0; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM
OPERATING SYSTEM; PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
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978 TCATITICIGCICCGCAAGIATCGAGCCAAGGAGCIGGICACAAAGGCAGAAAIGCIGGA 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            553 ACCCGGCCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              858 CACTIGCIGGAGGCAACCCAAIGAGGGIICCAGCAAGAAGAAGAGGAGGGGCCAAGCAC 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493 CCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGGTTGAGGAACTGCGGAA 552
  APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Taversari, Catia TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor TITLE OF INVENTION: Rejection Antigens and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.4%; Score 39.6; DB 2; Length 2531; Best Local Similarity 44.4%; Pred. No. 0.54; Matches 159; Conservative 0; Mismatches 199; Indels 0
                                                                                                                                                                                                                                                                                                                                                                 Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: LUD 5253.4-US TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 07-807,043
FILING DATE: 12-DECEMBER-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATONEY/AGENT INFORMATION:
NAME: Hanson, No. 525729ma D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                               E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2531 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MAGE-41 gene
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                                                                                                                                        NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                     CITY: New York City
STATE: New York
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-142-368A-14
                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          553 ACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGC 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.4%; Score 39.6; DB 1; Length 2 Best Local Similarity 44.4%; Pred. No. 0.54; Matches 159; Conservative 0; Mismatches 199; Indels
                                                                                                                                                                                                                                                                PRIOR AFFILICATION DATA

FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATPORNEY AGENT INFORMATION:

REGISTRANCY DATE: 30,946
RESTERRENCE/DOCKET NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRANCY (212) 688-9200
TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 688-9200
TELEPRONE: (212) 688-9804
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARRACTERISTICS:

LENTH: 2531 base pairs
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 435
                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/US92/04354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08142368A Patent No. 5925729 GENERAL INFORMATION:
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
                                                                                                                                                                                                                        FILING DATE: 22-MAY-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MAGE-41 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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Sequence 14, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                          978 ICATITICIGCICCGCAAGIAICGAGCCAAGGAGCIGGICACAAAGGCAGAAAIGCIGGA 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1098 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACTACAC 1157
                                                   433 GTTCCCAGCCACAGAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAGGGCCTGC 492
                                                                                                                                                                                                                          918 CTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCCAGTAACAAGGTGGATGAGTTGGC 977
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373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGGAGCTGGCCACGGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    673 TCTGGTGGCCAACGGTGTGCGGCCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTT 730
                                                                                                                                                                                                                                                                                                      493 CCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 26-MARCH-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: PCT/US92/04354
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 12-MAY-1992
PRIOR APPLICATION DATE: 12-MAY-1991
PRIOR APPLICATION DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATE: 12-DECEMBER-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hanson, No. 6235525man D. REGISTRATION NUMBER: 30,946
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FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
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STREET: 805 Third Avenue
CITY: New York City
STATE: New York
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OPERATING SYSTEM: PC-DOS
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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APPLICANT: Gaugler, B atrice: Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                   1098 cergaagargareririgecarrgacgrgaaggaagrggaceecaccaggaagaceracca
613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672
                                                                                                                                                                                               673 TCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGAAGAAGCAGAGCTTT 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.4%; Score 39.6; DB 3; Best Local Similarity 44.4%; Pred. No. 0.54; Matches 159; Conservative 0; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/087,043
FILING DATE: 12-DECEMBER-1991
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PRIOR APPLICATION DATA: PAPLICATION NUMBER: 07/72R PRIOR PRIOR APPLICATION NUMBER: 07/72R PRIOR A
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REFERENCE/DOCKET NUMBER: LUD 535
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
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PRIOR APPLICATION DATA:
FILING DATE: 9-JULY-1991
PRIOR APPLICATION NUMBER: 07/705 707
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08967727
Patent No. 6025474
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STREET: 805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: qenomic DNA
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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978 TCATITICIGCICCGCAAGTAICGAGCCAAGGAGCTGGTCACAAGGCAGAAATGCTGGA 1037
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                                                                                                                                                                                                                                                                                                   373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGA 432
                                                                                                                                                                                                                                                                                                                                  553 ACCCGGCCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGC 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           673 TCTGGTGCCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTT 730
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                                                                                                                                                                                                                           Length 2531;
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CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFWWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                       Query Match 2.4%; Score 39.6; DB 4; Best Local Similarity 44.4%; Pred. No. 0.54; Matches 159; Conservative 0; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.4%;
Best Local Similarity 44.4%;
Matches 159; Conservative
INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 2531 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                              ; NAME/KEY: MAGE-41 gene US-08-037-230D-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KIPPS, THOMAS J. APPLICANT: WU, YUNQI
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493 CCTGTGCCTGTCCCCGCAGGCCCCRTTTCCCAAGCTGGGGTGAGGAACTGCGGAA 552
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APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT PILING DATE: 1998-01-14
EARLIER PLILING DATE: 1997-01-27
EARLIER PLILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
SEARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09007005B Patent No. 6258558 GENERAL INFORMATION:
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US-09-244-796-17/c
; Sequence 17, Application US/09244796
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US-09-007-005-17/c
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LENGIH: 289
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954 ACCCGGTGTCAGGCAACGTACTCCACATCCTCACACACAAAACGCCTGCTCAAGTTCCTGC 1013
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APPLICANT: Dietrich, Paul S.
APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: TAND USES
FILE REPERENCE: R0043B-RBG sequence listing
CURRENT PILING DATE: 1994-09-23
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT APPLICATION NUMBER: US/09/404,650
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 12
SEQ ID NO 1
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                 GENERAL INFORMATION:
APPLICANT: SCOSTAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS
FILE REFERENCE: 00786/350007
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFUND NOT: PASTSEQ for Windows Version 4.0
: SEQ ID NO 17
LENGTH: 289
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; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA ORGANISM: Artificial Sequence
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; LOCATION: (192)..(6716)
US-09-404-650-1
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ORGANISM: Homo sapiens
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Patent No.
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Query Match 2.4%; Score 38.8; DB 4; Length 6816; Best Local Similarity 47.5%; Pred. No. 1.3; Matches 115; Conservative 0; Mismatches 127; Indels 0
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sequence 3, Applisequence 70, Applisequence 559, Applisequence 5373, Applisequence 11098, A Sequence 2182, Applisequence 2472, Applisequence 2472,
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Sequence 16257, A
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4579.068 Million cell updates/sec
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/cgn2_6/ptodata//pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata//pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata//pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata//pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata//pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata//pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata//pubpna/USO8_REW_PUB.seq:*
/cgn2_6/ptodata//pubpna/USO8_REW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-198-846-2472
US-09-826-581-1
US-09-918-995-16257
US-09-864-761-693
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US-09-783-590-11098
US-09-864-761-20146
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US-10-184-634-332
US-09-983-965-2114
US-10-123-155-10
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US-09-925-297-2

US-09-925-297-2

US-09-826-581-4

US-08-826-581-3

US-10-108-605-70

US-09-822-846-559
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 & FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US/09/826,581
PRIOR APPLICATION NUMBER: 10 60/195,665
PRIOR FILING DATE: 2000-04-07
                  Sequence 18, Appl.
Sequence 17, Appl.
Sequence 20, Appl.
Sequence 114, Appl.
Sequence 114, Appl.
Sequence 395, Appl.
Sequence 402, Appl.
Sequence 402, Appl.
Sequence 402, Appl.
Sequence 346, Appl.
Sequence 346, Appl.
Sequence 1713, Appl.
Sequence 1, Appl.
Sequence 1, Appl.
Sequence 1, Appl.
Sequence 41, Appl.
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      Sequence
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DB 10;
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                Sequence 5, Application US/09826581 Patent No. US20020142310A1 GENERAL INFORMATION:
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; LOCATION: (20)...(1486)
US-09-826-581-5
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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    4444460000000000000000000000000000000
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Best Local Simi
Matches 1647;
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GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Db 1261 CATCAGTGTGGGAGAAGCCTGAGGGACACTATGTCTGGAGGGACTTTCCTG 1320	RESULT 2 US-09-826-581-2 Sequence 2, Application US/09826581 Sequence 2, Application US/09826581 Patent No. US20020142310A1 GENERAL INFORMATION: APPLICANT: Anderson, Leif APPLICANT: Luthman, L. Holger APPLICANT: APPLICANT OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUE TILE REFERENCE: 11145-007001 CURRENT FILING DATE: 2001-04-05 PRIOR APPLICATION NUMBER: US 60/195,665 PRIOR PILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 14 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 989 TYPE: DNA CORGANISM: Home sapiens US-09-826-581-2	Query Match 24.7%; Score 407.2; DB 10; Length 989; Best Local Similarity 99.3%; Pred. No. 8e-111; Aatches 409; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 247 AGGTCCCGGGTCCAGGCTGCTGGAGTCCACCGGGCTGGAGCCACATTCCCCAAGAC 306	Qy 367 CCTCCCCTCTGACTGACGCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGC 426 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
		CGGGCCATGGCGACTGGCCCCGGGGGGGGGGGGGGGGGG	TGAGGCAACGTCACACACCACACACGGATCCATCCTGCCTG	CATTICCGGGGCTGTGGTGCTGGGGCACCCTCTGTTTTTTTTTT

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APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 :
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR PILING DATE: 2000-04-07
                                                                                     TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGGCTTTGATGTGATTC 1226
                                                                                                                                              ACCTGGCTGCCCAGCAAACCTACAACCTGGACATGAGTGTGGGGAGAAGCCCTGAGGC 1286
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                            1107 TGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCAC 1166
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                                              TCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC 662
                                                                                                       1358 ATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGCCCAGCATCTTGGGC
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Pred. No. 1.1e-72;
0; Mismatches 7;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1014
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; Patent No. US20020142310A1
; GENERAL INFORMATION:
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ilarity 97.6%;
Conservative
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283; Conserv
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 GCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACCTGCTACGATGC
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                                                                       Length 1691;
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65.1%; Pred. No. 1.2e-106;
tive 0; Mismatches 311;
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TITLE OF INVENTION: Nucleic Acids, Proteins and FILE SEFERENCE: PAJO5
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-30-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1093)
) OTHER INFORMATION: n equals a,t,g, or US-09-925-297-2
                                                                                                                                                     : Sequence 2, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 580; Conserv
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10036 GTCCATGGAGCAGCTGGAAAAGCGGGAACCACGTGGCGGAGTAAGTGAAAACCCAC 10095
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                                                                                                    9856 CTCCGCCAAGTTGGTTGTCTTCACACCCAGCTTCTTGTAAAAGAAGGCCTTCTACGCCCT 9915
                                                                                                                                                                                676 GGTGGCCAACGCTGTGCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGG 735
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556 CGCCCCCAGAICIACAIGCGCTICAIGCAGGAGCACCCIGCIACGAIGCCAIGGCAAC
                                                                             616 TAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGAGTCAAGAAGGCCTTCTTTGCTCT
                                                                                                                                                                                                                                                                                                                 ------TCTACCTGCAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       858 GCTTCAAGCCTCTGGTCTCCATCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCC
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TITLE OF INVENTION: POLYNUCLECTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   978 ACATCCTCACACACACAAACGCCTGCTCAAGTTCCTGCACATCT 1019
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CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 559, Application US/09822846 Publication No. US20030027139A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/195,605 PRIOR FILING DATE: 2000-04-06
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Steininger II, Robert J.
Bowman, Michael R.
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LaVallie, Edward R.
Collins-Racie, Lisa A.
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Resnick, Richard J.
Gulukota, Kamalakar
Graham, James R.
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Wong, Gordon G.
Clark, Hilary
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Merberg, David
Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                           843 -----
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 559
LENGTH: 1446
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                       GENERAL INFORMATION:

APPLICANT: Andersson, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTIONS VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR APPLICATION NUMBER: US 60/195,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Randar, Kin
APPLICANT: Kandar, Kin
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOCASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THERBOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1129 TGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGG 1188
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 168.2; DB 10; Length 1722;
Pred. No. 9.3e-40;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.7%; Score 127.2; DB 9;
56.7%; Pred. No. 2.5e-27;
tive 0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 70, Application US/10108605; Patent No. US/2020/160934A1; GENERAL INFORMATION: APPLICANT: Broadus, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Drosophila melanogaster
                                      ; Sequence 3, Application US/09826581
; Patent No. US20020142310A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.69
Matches 173; Conservative
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 56.7
Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3
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LENGTH: 11527
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US-10-108-605-70
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US-10-108-605-70
                  US-09-826-581-3
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651 AGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGG 710
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APPLICANT: Haseltine, William A.
APPLICANT: Haseltine, William A.
APPLICANT: Haseltine, William A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Seeven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 1995-04-12
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1995-04-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN HELIOO, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN HELIOO, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN BOOK MARROW, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN LDNG, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 4.8
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ TRAKE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 3373
LENGTH: 378
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OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAP TO AC009974.3
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Best Local Similarity 94.6
Matches 88; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11098
LENGTH: 427
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: (53)
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OTHER INFORMATION:
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                        1130 GCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGGTCAACGAATGTGGT 1189
                                                                                                                                                                                                                                                                                                                                           1190 CAGGICGIGGGCCTCTATICCCGCTTTGAIGIGAITCACCIGGCIGCCCAGCAAACCIAC 1249
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                                                                                                                                                                                                                                                                                                                                                                             64
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                                                                                                         DB 9; Length 1446;
                                                                                                                                                              0; Mismatches 134; Indels
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                                                                                                   7.5%; Score 123.6;
60.4%; Pred. No. 1.6e
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CURRENT PILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3373, Application US/09864761 Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                        Best Local Similarity 60.4 Matches 204; Conservative
         ; ORGANISM: Homo sapiens
US-09-822-846-559
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US-09-864-761-3373/C
                                                                                                      Query Match
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APPLICANT: AGREEL, DATO A.

APPLICANT: CHEN, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FY
TITLE OF INVENTION: GNEE EXPRESSION AMALYSIS BY MICROARRAY
FILE OF INVENTION: GNEE EXPRESSION AMALYSIS BY MICROARRAY
FILE OF INVENTION: GNEE EXPRESSION AMALYSIS BY MICROARRAY
FILE OURRENT PELLAGATION NUMBER: US/09/864,761
CURRENT PILLING DATE: 2000-05-26
FRIOR RILING DATE: 2000-05-26
FRIOR PILLING DATE: 2000-06-26
FRIOR FILING DATE: 2000-06-26
FRIOR PELLING DATE: 2000-06-06
FRIOR PELLING DATE: 2000-06-06
FRIOR PELLING DATE: 2000-06-06
FRIOR PELLING DATE: 2000-09-27
FRIOR PILLING DATE: 2000-09-27
FRIOR PELLING DATE: 2000-09-27
FRIOR PELLING DATE: 2001-01-30
FRIOR RELING DATE: 2001-01-30
FRIOR RELING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: PCT/US01/0066
FRIOR 
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NN: EXPRESSED IN HELA, SIGNAL = 4

NN: EXPRESSED IN HEART, SIGNAL = 4.1

NN: EXPRESSED IN HEART, SIGNAL = 3.9

NN: EXPRESSED IN HAULOO, SIGNAL = 3.9

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 3.9

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8

NN: EXPRESSED IN FORTAL LIVER, SIGNAL = 4.8

NN: EXPRESSED IN BOAR MARROW, SIGNAL = 4.2

NN: EXPRESSED IN BRAIN, SIGNAL = 4.2

NN: EXPRESSED IN BRAIN, SIGNAL = 4.2

NN: EXPRESSED IN BRAIN SIGNAL = 4.3

NN: EXPRESSED SIGNAL SIGNAL = 4.3

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NN: EXPRESSED SIGNAL 
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100.0%; Pred. No. 3.1e-06;
tive 0; Mismatches 0; Indels
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PRIOR PELING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PLICATION NUMBER: US 69/204,687
PRIOR PLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PRIOR DATE: 2000-09-30
PRIOR PLICATION NUMBER: US 09/608,408
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PRIOR FILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR FILING DATE: 2001-01-30
Penn, Sharron G.
Rank, David R.
Hanzel, David K.
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SOFTWARE: Annomax Sequence
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 63.2; DB 10; Length 427; 59.0%; Pred. No. 9.4e-09; tive 0; Mismatches 82; Indels 4
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Sequence 20146, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:

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SEQ ID NO 2472
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                        LENGTH: 897
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Best Local S
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
FILE REFERENCE: MRI-049
CURRENT FILLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FASTSEQ for Windows Version 4.0
AGATCAAGAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCTC 1
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Publication No. US20030099974A1
GENERAL INFORMATION:
                                                                                                                                        ; Sequence 2282, Application US/10198846; Publication No. US20030099974A1
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; LOCATION: 2, 3, 4, 5

; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-2282
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Matches 111; Conservative
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US-10-198-846-2472/c
                                                                                              RESULT 11
US-10-198-846-2282/c
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APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
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                                                                                                    73, 462, 481, 540, 559,
774, 809, 849, 870, 873,
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.2%; Score 52; DB 10; I 100.0%; Pred. No. 2.4e-05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                        3.2%; Score 52.2; DB 9;
1 Similarity 56.8%; Pred. No. 2.2e-05;
96; Conservative 0; Mismatches 73;
                                             PEATURE:
NAME/KEY: misc_feature
LOCATION: 2, 16, 22, 23, 27, 28, 30, 36, 39,
LOCATION: 590, 604, 634, 636, 676, 680, 772,
LOCATION: 876, 886, 893, 895, 896, 897
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16257, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                            ; OTHER INFORMATION: n = A, T, C or G
US-10-198-846-2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09826581; Patent No. US20020142310A1; GENERAL INFORMATION:
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Best Local Similarity 100.v.,
...os 52; Conservative
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US-09-826-581-1
TYPE: DNA
ORGANISM: Homo sapiens
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1369 GCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTTTGGGCGTGGTCTCCCT 1428
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OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN BALLO, SIGNAL = 7.6
OTHER INFORMATION: EXPRESSED IN HBLIOO, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
US-09-864-761-693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 GTGGGACATTCTGCAAGCCCTGATCCTCACAGAGGTA 302
                                          PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 693
             PCT/US01/00661
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Job time: 521.839 secs
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Best Local Similarity 64.4%;
Matches 65; Conservative
           APPLICATION NUMBER: PCT, FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                                                                                         116 CGGCGAGGAGCAGGCCCACAGCTGCTCCACCCTGTCTGTAGAAGAGGCCGGC 175
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                                                                                                                                                                            Score 46; DB 9; Length 396
Pred. No. 0.0012;
0; Mismatches 145; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16257
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Patent No. US20020048763A1
                                                                                                                                                                            Query Match 2.8%;
Best Local Similarity 47.8%;
Matches 133; Conservative 0
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-918-995-16257
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US-09-864-761-693
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Gaps

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June 13, 2003, 01:49:14; Search time 192.613 Seconds (Without alignments) 9216.782 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                2054640 seqs, 14551402878 residues
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61
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
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2: 9D_ba:*
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6: 9D_ov:*
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em_htgo_other:*
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AX281582 Bukaryota March Lea

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AF214519 2115 bp mRNA linear PRI 03-JUN-2000
Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.
AF214519
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KNERHRLPVLDPVGRYNLHILTHRELLKFBLIPESPEFRZHTODLGIGFREN
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GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVINDETQHLLGVVSLSDTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQ1YM
RFWQEHTCYDAWATSSKLVIFDTWLEIKKAFFALVANGYRAAPLWDSKKQSFVGMLFI
                                                                                                                                                                                                                                                                                                                          PAT 02-APR-2001
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                                                                                                         100 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTC 159
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FR) ;
Ernst (DE)
                                                                                     1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGGGGGAAGGTCCCCGGTCC
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                                            Gaps
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Patent: WO 0120003-A 29 22-WAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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Length 2109;
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100.0%; Pred. No. 5.4e-08;
100.0%; Score 61; DB 6; 100.0%; Pred. No. 5.4e-08;
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                                          0; Mismatches
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Sequence 29 from Patent WO0120003.
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Query Match
Best Local Similarity 100.
Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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AF214519
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HLAAQQYYNHILDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRIVLVDE
TOHLLGVVSLSDLIQALVLSPAGIDALGA"

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 5.6e-08;
iive 0; Mismatches 0; Indels
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                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
20. .1489
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/db_xref="G1:13538811"
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Sequence 3 from Patent WO0120003.
AX099776
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/db_xref="taxon:9606"
                    Location/Qualifiers
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LVANCYRAALWDSKKQSYGMLTITPIDLULLHRYYRSPLVOYDYEEDGHKIETWREIY
LQCCRPLYSISPHDSLFEAVYTLIKHRIHRLPKPLLTHRKLLKTLHTF
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTPALDIFVDRAYSALPYVNECGQY
VGLYSRFDVTHLAAQOTYNHLDMSVGEBLIRKRPLCLEGGVLSCOPHESLGEVIDRIARE
QVHRLVLVDFTQHLLGVYSLSDLIGALVJSPAGIDPSGPEKI"
674 C 617 9 498 L
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sserirgkrrakalrwirgksyebgeeppggegprsrpaaestgleatfpkytplaga
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                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthbria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2290; Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit lisoforms and their role in AMP binding
Biochem. J. 346 Pt 3, 659-669 (2000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/product="AMP-activated protein kinase gamma 3 subunit"
                                                                                                                                                                                                                                                                 Carling,D.
Direct Submission
Submitted (12-CCT-1999) Carling D., Cellular Stress Group, M.
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 ONN, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="AMPK gamma 3"
/function="AMP-activated protein kinase regulatory
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100.0%; Pred. No. 5.3e-08;
iive 0; Mismatches 0;
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/db_xref="G1:6688201"
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Sequence 2 from Patent WO0177305.
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22. .1500
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EPPPGGGERSRRPTABAZTGLEAFFYTPLADADPAGVFPTFGWDCLPSDCTABAAG
SSTDDVELATEFFATBAWDCLLSCLLEEFFALCLSPAFFALGAPFRAGATW
RFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANCVRAAPLWDSKKQSFVGMLTI
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KNRHHRLPULDPVSGNVHJILTHRKLLKFLHIFGSLLDFSFLYRTJQDLGIGTFRDL
AVVLETAPILJALDIFVDRRYSALPVVHSCGQVVGLYSREDVHLAAQQYNHLDMSV
GEALRQRTICLEGVI.SCQPHESI.GEV IIN FARQVHRALVLVDETQHLGVYSLSDILQ
                                                                                                                                                                                                                                        A mutation in PRKAG3 associated with excess glycogen content in pig
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Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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AJZ49977 GI:6688200
AMP-activated protein kinase gamma 3 subunit aJZ49977.1 GI:6688200
AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
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                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2115)

Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.
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/protein_id="AAF73987.1"
/db_xref="GI:8215682"
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100.0%; Pred. No. 5.4e-08;
ive 0; Mismatches 0;
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Science 288 (5469), 1248-1251 (2000)
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/db_xref="taxon:9606"
/chromosome="2"
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AF214519.1 GI:8215681
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61; Conservative (
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Buguslarky, L. Budwin, J., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Budwin, J., Barna, N., Bastien, V., Beda, F., Boguslarky, L., BouthAgalter, B., Brown, A., Burkett, G., Campopiano, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, W., Doyle, M., Ferreina, P., Fitzhudh, W., Gage, D., Gand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J., Cant, G., Hagos, B., Heaford, A., Horton, L., Howland, J., LaRocque, K., Lamazares, R., Landers, T., Lahoczky, J., Kartes, N., McCarthy, M., McEwn, P., McGurk, A., McKernan, K., McDeeters, R., McInn, J., Meneus, L., Minoan, T., Minanda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Morman, C. H., O'Connor, T., O'Donell, P., O'Neil, D., Olivar, T., Minoan, T., Mitoy, R., Kogov, P., Rothman, D., Pisani, C., Pollara, Y., Kaymond, C., Rilly, R., Kogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Sphramanian, A., Talamas, J., Taskers, M., Trigillo, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Trigillo, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Tavers, M., Trigillo, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Oln, Y., Willer, K., Volot, His, sequence version replaced gi:7342115.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://free property of the same property of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC027416 152129 bp DNA linear HTG 07-JUN-2000
HOMO Sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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------- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Assembly program: Phrap; version 0.960731
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                                                                                                                                                                Score 51; DB 6; Length yos;
Pred. No. 5e-05;
                                                                                                                                                                                             Length 989;
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Unpublished
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                                                                                                                                                                      83.6%; Sco...
100.0%; Pred, No. ...
... 0; Mismatches
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306 c 286 q 168
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NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                            Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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Consensus quality: 135376 bases at least Q40 Consensus quality: 143264 bases at least Q30 Consensus quality: 146503 bases at least Q20
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15043; contig of 2387 bp in length
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33968: contig of 3698 bp in length
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contig of 1980 bp in length
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contig of 2640 bp in length
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85022: contig of 7807 bp
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21928: contig of 2362 bp
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60595: contig of 4624 bp
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93415 101193: contig
101194 101293: gap of
101294 113090: contig
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27059: cont
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12556: con
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51285: cont
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6161: com
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113091 113190: gap of 100 bp
113191 123496: contig of 10306 bp in length
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AC009974 206854 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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Submitted (OB-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 206854)
Waterston, R. H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 206854)
Sulston, J.E. and Waterston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                       Gaps
                                                                                                                     2925 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 2875
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Center code: WUGSC
                                                                                            1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51
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  Length 152129;
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
Unpublished (2001)
3 (bases 1 to 206854)
Waterston,R.H.
83.6%; Score 51; DB 2; Length 152
100.0%; Pred. No. 2e-05;
iive 0; Mismatches 0; Indels
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Contact: sapiens@watson.wustl.edu
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Waterston, R.H.
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Waterston, R.
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281. .344
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/note="match to EST BI059713 (NID:914467240)"
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594. .763
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/note="match to EST BF304755 (NID:g11251653)"
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599. .763
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/note="similar to Homo sapiens EST BI114348
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967. .1085
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The RPCI-11 human.

The RPCI-11 human.

The RPCI-11 human.

Tateno, M., Catanese, J.J. and de Jong, P.Y., [1998] An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:1:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer institute (http://bacpac.med.buffalo.edu)
                                                                                         Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Mashington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NID:98364652) tz39c01.y1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="match to EST A1670836 (NID:94850567) wa04910.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match to EST BE047599 (NID:g8364652) tz39c01.yl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="match to EST A1670836 (NID:94850567) wa04910.x1"
  ρλ
from more than one subclone; and the assembly was confirmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="match to EST AL567345 (NID:g12920610)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="match to EST BF183086 (NID:911061273)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note-"match to EST BF304755 (NID:911251653)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match to EST BG477625 (NID:g13409904)"
1. .37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match to EST BI059713 (NID:g14467240)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match to EST BG470047 (NID:913402322)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="match to EST AL567345 (NID:g12920610)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="match to EST BE908408 (NID:g10402954)"
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/note="similar to Homo sapiens EST BI114348
(NID:g14565249)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match to EST C05773 (NID:g1502549)"
220. .221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note" match to EST BE047599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone-"RP11-459119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11"
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281. .344
                                                                     MAPPING INFORMATION:
                                                                                                                                                                                                                SOURCE INFORMATION;
                           restriction digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="2"
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HFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKÖSFVGMLTI
TDFIIVYLHYYRSPLVOLYTEIEBHKIETWREITLGGCFKFLVSISPNDSLFERAYALI
KNRIHRLPVLDPVSGAVLHILTHKRLIKFLHIFGTLLPRPSFLYRTIQDLGIGFRDL
AVVLETAPILTALDIFVDRRVSALPVVNHSTGQVVGLYSREDVIHLAAQQTYNHLDMNV
GEALRQRTLCLEGGVLSCQPHETLGEVIDRIVBEQVHRLVLVDETQHLLGGVVSLSDILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gailland,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 1873) Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
1. 1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="AMP-activated protein kinase gamma subunit"
/protein_id="AAF73988.1"
/db_xref="GI:8215684"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                        /tissue_type="skeletal muscle"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  /gene="PRKAG3"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AMPKG3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="PRKAG3"
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                                                                                                                                                                                                                                                                                                                      /map="15q
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Matches 49; Conservative
                                                                                                                                                                                                                                   .1873
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                      10818001
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ACCESSION
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                                       REFERENCE
AUTHORS
                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                gene
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MEDLINE
                      PUBMED
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                                                                                                                                                                                                             FEATURES
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lwdskkosfydmlitopilvlhryyrsplvQiyeleehkiethreikfotldprsprus
Ispndsleavyaletheikfultopidysdavlailthkalkfelhifotllafotldprspru
Yrtiodigigterolavulethallylaldifydrrysaleyvnergoyogiysredy
Hlaaqqtynhldmnygealrolethgvilclegvlscophetlgevidrivyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF214520 1873 bp mRNA linear MAM 03-JUN-2000 Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
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                                                                                 PAT 02-APR-2001
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
and Andersson,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                       Variants of the gamma chain of ampk, dna sequences encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                   INSTITUT NATIONAL DE LA RECHERCHE ÀGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACAAGGCAGAAGTCGGTGGAGGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC
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Pred. No. 0.021;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product"
                                                                                 DNA
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583 c 529 g 375 t
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                                                                                                                                                                                                                                                                                                                                                                           same, and uses thereof
Patent: WO 0120003-A I 22-MAR-2001;
                                                                          AX099774 1867 bp
Sequence 1 from Patent W00120003.
AX099774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAC35798.1"
/db_xref="GI:13538809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sus scrofa"
/db_xref-"taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .1867
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DSNDPLDLDGIEFSAASAGGBEGLQVEEKPAPCPSPPRVLLEPGAWDDELCKPGAQVYM
HFWGGHTCYDAAMTSSKLVIFDYMLETKKAFPALVAGVRAAPLAWDSKKQSFVGMLT
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISNDSLFERAYPALI
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AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRPDVIHLAAQQTYNHLDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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Sus scrofa
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Plastow,G.
as genetic markers for
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Pred. No. 0.021;
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Novel prkag3 alleles and use of the same as genetic reproductive and meat quality traits
Patent: WO 0220850-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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AX398333
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/organism="Sus scrofa"
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/db_xref="G1:21261107"
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DSNTDHLDLGIEFSASAARGDELGLVPEKRAPCPSFPCLLPRLGMDEDGKPGAQVYM
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KNRIHETAPLLASPSGAVLHILTHRKILKFLHFGTLLLRSSPLXRTIODGGGGFFRDL
AVULETAPILTALIFUDRYGALPVVNETGQVVGIXSREDVIHLAAQOTYNHLDMN
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HFWQEHTCYDAMATSSKLVIFDFMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 022085-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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nilarity 80.3%; Pred. No. 0.021;
Conservative 0; Mismatches 12; Indels 0.
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organism="Sus scrofa"
                  /db_xref="taxon:9823"
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TDFILVLHRYRESPLYQOY ELEEHK IETWREIYLGGCFRTLVSTSPNDSLFBAYALI
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GPPGFREGPGSRFVARSTGGEARPFRAIPLAQAAPLAEVDNPFTERDILPSDCAAASAS
                                                                                                                                                                                                                                                                                                                                                                       DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
HFWQEHTCYDAMAISSKLVIFDIWLEIKKAFFALVANGIRAAPLWDSKKQSFVGMLTI
                                                                                                                                                                                                                                                                                                                                                                                                                 TDFILVLHRYTRSPLVQIYEIEEHKIETWREIYLGGCFKPLVSISPNDSLFEAVYALI
KNRTHRLFULDYDGYVGGAUHLGTHRKELKFLHFGTLLRSPSELYRTJQDGGGFFBDL
AVVLETAPILTADIFVDRAVSALPVNNETGQVVGLYSRFDVIHLAAQQTHLDMY
GEALRQFTLCLEGVLSCQPHETLGEVIDRIVREQVHALVLVDETQHLGVYSLSDILO
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DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGKDDELQKPGAQVYM
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 714-MAR-2002;
IOWA State University Research Foundation, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220856-A 9 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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/protein_id="CAD32629.1"
/db_xref="G1:21261115"
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Sequence 9 from Patent W00220850.
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/db_xref="taxon:9823"
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Pred. No. 0.021;
0; Mismatches 12; Indels 0
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Job time: 194.613 secs
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ALVLSPAGIDALGA"
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80.3%;
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                                                                      Best Local Similarity
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Pig Pr. Pig PRKAG3 y_ Pig PRKAG3 gene > DNA encoding novel Human breast cance "NA encoding novel" " activated" hanr

AAD36458 AAD36461 AAD36462 AAS84523 AAS84523

Calcium activated Human Ecalcium activated Human IRca channel T. thermophilus gar Thermus thermophil Human Lobo homolog Human retina speci Human retina speci Human retina speci

AAX21373 AAZ23900 ABK95404 ABK95403 ABK95403

CDNA encoding nove Gene #2184 used to Drosophila melanog Murine bone morpho

ABL27039 AAZ95746 AAQ74084

AAS45150 ABN95686

AAZ32059 AAC90316 AAS62392 ABL27038 ABK13766

AAS40665 AAL06553

AAF30037

AAQ35243 AAH16987

Murine BMP-9 cDNA. Encodes murine bon

Human cDNA sequenc cDNA sequence #179 CDNA encoding huma DNA encoding humar

Human reproductive Apolipoprotein A-I

ALIGNMENTS

Human IL-2R beta c Human METH2 relate

X16619 CDNA clone.

Human prostate exp Human prostate exp

Ovary cancer relat

ABV29324 ABL68109 AAQ05872 AAQ06331

Sequence encoding

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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                     2185239 seqs, 1125999159 residues
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1 acaaggganaagta
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			Description	PRKAG3 CDNA. HOMO	Human AMPK gamma s	Human AMPK gamma s	PRKAG3 intron 2 -	Pig AMPK gamma sub	Pig AMPK gamma sub	Pig wild-type PRKA	Pig PRKAG3 polymor	Pig PRKAG3 polymor
SUMMARIES			ΩI	AAH43685	AAD03296	AAD03320	AAH43682	AAD03295	AAD03319	AAD36456	AAD36457	AAD36459
			DB	22	22	22	22	22	22	24	5 4	24
		Query	Length	1647	2109	2115	686	1867	1873	1873	1873	1873
	æ	Query	Match	100.0	100.0	100.0	83.6	68.5	68.5	68,5	68.5	68.5
			Score	61	61	61	51	41.8	41.8	41.8	41.8	41.8
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/product- "Human Prkag3 protein"
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                                                                                                                                                                   New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                          AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A, in exon 4 variation may be a substitution of a c at nucleotide 550; and in exon variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                              nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
                                                                                                                                                                                                                                               sequence represents the full length cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 61; DB 22; Length 1647; 100.0%; Pred. No. 6e-10; 1. Indels 0; Mismatches 0; Indels 0;
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-haq 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
                                                                                                              Andersson L, Luthman H, Marklund S;
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                                                                                                                                                                                                                            Disclosure; Fig 5; 25pp; English.
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                                          06-APR-2001; 2001WO-SE00765.
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Matches 61; Conservative
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P-PSDB; QQB47679.
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WO200177305-A2
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(AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, which are the continuous and the carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such sa supparity and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic and its functionally altered mutants are useful for the diagnostic callerably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3 are useful for detecting and protonois of an activity and expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a CDNA encoding human adenosine monophosphate
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(ANDE/) ANDERSSON L.
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PRKAG3 intron 2 - intron 4.

(first entry)

21-JAN-2002

AAH43682;

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AAH43682 standard; DNA; 989 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in sketatal muscle-specific isoform, carbohydrate metabolism, particularly in sketatal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as myopathy and cardovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PFKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and proquosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for escending PRKAG3 is useful for detecting mutations in a PKRAG3 domain and provided and a print provider activity. Nucleic acid and a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                        PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                            Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a cDNA encoding human adenosine monophosphate
                                                                                      Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                   /product= "Human complete Prkag3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 65-68; 71pp; English.
                                                                                                                                                                                                                                     Location/Qualifiers
1..1395
                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-2000; 2000WO-EP09896.
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18-MAY-2000; 2000EP-0401388.
  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANDERSSON L.
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                                                                                                                                                                                             Homo sapiens
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13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2001
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New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3) Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, as subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of substitution p71A, in exon 4 variation may be a substitution of substitution of a C at nucleotide 320, resulting in the amino acid substitution of a rior a C at nucleotide 550; and in exon 10 variation may be a substitution of a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
Human, AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAH43681-84 represents genomic fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "5' portion of intron 4"
                                                                                                                                                                                                                                           /note= "3' portion of intron 2"
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/number = "Intron 2"
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r= "Intron 3"
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r= "Intron 4"
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Exon 4"
                                                                                                                                                                                                                                                                                                                             'number= "Exon 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid substitution R340W.
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                                                                                  Homo sapiens
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100.08; 100.0%;

l Similarity 100.0 61; Conservative

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Query Match Best Local S

Matches

Length 2115; Indels 9

106 ACAAGGCAGAAGTCGGTGGAGGAAGGGAACCACCAGGTCAGGGGGAAGGTCCCCGGTCC 165

ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC

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Andersson L,
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Best Local 8
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                                                                                                                                                                                                                                  PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                          gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                             1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51
                                                 ö
                                                                                                                                                                                                    Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                        Best Local Similarity 100.0%; Pred. No. 7.5e-07; Matches 51; Conservative 0; Mismatches 0; Indels
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/product= "Sus scrofa PRKAG3 protein"
1390.1867
/ttag= c
        Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
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                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                         AAD03295 standard; cDNA; 1867 BP.
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18-MAY-2000; 2000EP-0401388
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472..1389
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                                                                                                                                                                                                                                                                 chromosome 15; ss
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such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder.

preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3.

Transpenic animal and host cell transformed with PRKAG3 or a
heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.5%; Score 41.8; DB 22; Length 1867; 80.3%; Pred. No. 0.00058;
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J, Le Roy P, Chardon P;
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0; Mismatches
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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18-MAY-2000; 2000EP-0401388.
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Iannuccelli N, Gellin J,
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/product=
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es 49; Conserva
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     variation
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                                                                                                                                            (AMP) activated Kinase (AMPK) gamma subunit muscle-specific isoform, complete PRRAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as the captured for treating carbohydrate metabolism disorders such as captured as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered aliele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a sequence encoding the first cystathione beta synthase (CBS) domain PRKAG3 and is useful in gene therapy.
New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                           heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                The present sequence is a cDNA encoding pig adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.5%; Score 41.8; DB 22; Length 1873; 80.3%; Pred. No. 0.00058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Pig PRKAG3 wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.00
0; Mismatches
                                                                                            Claim 12; Page 62-64; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace (154, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD36456 standard; DNA; 1873 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pig wild-type PRKAG3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                     myopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma subunit gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product- "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig wild-type PRKAG3 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 0,00058;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
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1..1395
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80.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                         10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                          08-JAN-2001; 2001US-260239P. 18-JUN-2001; 2001US-299111P.
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us-09-826-581-5_copy_200_260.rng

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1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality trails. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality trails and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
                                                                                                                                                                                                                                                                                                                                          Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                    /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.5%; Score 41.8; DB 24; Length 1873; 80.3%; Pred. No. 0.00058; Dred. No. 0.0058; Live 0; Mismatches 12; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                             Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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     replace (595, A)
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                                                                                                                                                              2000US-231045P.
2001US-260239P.
2001US-299111P.
                                                                                                                                10-SEP-2001; 2001WO-US28283.
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                                                                                                                                                                                                                                                                                           WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                          P-PSDB; AAE22987
                                                                    WO200220850-A2
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                                                                                                                                                              08-SEP-2000;
                                                                                                                                                                               08-JAN-2001;
18-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                            subunit gene
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                                                                                                    14-MAR-2002
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      variation
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AAD36460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant DNA (PRRAG3-30).
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                                                                                                                                                                                                                                                                                                                                        Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                 /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                           Rothschild MF, Ciobanu DC, Malek M, Plastow G;
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1..1395
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replace (89, C)
/*tag= b
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08-JAN-2001, 2001US-260239P.
18-JUN-2001, 2001US-299111P.
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                                                                 WO200220850-A2
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                                                                                                14-MAR-2002
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   variation
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The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 gene is located in the RN locus of carbohydrate metabolism disorders as achieved by the appearance of the present of the analysis of carbohydrate metabolism alsorders such as myopathy and disorders associated with muscle metabolism cardiabetes, obesity, and disorders associated with muscle metabolism cardiabetes, obesity, and disorders associated with muscle metabolism cardiabetes, obesity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dystunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3, are transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
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    /product= "Sus scrofa Prkag3 splice variant"
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80.3%; Pred. No. 0.00059;
ive 0; Mismatches 12;
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L.
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                                                                                                                                                11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                         10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
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ANDERSSON I
LOOFT C.
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                                                                                                                                                                                                                                                                                                                                    (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                           Iannuccelli N,
                                                     WO200120003-A2
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                                                                                                 22-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myopathy
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AC AAD3
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DT 09-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 102-104; 109pp; English.
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1..1545
/*tag= a
replace (599, A)
/*tag= b
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80.3%;
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08-JAN-2001, 2001US-260239P.
18-JUN-2001, 2001US-299111P.
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Matches 49; Conservative
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       variation
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Sus scrofa

variation

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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; polymorphism; short interspersed element; pig; SINE; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32.6; DB 24; Length 1095;
Pred. No. 0.41;
2; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                            /rpt_type= "DIRECT"
/note= "Direct repeat present between short
interspersed element (SINE)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon, intron and short interspersed element (SINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rothschild MF, Ciobanu DC, Malek M, Plastow G;
              Pig PRKAG3 gene 5' flanking region with SINE.
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                                                                                                                                                                       Location/Qualifiers
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nilarity 74.5%;
Conservative 2
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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/*tag= b
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732..749
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826..979
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es 38; Conserv
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                                                                                                                                                                                                                                                                                                            repeat_region
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                                                                                                                                Sus scrofa
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                /*tag= a
/product= "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
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/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                   AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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Pred. No. 0.0018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                  Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
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                                                                                                                                                                         Location/Qualifiers
1..1395
                                                                                                                                                                                                                                                     replace (154, A)
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78.7%;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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Best Local Similarity 78.7
Matches 48; Conservative
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09-AUG-2002

AAD36462;

RESULT 14 AAD36462 Sus scrofa

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and green chair reaction (PCR) primars, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The color intrifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques for restore normal activity of (II) or to treat disease states involving (II). (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and to produce other types of data and products dependent on DNA and amino acid sequences. AASG4197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO
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                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                  DNA encoding novel human diagnostic protein #20327.
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                      AAS84523 standard; cDNA; 2541 BP.
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Best Local Similarity 67.3%;
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                       Homo sapiens.
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23-AUG-2000;
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AAS84523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 gene 5' flanking region including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                            Pig PRKAG3 gene 5' flanking region including exon and intron.
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                                                                   AAD36462 standard; DNA; 808 BP.
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subunit gene

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Gaps

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18; DB 23;

Pred. No. 43; 0; Mismatches

Score 26.2;

Length 2541; Indels

Query Match

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B1775360 A1664508 AA787203 AW693375 BJ0800431 BB306360 BM466469 BM466469 BG24494 CNSQ14199 A2166563	AW353555 AW353555 AW362678 AW36260 BE1359806 BE1359806 BE135819 BE135811 BE135811 BE13102 BE13102 BE13102 BE13102 BE150102 BE12102 BE15010	ALIGNMENT ALIGNMENT ALIGNMENT ALIGNMENT 621 bp 621 bp 621 bp 621.15399483 61:15399483 61:15399483 F. GI:15399483 F. GI:153998483
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227.2.2.4.4.6.6.6.6		BB628877 BB628877 BB628877 BB628877 BB628877.1 BB628877.1 GI BSG7. Mus musculus Bwarmalia; Buth Mammalia; Buth Musmamalia; Buth Musmamalia; Buth Musmamalia; Buth Tagami, M.,
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Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Kouda Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN WOUSE ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Tukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammallai Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 655)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazakı,Y., Muramatsu,M. and Haysshizakı,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN)
1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fal: 81-45-503-9226
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         BB629521 RIKEN full-length enriched, adult male bone Mus musculus cDNA clone 9830138C07 5', mRNA sequence.
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/clone="9830138C07"
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Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encyclopedia: real-time sequence clustering for construction of a nonredundant cloud library. Genome Res. 11 (2), 281-289 (2001) Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fukuda,S., Hara,H., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDN&s on mouse chromosomes. J. Struct. Punc. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Mutamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="site_1: Sal1; Site_2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="9630039L22"
/clone_lib="RIKEN full-length enriched, 16 days neonate
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 685)
Arakawa T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.
Hiramoto, K., Hori, F., 1shi, Y., Ito, M., Kawai, J., Konno, H., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyoswa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGARTICTGAGTIAATTAAATTAAATTAAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
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Email: genome-res@gsc.riken.go.jp,
UNR.http://genome.gsc.riken.go.jp,
carninci.p., Shibata,Y., Hayatsu.N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Bayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length CDNA libraries for rapid discovery of new
"wagi.K., Fujiawake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wathiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 26-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic
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                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB630381 RIKEN full-length enriched, 6 days neonate skin Musmusculus cDNA clone A030014A04 5', mRNA sequence.
                                                                                                                                                                                                                                                                 Length 655;
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0.17;
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                                                                                                                                                                                                                                                            Score 38.6; DB Pred. No. 0.17; 0; Mismatches
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Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                            63.38;
                                                                                                                                                                                                                                                                                      77.0%;
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Best Local Similarity 7/.vv.,
"..hos 47; Conservative
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-WcKown, C.G.,
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                                                                                                                                                                                                                                                                                                                                                                        Anotes Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGGAGGAGGAGGAGGCCTTTTTTTTTTTTTTTTV 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC 60
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                            /clone="A030014A04"
/clone_lib="RIKEN full-length enriched, 6 days neonate
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USDA, ARS, US Meat Animal Research Center
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0; Mismatches
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                                                                                                                                                                                                                                                                                                     /tissue_type="skin"
/dev_stage="6 days neonate"
/lab_host="DH10B"
                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                     /db_xref-"taxon:10090"
                                                                                                                            Location/Qualifiers
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AW356079.1 GI:6860085
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l Similarity 77.0%;
47; Conservative (
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Best Local Similarity
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Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
'G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                              /note="Yector: pcMv SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCGGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                60.7%; Score 37; DB 10; Length 422; 75.4%; Pred. No. 0.46; ive 0; Mismatches 15; Indels
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NO Box 16c, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                         /clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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/tissue_type="pooled"
/lab_host="DH10B"
                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
    Plate: 32 row: F column: 22
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: ATTTAGGTGACACTATAG.
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Plate: 57 row: H column: 11
                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                           125 g
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                                                                                                                                                                                                                                                                                                                136 c
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                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 75.4 Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR PRimers
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BF890374
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USDA, ARS, US Meat Animal Research Center
PO Box 166, clay center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Fax: 402 762 4390
Single pass sequencing. Bases called and trimmed with phred
V0.880904 e. Vector identified by cross_match with the -minscore 20
                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR PRimers
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1 (bases 1 to 422)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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Mammalla; Eutheria; Cetartlodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pcMv SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 bp mRNA linear 63185 WARC 3BOV Bos taurus cDNA 5', mRNA sequence. AW427435 AW427435.1 GI:6955382 BST.
PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adrenal, and endometrium.
                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="MARC 2BOV"
                                                                                                                                                                                                         BACKWARD: GTTTTCCCAGTCACGACG
Plate: 17 row: P column: 9
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                        FORWARD: AGGAAACAGCTATGACCAT
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es 46; Conserv
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AW427435
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EST 25-APR-2001

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Gaps ..

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/Clone_lib="Suparan mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/dev_stage="embryo, 14 dpc"
/dev_stage="embryo, 14 dpc"
/deb_nost="bHi08"
/note="Vector: pME18S-FL3; Site_l: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACATGTG]. XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CGACCTGCAGCTGCGACAC."
                                                                                                                                                                                                                                                                                                                                                                                                                   E. T. (bases 1 to 516)

Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylle, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, F., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The Washul-NOT Mouse EST Project 1999

L. Unpublished (1999)

L. Unpublished (1999)

L. Ocher_ESTS: uk25b05.x1

Conter_ESTS: uk25b05.x1

Conter_ESTS: uk25b05.x1

Context: Marra M/Washur MCI Mouse EST Project 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1800
                                                                                                                                                                                  EST 10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                    uk25b05.yl Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1970001 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 516;
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                                                                                                                                                                                  mRNA
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t
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/organism="Mus musculus"
/strain="C57bL"
/db_xref="taxon:10090"
/clone="IMAGE:1970001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: custom primer used
High quality sequence stop: 484.
Location/Qualifiers
                                                                                                                                                                                516 bp
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                                                                                                                                                                                                                                                                                                                               house mouse.
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     61 A 61
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AA787203/c
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AI664508
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
1 (bases 1 to 548)
2 (bases 1 to 548)
2 (bases 1 to 548)
2 (arosse, W. M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
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Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle." 139 g 67 t
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Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pcMv SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, thymus, esmitendonosus muscle, longissimus muscle, pancreas, adversal and endometrium "
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                                                                                                                                                      Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                        BI775360 548 bp mRNA linear 467815 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                    Indels
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PO Eox 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                    Score 34.2; DB 12;
Pred. No. 3;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adrenal, and endometrium.
173 c 163 g 93
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/clone_lib="MARC_2BOV"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: 1 column: 16
Seg primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI775360.1 GI:15776346
                                                                                                                                                    Query Match 56.1%;
Best Local Similarity 76.4%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Conservative
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Best Local Similarity
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BJ080431 669 bp mRNA linear EST 12-DEC-2001 BJ080431 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL075j16 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="stage 25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                          Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="XL075j16" /clone_lib="NIBB Mochii normalized Xenopus tailbud
                                                                    Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7568111.
Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Pooled developmental"
/note="Vector: Lambda 2ap; Contains a mixture of
internodal stem segments"
107 c 137 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 10; Length 618;
Pred. No. 2e+02;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACAAGGCAGAAGTCGGTGGAAGGGGAGCCACCAGGTCAGGG 44
                                                                                                                                                                                           USA
                                                                                                                                     Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 660 Std Error: 0.00
Plate: 063 row: H column: 10
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
Contact: Tadasu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                       truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed genes in X. laevis embryo
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/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3880"
/clone="NF063H10ST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Medicago
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="stem"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         African clawed frog.
Xenopus laevis
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Best Local Similarity
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BJ080431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cnNA lambda zap library" / tissue_type="vegetative nycella, asexual structures" / note="vector: pBlueScript SK-; Site_l: EcoRI; Site_2: XhoI; S; end of cDNA cloned into EcoRI site of pBluescript a cloned into XhoI site of pBluescript" a ll8 c 96 g 58 t
AA787203 365 bp mRNA linear EST 31-JUL-1998 m8d07al.rl Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW693375 618 bp mRNA linear EST 20-DEC-2000 NF053H10ST1F1000 Developing stem Medicago truncatula cDNA clone
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Bukaryocha; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: broefou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAAGGCAGAAGTCGGTCGAGGAAGGCGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTCC 60
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He.X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
.C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ACAAGGCCGGGTGCGCGGAAGAAGCGCGACCACACAGAGGGGAAAGAGGTAGCTGGTCC 3
                                                                                                                                                                                                                                                                             Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
Prade,R. and Roe,B.
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4012
Fax: 405 325 7762
                                                                                                                                                           Emericella nidulans.

Emericella nidulans

Emericella nidulans

Emericella nidulans

Euroxycota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Euroxilaies; Trichocomaceae; Emericella.

[ (bases 1 to 365)
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Pred. No. 95;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Emericella nidulans"
/strain="FGSG A26"
//db_xref="taxon:162425"
/clone="m8d07a1"
                                                                                                                                                                                                                                                                                                                           An Aspergillus nidulans EST Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 346.
Location/Qualifiers
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                                                                 m8d07a1 5', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                       Other_ESTs: m8d07al.fl
                                                                                                               AA787203.1 GI:2847434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.5%;
Best Local Similarity 67.2%;
Matches 41; Conservative (
                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
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Gaps

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/note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Breast,leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM466469 1029 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6456404 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5579448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="pgm2n.pk010.p18"
/clone_lib="Wormalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1029)
clone pgm2n.pk010.p18 5' similar to ref|NP_060575.1 (NM_018105) hypothetical protein FLJ10477 [Homo sapiens] dbj|BAA91635.1| (Ak001339) unnamed protein product [Homo sapiens], mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Breast muscle, leg muscle and epiphyseal
                                                                                                                                                                                                                              (bases 1 to 590)
Cogburn,L.A. and Monsonego-Ornan,E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate CDNA library, USDA/IFAFS Animal Genome
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National Institutes of Health, Mammalian Gene Collection (MGC)
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69.8%; Pred. No. 3e+02;
iive 0; Mismatches 16;
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Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Contact: Larry A. Cogburn
University of Delaware
                                                                                    BM489457.1 GI:18610388
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BM466469.1 GI:18515511
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1 (bases 1 to 808)
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according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute). " 1 others 128 c 196 g 150 t
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243 c 241 g 161 t
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM561 row: n column: 19
High quality sequence stop: 652.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                            Length 669;
                                                                                                               0; Mismatches
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/strain="CZECH II"
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Gaps

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SM Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
E 1 (pases 1 to 151)
Naith-MCC http://mgc.nci.nih.gov/.
Naitonal Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs = featinh.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                            /clone="Indage: 5579448"
/clone="Indage: 5579448"
/clone=lib="N.H_MCC_67"
/tissue_type="retinoblastoma"
/lab.nost="NuH10B (phage-resistant)"
/note="Organ: eye: Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LimAga.llnl.gov
High quality sequence stop: 681.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lli.gov
Plate: LLAM10330 row: h column: 16
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/dev_stage="10 months, virgin"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                 /organism-"Homo sapiens"
/db_xref-"taxon:9606"
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/db_xref="taxon:10090"
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Tissue Procurement: ATCC
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Sequence 214, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TANIGUCHI, TADATSUGU; HATAKEYAMA, MASANORI; MINAMOTO, SEJIRO; KONO, TAKESHI; DOI, TAKESHI; MIYASAKA, MASAYUKI; TSUDO, MITASASOYAMA, HAJIME TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2 NUMBER OF SEQUENCES: 12 CURRENT APPLICATION DAIA: APPLICATION NUMBER: 05/08/88,592 FILING DATE: 9-JUL-1993 PRIOR APPLICATION NUMBER: 465,155 FILING DATE: 08-APPLICATION NUMBER: 467,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICAMY: TANIGUCHI, TADATSUGU; JATAKEYAMA, MASANORI;
MINAMOTO, SEJIRO; KONO, TAKESHI; DOI, TAKESHI; MIYASAKA, MASAYUKI;
FULDO, MITSURU; KARASUYMA, HAJIME
TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
UNDERR OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 6; Length 4035;
Pred. No. 16;
0; Mismatches 20; Indels
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tive 0; Mismatches 20; Indels
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US-09-103-840A-1

US-09-103-840A-1

US-09-182-145-34

US-09-182-145-13

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US-09-182-145-13

US-09-182-145-14

US-09-182-145-14

US-09-182-145-14

US-09-18-145-14

US-09-18-275A-10

US-09-18-275A-10

US-09-23-42

US-08-410-54-4

US-08-72-56-1

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US-09-298-568-1

US-09-298-568-1

US-09-230-371A-20

US-09-230-371A-20
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64.98;
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Best Local Similarity 64.99
Matches 37; Conservative
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Best Local Similarity 64.9
Matches 37; Conservative
   RESULT 2
5449756-1/c
;Patent No. 5449756
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: LENGTH: 4035
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;Patent No. 5198359
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; LENGTH: 4035
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Patent No. 5198359
Patent No. 5449756
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Patent No. 5449756
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                                                                                                                          June 13, 2003, 02:39:09 ; Search time 4.64516 Seconds (without alignments) 4027.262 Million cell updates/sec
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Sequence 3
Sequence 3
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/barcCMB.seq:*
6: /cgn2_6/ptodata/1/ina/barcKilles1.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-194-145-1

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US-09-556-870A-1

US-07-918-314-5

US-07-918-314-5

US-08-469-412A-3

US-08-469-412A-1

US-08-64-412A-1

US-08-64-412A-1

US-08-69-12A-1

US-08-69-12A-1

US-08-826-134-3
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US-08-05-132A-1

US-08-15-652B-1

US-08-24-35A-1

PCT-US92-0534A-1

PCT-US92-07084-1

US-09-15-177A-7

US-09-17-177A-7

US-08-11-777A-7

US-08-451-77A-7

US-08-750-580-1
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                                                                                                                                                                                                                                                                                                                             441362 seqs, 153338381 residues
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                                                                                                                                                                                     US-09-826-581-5_COPY_200_260
61
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Maximum Match 1008
Listing first 45 summaries
                                                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match I
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1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCC 55
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                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,222A
FILING DATE: 04-DEC-1996
CLASSIFICATION NUMBER: 435
PRIOR APPLICATION NUMBER: 08/254,353
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
ATREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
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RESULT 4
US-08-750-222A-1
Sequence 1, Application US/08750222A
Fatent No. 6034061
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Rosen, Vicki A.
TAPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
TAPLICANT: Song, Jeffrey
TITLE OF INVENTION: BMP-9 COMPOSITIONS
UNMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Rapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: 61 5186B
TELEPONNUICATION INFORMATION:
TELEPONE: (617) 876-1170
TELEPONE: (617) 876-1170
INFORMATION FOR EEE ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
STRAIN: C57846xCBA
TISSUE TYPE: liver
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1564..1893
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STRANDEDNESS: double
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UNITS: bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
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02140
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LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
US-08-750-222A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WOZNEY, JOHN M.
APPLICANT: WOZNEY, JOHN M.
TITLE OF INVENTION: BMP-9 COMPOSITIONS
INMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OCMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,132A
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                                                                                                Sequence 1, Application US/08050132A
Patent No. 5601007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
FILING DATE:
CLASSIFICATION: 435
ATORNEY AGENT INFORMATION:
NAME: RADINGS, Bilen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDENDESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse liver cDNA
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STRAIN: C57846xCBA
TISSUE TYPE: liver
IMMEDIATE SOURCE:
LIBRARY: MOUSE liver CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 65.5
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat_peptide
LOCATION: 1564..1893
FEATURE:
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610..1896
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POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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Sequence 1, Application PC/TUS9507084
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Geleste, John M.
TILLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kapinos, Ellen J.
REGIERRATION WUBBER: 32,245
REFERENGA/DOCKET NUMBER: 31,245
REFERENGA/DOCKET NUMBER: 31,245
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 876-1210
TELEFAX: (617) 876-1210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 4, Application US/09750580; Patent No. 6455280; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 65.5%;
Matches 36; Conservative [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
1564..1893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN: C57B46xCBA
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
1..2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: ML14A
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                 rry: US
02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY:

, LOCATION:

PCT-US95-07084-1
                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-09-750-580-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920625
CLASSIFICATION:
                                                                                                                                                               APPLICANT: Worney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STRET: Legal Affairs - 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI 5186A
                                                                                                                   Sequence 1, Application PC/TUS9205374A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTORNOLIVE AND ADDRESS ADDRESS AND ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: Mouse liver cDNA CLONE: ML14A POSITION IN GENOME: UNITS: bp FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.3%;
Best Local Similarity 65.5%;
Matches 36; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
STRAIN: C57846xCBA
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide
LOCATION: 1564..1893
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 610.1896
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; LOCATION: 1..2447
PCT-US92-05374A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sn
                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA COUNTRY: US ZIP: 02140
                                                                                       PCT-US92-05374A-1
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PCT-US95-07084-1
                                                              RESULT 7
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 TCGGTGGAGGAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTC 59
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SCHWARE: Patentin Neberse #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOBER: 0S/08/451,777A
FILING DATE: 26.48Y-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: 709 Swedeland Road/UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 320..338
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 3194..3212
OTHER INFORMATION: 17-41-250.mis
LOCATION: 3232
OTHER INFORMATION: 17-41-250.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambollan, Dwight
TITLE (INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                        NAME/KEY: primer_bind
LOCATION: 1441..12461
LOCATION: 1441..12461
NAME/KEY: primer_bind
LOCATION: 1632..12651
OTHER INFORMATION: 17.40.rp complement
NAME/KEY: primer_bind
LOCATION: 2964..13984
OTHER INFORMATION: 17.41.pu
                                                                                                                                                                                                                                                           NAME/KET: primer_bind
LOCATION: 3422.14454
OTHER INFORMATION: 17-41.rp complement
NAME/KET: primer_bind
LOCATION: 300..318
OTHER INFORMATION: 17-42-319.mis
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_binding
LOCATION: 3201..3225
CHER INFORMATION: 17-41-250.probe
08-09-750-580-4
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OTHER INFORMATION: 17-42-319.probe
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US-08-451-777A-7/c
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                                                                 APPLICANT: Bihain, Bernard
APPLICANT: Bihain, Bernard
APPLICANT: Bunas Milne Edwards, Jean-Baptiste
APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Dundcart, Aymeric
APPLICANT: Bouclert, Lydie
APPLICANT: Bouqueleret, Lydie
APPLICANT: Ebbets:Reed, Dana
APPLICANT: Bouvouleret, Lydie
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR PILING DATE: 2000-06-21
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
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LOCATION: 1447
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
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LOCATION: 1241
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NAME/KEY: primer_bind
LOCATION: 553.11575
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 899.11920
OTHER INFORMATION: 17-39.pu
NAME/KEY: primer_bind
LOCATION: 1246.11267
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LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: exon 4
NAME/FET insc.feature
LACAG/TRON: 3941..5381
OTHER INFORMATION: 3'regulatory region
Yen, Frances
Denison, Blake
Bour, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 919..930
OTHER INFORMATION: exon 1
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OTHER INFORMATION: exon 2
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OTHER INFORMATION: exon 3
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LOCATION: 319
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LOCATION: 3213
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LENGTH: 5381
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                                                                                                                                                                                                                                                                                                                                                            Indels
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APPLICATION NUMBER: US/08/451,778A FILING DATE: 26-MAY-1995 CLASSFRICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            Query Match 40.3%; Score 24.6; DB 1; I Best Local Similarity 65.5%; Pred. No. 23; Matches 36; Conservative 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: 709 swedeland Road/UW220 CITY: King of Prussla STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Satent No. Sococia.
GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
APPLICANT: Stambolian, Dwight
APPLICANT: Stambolian, Dwight
APPLICANT: Stambolian, Dwight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
37,126
.... P50268-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P50268-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-451-778A-7/c; Sequence 7, Application US/08451778A; Patent No. 5830649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Eagle, Alissa M.
RECISTRATION NUMBER: 37,126
REFERENCE/DOCKET NUMBER: PS/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
      REGISTRATION NUMBER: 37,126
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
                                                                                     TELERAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic) US-08-451-7778-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 7676 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11:
MOLECULE TYPE:
                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-451-778A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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3 AAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGG 57

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3 AAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGG 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stambolian, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/998,208
                                                                                                                                                                                                                                                                              ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: 709 Swedeland Road/UW2220
                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24.6; DB; Pred. No. 23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/451,777
FILING DATE: 26-MAY-1995
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P50268-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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                                                                                                                    ; Sequence 7, Application US/08998208
; Patent No. 5880105
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-998-208-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
40.3%;
Best Local Similarity 65.5%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 610-2/2
INFORMATION FOR SEQ ID NO: 7'
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                  STREET: 709 Swedeland
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 7676 base I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                            RESULT 12
US-08-998-208-7/c
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OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KET: DITMET_DING
LOCATION: 1357...137
LOCATION: 1357...137
LOCATION: 12029...12060
CUBER INFORMATION: 17-42.pu
NAME/KET: primer_bind
LOCATION: 12029...1260
CUBER INFORMATION: 17-42.pu
NAME/KET: primer_bind
LOCATION: 12591...12603
CUCATION: 12591...12603
LOCATION: 14992...15012
LOCATION: 14992...15012
LOCATION: 14992...15012
LOCATION: 14960...15402
LOCATION: 15460...15482
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NAME/KEY: primer_bind
LOCATION: 45863.45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer_bind
LOCATION: 76644.76664
OTHER INFORMATION: 20-853.pu
                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 14271...15968
OTHER INFORMATION: exon 4
NAME/EXT: misc_feature
LOCATION: 15969...17969
OTHER INFORMATION: 3'regulatory region
                                                                                            NAME/KEY: misc_feature
LOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JTHER INFORMATION: 17-41.rp complement NAME/KEY: primer_bind LOCATION: 42070..42090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 20-841-149
NAME/KEY: allele
LOCATION: 45442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 20-828-311
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIHER INFORMATION: 20-842-115
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NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THER INFORMATION: 17-41-250
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                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: exon 3
                                                                                                                                                                                                                   INFORMATION: exon 1
                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 13470..13526
                                                                                                                                                                      NAME/KEY: exon
LOCATION: 12947..12958
                                                                                                                                                                                                                                                                                                                                        LOCATION: 13641..13752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 45328..45347
                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
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LOCATION: 42218
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                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
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  LENGTH: 81001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
Dundas Milne buwall.
APPLICANT:
Bougueleret, Lydie
APPLICANTON:
METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE OF INVENTION:
BRIOR PLING DATE: 2000-10-22
PRIOR FILING DATE: 2000-06-21
PRIOR FILING DATE: 1999-12-20
PRIOR PLICATION NUMBER: US 49/469/099
PRIOR PLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1999-12-22
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFFWARR: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.3%; Score 24.6; DB 5; Length 7676; Best Local Similarity 65.5%; Pred. No. 23; Matches 36; Conservative 0; Mismatches 19; Indels 0
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/06743 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yen, Frances
Denison, Blake
Bour, Barbara
Bihain, Bernard
Dumas Milne Edwards, Jean-Baptisle
                                                                                                                                                                                                                                                        PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-SEP-1944
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: PF0268-1
TELECOMMUNICATION INFORMATION:
TELEPHOME: 610-270-5024
TELECOMMUNICATION SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TTPE: nucleic acid
STRANDEDNESS: double
                                       ZIP: 19406-0939
COMPUTER READABLE FORM:
COMPUTER: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09750580 Patent No. 6455280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Yen, Fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-06743-7
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US-09-750-580-1
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APPLICANT:
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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC
                      APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENER, John C.
TITLE OF INVENTION: DAS REQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFRENCE: 24366-20007.00
CURRENT APPLICATION NEWER: US/09/103,840A
CURRENT APPLICATION NOS: 2
SOFTWARE: PATENTIN VOY: 2.1
SEQ ID NO 2
LEMETH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.7%; Score 24.2; D
Best Local Similarity 62.3%; Pred. No. 40;
Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: June 13, 2003, 06:01:06
Job time : 11.6452 secs
                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mycobacterium tuberculosis
      APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3821367 A 3821367
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US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 TCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTC 59
                               OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220.
LOCATION: 1220.
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 20-853-415.mis complement NAME/KEY: misc_binding LOCATION: 1227.1251
OTHER INFORMATION: 20-828-311.probe
                                                                                                                                                                                                           OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348.1.2366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15522.15240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_binding
LOCATION: 12335, 12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15229, 1523
OTHER INFORMATION: 17-41-250.probe
NAME/KEX: misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 20-842-115.probe NAME/KEY: misc_binding LOCATION: 77046..77070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 20-841-149.probe NAME/KEY: misc_binding LOCATION: 45430..45454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 20-853-415.probe
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US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6284328
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 20-853-415.mis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: primer_bind
LOCATION: 77059..77077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 42206..42230
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 33; Conserva
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0; Gaps

23;

DB 4; Length 4403765; Indels

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Sequence 5, Appli
Sequence 1640, Ap
Sequence 1640, Ap
Sequence 32, Appl
Sequence 30, Appl
Sequence 69, Appl
Sequence 1184, Ap
Sequence 119, App
Sequence 179, App
Sequence 9241, Ap
Sequence 9241, Ap
Sequence 4, Appli
Sequence 1, Appli
                                           (without alignments)
4579.068 Million cell updates/sec
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                         June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
                                                                                                                     1 acaaggcagaagtcggtgga.....ggggggaaggtcccggtcca
                                                                                                                                                                                                                                                                                                                                                            Published_Applications_NA:*

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4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 US-09-826-581-5
10 US-09-826-581-2
10 US-09-960-352-1640
9 US-10-175-523-67
9 US-09-995-793A-32
9 US-09-995-793A-30
10 US-09-995-793A-30
10 US-09-995-793A-30
10 US-09-957-76A-301
9 US-10-091-572-817
9 US-10-091-572-817
9 US-09-764-891-9241
9 US-09-764-891-9241
9 US-09-764-891-9241
10 US-09-80-107-2228
10 US-09-80-107-2228
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US-09-764-891-5478
US-09-764-891-10205
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                                                                                                                                                                                              1029858 seqs, 724030393 residues
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                                                                            US-09-826-581-5_COPY_200_260
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
OM nucleic - nucleic search, using sw model
                                                                                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                          seq length: 0 seq length: 20000000000
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Match Length DB
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389
389
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33795
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Perfect score:
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Maximum DB :
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US-09-962-832-154 Sequence 154, App US-09-962-832-154 Sequence 1950, App US-09-294-093B-950 Sequence 1950, App Sequence 1950, App US-09-84-761-5 Sequence 1950, App US-09-864-761-19652 Sequence 1952, App US-09-864-761-19652 Sequence 1952, App US-09-864-761-19652 Sequence 1952, App US-10-198-846-1313 Sequence 1952, App US-10-198-846-1313 Sequence 132, App US-09-398-34 Sequence 132, App US-09-398-34 Sequence 16, App US-09-39-254-16 Sequence 16, App US-09-39-254-16 Sequence 16, App US-09-39-254-16 Sequence 16, App US-09-991-537 Sequence 5637, App US-09-981-537 Sequence 5637, App US-09-981-537 Sequence 5637, App US-09-860-352-9661 Sequence 298, App US-09-992-598-298 Sequence 298, App US-09-993-298 Sequence 298, App US-09-999-338-298 Sequence 298, App US-09-999-338-298 Sequence 298, App US-09-999-338-298 Sequence 298, App US-09-989-735-298 Sequence 298, App US	ALIGNMENTS	Score 61; DB 10; Length 1647; Pred. No. 3.1e-11; 0; Mismatches 0; Indels 0; Gaps 0;
C 20 24.4 40.0 302250 10 21 24.2 39.7 139 10 22 24.2 39.7 1448 9 0 22 24.2 39.7 451 10 24 24.2 39.7 451 10 24 25 24.2 39.7 451 10 24 25 24.2 39.7 1448 9 0 25 24 29.3 26.8 10 24 39.3 26.8 10 24 39.3 26.8 10 24 39.3 26.8 10 24 39.3 26.8 10 24 39.3 26.8 10 24 23.6 38.7 26.9 0 23.6 38.7 26.9 0 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 38.7 26.9 2 0 24 23.6 23.6 38.7 26.9 2 0 24 23.6 23.6 23.6 2 0 24 23.6 23.6 23.6 2 0 24 24.7 26.9 2 0 24 23.6 23.6 23.6 23.6 23.6 23.6 23.6 23.6	ALIGNMER US-09-826-581-5 Sequence 5, Application US/09826581 Patent No. US20020142310A1 GENERAL INFORMATION: APPLICANT: Andersson, Leif APPLICANT: Marklund, Stefan TITLE OF INVENTION: VARIANTS OF THE HUMA, FILE REFERENCE: 11145-007001 CURRENT APPLICATION NUMBER: US/09/826,58 FILE REFERENCE: 11145-007001 FILE REFERENCE: 11145-007001 CURRENT FILING DATE: 2001-04-05 PRIOR APPLICATION NUMBER: US 60/195,665 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 14 SOFTWARE: FRASESO for Windows Version 4. SEQ ID NO 5 IENGTH: 1647 TYPE: DNA ORGANISM: HOMO SapienS FEATURE: NAME/KEY: CDS LOCATION: (20)(1486)	Query Match 100.0%; Best Local Similarity 100.0%; Matches 61; Conservative

90 da

RESULT 2 US-09-826-581-2 ; Sequence 2, Application US/09826581 ; Patent No. US20020142310A1

61 A 61 | 260 A 260

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Sequence 3.2. Application US/09995793A; Sequence 3.2. Application US/09995793A; Sequence 3.2. Application No. US2003005446A1; Publication No. US20030054446A1; GENERAL INFORMATION:

APPLICANT: Webor, Bernard H.F.; APPLICANT: Stochr, Heidi ...
TITLE OF INVENTION: No. US20030054446A1e1 retina-specific human proteins C7orf9, (CTRENT PREERINCE: 033488-001
CURRENT RELIAN DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/253,751
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/253,751
PRIOR FILING DATE: 2001-11-29
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
SORTWARE: SO ID NOS: 71
FIRE THE TENGRET: 50
TYPE: DNA
SORANISM: Homo sapiens
## APPLICANT: Rajan, Prithi
### TITLE OF INVENTION: WULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
### FILE REFRENCE: 3235/1J795-US3
### CURRENT APPLICATION WUMBER: US/10/175,523
### CURRENT FILING DATE: 2002-06-18
### PRIOR FILING DATE: 2001-09-151
### PRIOR FILING DATE: 2001-09-05
### PRIOR FILING DATE: 2001-09-05
### PRIOR FILING DATE: 2001-09-25
### PRIOR FILING DATE: 2001-09-25
### PRIOR FILING DATE: 2001-09-25
### PRIOR FILING DATE: 2001-11-14
### PRIOR FILING DATE: 2002-01-18
### PRIOR FILING DATE: 2002-03-04
#### PRIOR FILING DATE: 2002-03-04
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OTHER INFORMATION: genomic DNA, Exon from 101 to 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.3%; Score 27; DB 85.7%; Pred. No. 2.2; iive 0; Mismatches
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Best Local Similarity 64,99
Matches 37; Conservative
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US-10-175-523-67
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US-09-995-793A-32
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                                                          APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR RAPLICATION NUMBER: US 60/195,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1640, Application US/09960352
Patent No. US2002013713941
GENERAL INFORMATION:
Patent No. US2002013713941
GENERAL INFORMATION:
BAPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: MACHialagan, Ngqappan
APPLICANT: MACHialagan, Ngqappan
APPLICANT: MACHIALAGAN, NGCLE AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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. ORGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 08-LIH188-005-Q1-E1-B7
US-09-960-352-1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 83.6%; Score 51; DB 10; I
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ 10 2
LENGTH: 989
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Publication No. US20030096264A1
GENERAL INFORMATION:
APPLICANT: Brockman, Jeffrey
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Hook, Derek
Klimczak, Leszek
Laeng, Pascal
Palfreyman, Michael
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Matches 40; Conservative
                                                APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-826-581-2
                GENERAL INFORMATION:
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US-09-960-352-1640
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APPLICANT:
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APPLICANT:
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5 GGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCCA 61
TITLE OF INVENTION: Methl and Meth2 Polynucleotides and Polypeptides CURRENT APPLICATION NUMBER: US/09/373,658
CURRENT APPLICATION NUMBER: US/09/373,658
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 125
SEQ ID NOS: 125
SEQ ID NO 69
LENGTH: 8670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2184, Application US/09880107
Fatent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: HOLNE, Darci T.
APPLICANT: Scherf, Useph G.
APPLICANT: Scherf, Use C.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REPERENCE: 44921-5028-W0
CURRENT PLING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-16-14
PRIOR REPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOUTHWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L25880
US-09-880-107-2184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 9; Length 8670;
Pred. No. 12;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Unknown Organism:Unknown US-09-373-658-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 179, Application US/09822830A
; Patent No. US20020142952A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agostino, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Howes, Steven H.
Resnick, Richard J.
Gulukota, Kamalakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.9%;
Matches 37; Conservative
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Clark, Hilary
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-822-830A-179
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LENGTH: 33795
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT APPLICATION NUMBER: US/00/236,109
PRIOR FILING DATE: 2000-09-28
APPLICANT: Stoehr, Heidi
TITLE OF INVENTION: No. US20030054446Alel retina-specific human proteins C7orf9, C12d
FILE REPERENCE: 033488-001
CURRENT APPLICATION NUMBER: US/09/995,793A
CURRENT FILING DATE: 2001-11-29
PRIOR PLIJNG DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
; OTHER INFORMATION: artificial sequence, Translation start at 347, stop at 604
US-09-995-793A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 9; Length 1188;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 301, Application US/09967768A Patent No. US20020150877A1
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Publication No. US20030092900A1
GENERAL INFORMATION:
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SOFTWARE: Patenlin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.0%;
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Best Local Similarity 64.94
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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US-09-373-658-69/c
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2000-08-3

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PRIOR APLICATION NUMBER: 60/229, 343
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-05
PRIOR PELICATION NUMBER: 60/229, 513
PRIOR APPLICATION NUMBER: 60/229, 509
PRIOR PILING DATE: 2000-09-05
PRIOR PILING DATE: 2000-09-05
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-10-02
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PRIOR FILING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-39
PRIOR PLING DATE: 2000-10-13
PRIOR PLING DATE: 2000-10-0-19
PRIOR PLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241, 787
PRIOR PRIOR PLING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR APPLICATION NUMBER: 60/241, 785
OR FILING DATE: 2000-10-20
OR FILING DATE: 2000-11-01
OR APPLICATION NUMBER: 60/224, 617
OR FILING DATE: 2000-11-01
OR APPLICATION NUMBER: 60/225, 268
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/236, 368
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/251, 856
OR APPLICATION NUMBER: 60/251, 868
OR FILING DATE: 2000-12-08
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/251, 868
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/251, 868
OR FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                     DR APPLICATION NUMBER: 60/220,964

DR FILING DATE: 2000-07-26

DR APPLICATION NUMBER: 60/241,809

DR FILING DATE: 2000-10-20

DR APPLICATION NUMBER: 60/249,299

DR FILING DATE: 2000-11-17
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PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/236,370
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,802
                                                                             APPLICATION NUMBER: 60/224,518
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/236,369
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APPLICATION NUMBER: 60/237,037
FILING DATE: 2000-10-02
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APPLICATION NUMBER: 60/234,997
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APPLICATION NUMBER: 60/249,210
                                                                                                                                                                                                            APPLICATION NUMBER: 60/224,519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/236,327
FILING DATE: 2000-09-29
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                APPLICATION NUMBER: 60/228,924
                                                                                                                                                                              FILING DATE: 2000-09-29
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                                                                                                                                                                                                                                       FILING DATE: 2000-08-14
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
SEQ ID NOS: 631
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 179
LENGTH: 2996
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24.6; DB 10; Length 2996;
Pred. No. 19;
0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 817, Application US/10091572
Publication No US20030054373A1
Publication No US20030054373A1
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAILSCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/091,572 CURRENT FILING DATE: 2002-03-07
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PRIOR PELICATION NUMBER: 09/764,850
PRIOR FILING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2000-01-31
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-14
PRIOR PELING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR PELING DATE: 2000-07-16
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-08-14
PRIOR PELING DATE: 2000-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-09-21
APPLICATION NUMBER: 60/234,223
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 65.5%;
Matches 36; Conservative 0
                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-179
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PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/226,681
PRIOR APPLICATION NUMBER: 60/225,759
PRIOR PLING DATE: 2000-08-14
PRIOR PELING DATE: 2000-09-16
PRIOR PELING DATE: 2000-09-16
PRIOR PELING DATE: 2000-09-16
PRIOR PELING DATE: 2000-09-16
PRIOR PELING DATE: 2000-19-17
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000
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FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/241,786
FILING DATE: 2000-10-20
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APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bour, Barbara
APPLICANT: Bour, Barbara
APPLICANT: Bour, Barbara
APPLICANT: Bour, Branch
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: APOLIPOPROTEIN A-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNDICANT:
TITLE OF INVENTION: APOLIPOPROTEIN A-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNDICANT:
TITLE OF INVENTION: APOLIPOPROTEIN A-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNDICATION NUMBER: US 09/894,364
CURRENT FILING DATE: 2001-04-22
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9241, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
    FILE REFERENCE: PCOOR
    CURRENT APPLICATION NUMBER: US/09/764,891
    CURRENT FILING DATE: 2001-01-17
    Prior application data removed - consult PALM or file wrapper
    NUMBER OF SEQ ID NOS: 10231
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 9241
    LENGTH: 5312
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                                                                                                                                                                                                                       DB 9;
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                                                                                                                                                                                                                   Query Match 40.3%; Score 24.6; DB Best Local Similarity 65.5%; Pred. No. 18; Matches 36; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09842364; Publication No. US20030032783a1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yen-Potin, Frances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-764-891-9241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patent.pm
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US-09-842-364-4
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MANEAKER: COULLICL
LOCATION: 147
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
NAMEKER: primer_bind
LOCATION: 1.1022
OTHER INFORMATION: 17-42.pu
NAMEKER: primer_bind
LOCATION: 53:.11575
OTHER INFORMATION: 17-39.pu
NAMEKER: primer_bind
LOCATION: 19-9..11920
OTHER INFORMATION: 17-39.pu
NAMEKER: primer_bind
LOCATION: 12-6..12267
OTHER INFORMATION: 17-39.pu
NAMEKER: primer_bind
LOCATION: 12-6..12267
OTHER INFORMATION: 17-39.pu
NAMEKER: primer_bind
LOCATION: 23-64..1384
OTHER INFORMATION: 17-41.pu
NAMEKER: primer_bind
LOCATION: 33-1.414.pu
NAMEKER: primer_bind
LOCATION: 31-3..1454
OTHER INFORMATION: 17-42.319.mis complement
NAMEKER: primer_bind
LOCATION: 313-1.4154
OTHER INFORMATION: 17-42-319.mis complement
NAMEKER: primer_bind
LOCATION: 319-3.33
OTHER INFORMATION: 17-42-319.mis complement
LOCATION: 314-.323
OTHER INFORMATION: 17-41-250.mis complement
NAMEKER: primer_bind
LOCATION: 314-.323
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OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: CONTLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 3213
OTHER INFORMATION: 17-41-250 : polymorphic base C or
NAME/KEY: conflict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 17-42-319 : polymorphic base C or NAME/KEY: allele
                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 2243..3940
OTHER INFORMATION: exon 4
NAME/KEY: misc_feature
LOCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 919..930
OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                              LOCATION: 1442..1498
OTHER INFORMATION: exon 2
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OTHER INFORMATION: exon 3
                                                                     ORGANISM: Homo sapiens
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SEQ ID NO 4
LENGTH: 5381
                                                   TYPE: DNA
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                                                                                               FEATURE:
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APPLICANT:
APPLICANT:
APPLICANT:
Dumas Milne Edwards, Jean-Baptiste
APPLICANT:
Bougueleret, Lydie
APPLICANT:
Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWT)
FILE REFERENCE:
BOUGUERENT APPLICATION NUMBER: US/09/751,877
CURRENT APPLICATION NUMBER: US/09/751,877
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 4
LENGTH: 5381
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                                                                                                                                               Query Match
40.3%; Score 24.6; DB 9; Length 5381;
Best Local Similarity 70.2%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                            13 TCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTC 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1447
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
MANE/KEY: Primer bind
LOCATION: 1..11022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
LOCATION: 919..930
OTHER INFORMATION: exon 1
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OTHER INFORMATION: exon 4
NAME/FEY: misc_feature
LOCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
CTHER INFORMATION: 17-42-319.probe NAME/KEY: misc_binding LOCATION: 3201..325 CTHER INFORMATION: 17-41-250.probe US-09-842-364-4
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09751877
; Patent No. US20020142949A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bihain, Bernard
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APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
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LOCATION: 1442..1498
OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1613..1724
OTHER INFORMATION: exon 3
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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LOCATION: 319
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US-09-751-877-4
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Sequence 2228, Application US/09880107
Sequence 2228, Application US/09880107
Sequence 2228, Application
Sequence Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REPERBUCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
SPRIOR FILING DATE: 2000-06-14
SUMMER OF SEC ID NOS: 3950
SOFTWARE: PACENTIN VOS: 3950
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Live 0; Mismatches 14; Indels 0;
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             COCATION: 553..11575
COCATION: 553..11575
COCATION: 553..11575
COCATION: 553..11575
COCATION: 899..11920
COCATION: 899..11920
COCATION: 1246..12267
COCATION: 1246..12267
COCATION: 1441..12461
COCATION: 1441..12461
COCATION: 1632..12651
COCATION: 1632..12651
COCATION: 1632..12651
COCATION: 1632..12651
COCATION: 2646..13984
COCATION: 2644..13984
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COCATION: 2646..13984
COCATION: 2604..13984
COCATION: 320..388
COCATION: 3214..3232
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OTHER INFORMATION: 17-42-319.probe
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Matches 33; Conservative
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LOCATION: 3201..3225
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ORGANISM: Homo sapiens
NAME/KEY: primer_bind
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LENGTH: 8095
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US-09-751-877-4
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June 13, 2003, 01:49:14; Search time 192.613 Seconds (without alignments) 9216.782 Million cell updates/sec
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1 999ctgggatgacgaactgc.....acatgcgcttcatgcaggag
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            2054640 segs, 14551402878 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenEmbl:*

1: gb_ba:*

2: gb_htg:*

4: gb_om:*

5: gb_pt:*

7: gb_pt:*

8: gb_pt:*

9: gb_pt:*

10: gb_cx:*

10: gb_cx:*

11: gb_sx:*

11: gb_sx:*

12: gb_sx:*

13: gb_li:*

14: gb_vi:*

15: gb_sx:*

16: m_bun:*

17: m_bun:*

18: m_bun:*

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em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a

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Result No.	Score	Query Match	Length	图	QI QI		Descript	tion
7 7	61	100.0	989 1647	99	AX281579 AX281582		AX28157	Seque
m ~	61	100.0	2109	w w	AX099776		\mathbf{a}	6 Sequence
* rv	61	100.0	2115	9 00	AF214519		AF21451	s sequence 9 Homo sapi
υ r	61	100.0	152129	n o	AC027416		AC02741	6 Homo sapi
	57.8	94.8	2290	י סי	HSA249977		AJ24997	7 Homo sapi
φ Έ	48.2	79.0	1867	9 4	AX099774		AX09977	4 Sequence
11	48.2	79.0	1873	rφ	AX099800		AX09980	O Sequence
12	48.2	79.0	1873	w w	AX398331		AX39833	1 Sequence
14	48.2	79.0	1873	ى م	AX398335		AX39833 AX39833	3 Sequence 5 Sequence
15	48.2	79.0	1873	ωı	AX398337		AX39833	7 Sequence
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1 .	48.2	79.0	5888	4	AF214521		AF21452	1 Sus scrof
c 19	47.2	77.4	227724	N 0	AF336381		AF33638	Mus mus
21	41.8	68.5	190183	4 (7	AC129703		AC12970	3 Rattus no
7 7	41.8	68.5	192968	(1)	AC127107		AC12710	7 Rattus no
c 24		44.9	35018	n m			AC00589	3 Leishmani
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27		4 4 5 8 5 9 7 0	14856	-	AE009112 AE008077		AE00911 AE00807	<pre>4 Agrobacte 7 Agrobacte</pre>
79 39	26.2	43.0	14101	-10	AE009874		AE00987	4 Pyrobacul
M W		42.3	1917	10	AC113363 AF002245		AC11538 AF0022	s kattus no 45 Cricetulu
31		42.3	4279	10	AF039574		AF0395	Mus musc
nm	25.8	42.3	17570	7 -	AE007063		AF1128 AE00706	3 Mycobacte
c 34		42.3	39430	н.	MTCY49		273966	Mycobacteri
36	25.6	42.3	183496 217		AC125075 HSJ110B2		AC12507 AT.1593	5 Mus muscu 76 STS from
c 37		42.0	38819		AC091120		AC09112	0 Leishmani
30 88		42.0	110000		AC121230 AC124396 2		AC12123	0 Leishmani ation /3 of
4		41.6	15586				AE00007	8 Rhizobium
0 41 5	25.4	w w	140053		AC099721		AC09972	1 Homo sapi
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44	25.4	41.6	158808		AC106429		AC10642	AC106429 Rattus no
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ACCESSION VERSION		AX281579 AX281579.1	GI:1	:16608830	330			
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PEFFRENCE		Mammalia; E	Eutheria;	ia;	mates;	Ġ	i; Hominidae; H	Ношо.
AUTHORS		Andersson, L., Luthman, F Variants of the human a	L., Lui	Luthman, H e human a	d. and	Marklund, S.	kinase gamma	ma 3 գոհորոք
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LVANGVRAAPLWDSKKQSFVGMLTTTDF1LVLHRYYRSPLVQIYEIBQHX1ETWREIY
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VGLYSRFDVTHLAAQOTYNHLDMSVGBALRQRTLCLEGVLSCQPHESLGEVIDRIARE
OVRILVILVBTQHLGVYSLSDTLGALVLSPAGIDALGA"
502 c 462 g 337 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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I Similarity 100.0%; Pred. No. 3.3e-10;
61; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 61; Conservative 0; Mismatches 0;
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20. .1489
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Sequence 5 from Patent W00177305.
AX281582
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/db_xref="taxon:9606"
306 c 286 g 168
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LWDSKKQSFVGMLTITDFILVLHRYTRSPLVQIYEIEQHKIETWREIYLGGCFKPLVS
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HLAAQOTYNHLDANSVGEALRQYTLCLEGVLSCQPHESLGEVJDRIAREQVHRLVLVDB
TQHLLGVVSLSDILQALVLSPAGIDALGA"

621 c 560 g 470 t
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 2115)

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Tannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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1 Similarity 100.0%; Pred. No. 3.4e-10;
61; Conservative 0; Mismatches 0;
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AX099776 2109 bp
Sequence 3 from Patent W00120003.
AX099776
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RFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLMDSKKQSFVGKLTI
TDFILVLHRYRRSPLOQIYELEQHKIETWRELYLQGCFKBLVSISPUNGLFEAVYTLI
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AVVLETAPTLIADIFVDRRVSALPVVNRCGOVVGLYSRFDVIHLAAQOTVHLDMSV
GEALRQRTLCLEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
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Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
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SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAFFPKLGWDDELRKPGAQIYM
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PEPGGGERRRPTALGADPAGGGTPPTGMCLESDCTASAAG
SSTDDVELATEFPTAMECELEGLEERPALCLSPQAPPTGMDCLRSPGTARGES
SSTDDVELATEFPTAMECELEGLEERLEARALANGVRAAPLGMDDELKRFRAGITM
RENGESTCYDAMSTSKLVJFOTMLEIKKAFFALVANGVRAAPLUNDSKKQSFVGMLTI
TDFILVLHRYTRSPLVOTYEIROHKIETWREITLOGCFRUDSISPROSELREWYTLI
KNRTHHLAUDDVSGNVHLHITHWRLLAKPHLHFGSLLPRPSFLYFTIOLGGGGGGTRDL
AVVETAPILTALDIFVDRRYSALDVVURGCGVVGITSREPSITYRTIOLGGGGGGTRUDMSY
GEALRQFTLCLEGVLSCQPHESLGEVIDRIARREQVHRLVLVDETQHLLGVVSLSDILQ
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Milan,D. Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paull,S., Tannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gallardt,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
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                                                                                                                                                                                                                                                                                                                                                      Length 2115;
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l Similarity 100.0%; Pred. No. 3.4e-10;
61; Conservative 0; Mismatches 0; Indels
                       /note="unnamed protein product"
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Science 288 (5469), 1248-1251 (2000)
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                                             /codon_start=1
/protein_id="CAC35801.1"
/db_xref="G1:13538837"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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AF214519
AF214519.1 GI:8215681
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...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                     Center Clone name: 504.6_11

Center Clone name: 504.6_11

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 145264 bases at least Q30
Consensus quality: 145264 bases at least Q30
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12557 12656: gap of 100 bp 12657 12656: gap of 100 bp 12657 15044 1513: contig of 1387 bp in length 15144 15123: contig of 1980 bp in length 17124 1723: gap of 100 bp 1724 19466: contig of 1243 bp in length 19467 19566: gap of 100 bp 1955 22028: contig of 2243 bp in length 21952 22028: gap of 100 bp 22028: gap of 2291 bp in length 22029 24319: contig of 2291 bp in length
                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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27059: contig of 2640 bp in length

27159: gap of 100 bp

30170: contig of 3011 bp in length

30270: gap of 100 bp

33968: contig of 3698 bp in length
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12556: contig of 2473 bp in length
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38179; contig of 4111 bp in length
38279; gap of 100 bp
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46855: contig of 3899 bp in length
46465; gap of 100 bp
51285: contig of 4820 bp in length
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66595: contig of 5900 bp in length
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                                                                                                                          Center project name:
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66596 66695; gap of 100 bp 66696 73218; contig of 6523 bp in length 73219 77115; contig of 3797 bp in length 77215; gap of 100 bp 77319 77115; contig of 3797 bp in length 77215; gap of 100 bp 100 bp 77316 77215; gap of 100 bp 100 bp 85123 93314; contig of 8192 bp in length 93315 101193; contig of 8192 bp in length 101194 101293; gap of 100 bp 101294 113090; contig of 1779 bp in length 101294 113090; contig of 11797 bp in length 113091 gap of 100 bp 113191; gap of 100 bp 113191; gap of 100 bp 113191; and specified in length 11391; gap of 100 bp 113938 137937; gap of 100 bp 113938 152129; contig of 14192 bp in length.
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66696. .73218
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Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2001 this sequence version replaced gi:13431203.
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Submitted (08-SEP-1999) Cenome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 206854)
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Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Catarrhini; Hominidae; Homo.
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Center code: WUGSC
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                  100.0%; Score 61; DB 2; I
llarity 100.0%; Pred. No. 4.1e-10;
Conservative 0; Mismatches 0;
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                                     77216. .eo.22
/note="assembly_fragment"
85123. .93314
/note="assembly_fragment"
93415. .101193
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/note="assembly_fragment"
101294. .113090
/note="assembly_fragment"
                  /note="assembly_fragment"
77216. .85022
'note="assembly_fragment"
73319. .77115
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Mammalia; Eutheria; Primates;
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Sulston, J.E. and Waterston, R.
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5 (bases 1 to 206854)
Waterston, R.H.
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3 (bases 1 to 206854)
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Best Local Similarity
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catransee, J.J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Louis
                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

Location/Qualifiers

1. 206854
                                                                                                                                                                                                                                                                                                                                                                                                                       all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >> 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. I MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Data from AC079810 and AC073128 was used to finish this clone,
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/note="match to EST BI059713 (NID:914467240)"
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/note="match to EST BG477625 (NID:913409904)"
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    /note="match to EST AW880850 (NID:g8042860)"

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/note="match to EST BE314060 (NID:g9134719)"
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/note="similar to Homo sapiens EST BI114348
(NID:g14565249)"
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence, see http://genome.wustl.edu/gsc
                                                                                                       Center project name: H_NH0459119
                                                                          Summary Statistics
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/db_xref="taxon:9606"
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LSPQAPFPKLGWDDELRKPGAQIYMRFIEBHTCYDAMATSSKLVIFDTMLEIKKAFFA
LVANGVRAAPLWDSKKOSPYGMLITDFILVLHRYTRSPLVQIYELEGUK EFFWREIT
LOGGCKFPLVSISPSLFAVYTLIKNRIHRLPVLDPVSGVVLHILTHKRLIKFLHIF
GSLLPREPSFIYETIODIGIGTFRDLAVVLEFARIIGALDIFVDRRVSALPVVNBCGQV
VGLYSRFDVIHLAAQQIYNHLDMSVGEALRKRILCLEGVLSCQPHESLGEVIDRIARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit (AMPK gamma 3 gene).
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DPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC
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1 (bases 1 to 2290; Cheung, P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D. Characterization of Amractiated protein kinase gamma-subunit lisoforms and their role in AmP binding

Blochem. J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
Homo sapiens.
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/product="Amb-activated protein kinase gamma 3 subunit"
/protein_id="CaB65117.1"
/db_xref="GI:6688201"
                                       /note-"match to EST AA043371 (NID:g1521226) zk53e10.rl"
967. .1090
                  /note="match to EST A1656812 (NID:g4740791) tt54b06.x1"
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                                                                                                                                                                                           Length 206854;
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/note="similar to Homo sapiens EST B1114348
(MD:914565249)"
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                                                                                                                                                                                           Query Match 100.0%; Score 61; DB Best Local Similarity 100.0%; Pred. No. 4.1 Matches 61; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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594. .763
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                                         4 . 37
/note="match to EST A1670836 (NID:94850567) wa04g10.x1"
                                                                                                                                                      281. .344
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281. .344
                                                                                                                                                                                                                                                                                                             /note-"match to EST BE047599 (NID:98364652) tz39c01.yl"
281. .344
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/note="match to EST AA043371 (NID:91521226) zk53el0.rl"
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/note-"match to EST BIO59713 (NID:g14467240)"
594. .763
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/note="match to EST BG992568 (NID:g14396638)"
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281. .344
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281. .344
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281. .344
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281. .344
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594. .763
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(NID:914565249)"
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                                                                                   /note-"match to EST C05773 (NID:g1502549)"
220. .221
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/db_xref="G1:815684"
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HEWQEHTCYDAMATISSKLVIFDTWLEIKKAFPALVANGVRAAPLWDSKRQSFVGMITT
TOFILVLHRYTRSPLVQITSIEBKHIFWREITYGGCKFRLVSTSPNDSLFRAVYALI
KNRIHALDVLDDVGSAVLHILTHKRLIKFLHFGTLLPRPSFLYRTIQDLGIGTFRUL
AVVLETAPILTALDIFVDRRSALPVNETGQVVGLYSREDVIHLAAQTYWHILDMNV
ALVLSFARGIDALGA"
ALVLSFARGIDALGA"
375 t
580 c
535 g
376 t
                                                                                                                                         A mutation in PRRAG3 associated with excess glycogen content in pig skeletal muscle Science 288 (5469), 1248-1251 (2000)
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                 Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundatron,R., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                   Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
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Pred. No. 7.2e-06;
0; Mismatches 8; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="skeletal muscle"
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AX099800
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1. 1873
/organism="Sus scrofa"
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/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="PRKAG3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AMPKG3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PRKAG3"
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KEYWORDS
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mRNA, complete cds.
AF214520
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LWDSKKQSFVGMLTITDFILVLHRYTRSPLVQIYEIEEHKIETHREIYLGGCFKPLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISPNDSLFEAVTALIKNRIHRLPVLDPVSGAVLHILFHKRLLKFLHFGTLLPRPSFL
YRTYQDLGTGTFRDLAVVLETAPILTALDIEVDRRYSALPVVNETGQVVGLYSRFDVI
HLAAQQYYNHLUMNVGEALNQRYLCLECVLSCQPHETLGEVIDRIVREQVHRLVLDB
YQHLLGVYSLDDILQALVLSPAGIDALGA"
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          same, and uses thereof
Patent: Wo 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Lelf (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variants of the gamma chain of ampk, dna sequences encoding the
                                                                      1 GGGTGGGATGACGAAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCGTTCATGCAGGA
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   Length 2290;
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Pred. No. 7.2e-06;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                           linear
                                      Indels
Score 57.8; DB 9;
Pred. No. 4.1e-09;
0; Mismatches 2;
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/note-"unnamed protein product"
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AX099774
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/organism="Sus scrofa"
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94.8%;
96.7%;
               Similarity 96.7 59; Conservative
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Best Local Similarity
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Sus scrofa
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AF214520
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AUTHORS
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TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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                  TOFTLVLHRYYRSPLVQIYEIEBHKIETWREIYLQGCFKPLVSISPUOSLFBAVYALI
KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQOLGIGTFRDL
                                                            AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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Novel prkag3 alleles and use of the same as genetic markers reproductive and meat quality traits
Patent: WO 0220850-A 3 14-MaR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 79.0%; Score 48.2; DB 6; Similarity 86.9%; Pred. No. 7.2e-06; 53; Conservative 0; Mismatches 8;
                                                                                                                                                                                         Score 48.2; DB 6;
Pred. No. 7.2e-06;
0; Mismatches 8;
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/db_xref="taxon:9823"
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86.9%;
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Sus scrofa
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GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPIAEVDNPPTERDILPSDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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TOFTLVLHRYTRSPLVOLYET BEHK ETWRELYLOGCFREDVSTSPONSLFBAYALL
TOFTLVLHLYDVDPVSGAVLHLTHRALKFHLHFGTLLDFRPSELYRTIQDLG IGTPRDL
AVVLETAPILTAPILFOLDFVORVASLPVVNETGOVVGLYSREDVIHLAAQOTYNHLDMVN
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVVBEQVHRLVLVDETQHLLGEVVSLSDILQ
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                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAFLAEVDNPPTERDILPSDCAASAS
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Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
Patent: WW 0020360.A 1 14-WAR-2002;
Iowa State University Research Foundation, Inc. (US)
                                                                                                                       same, and uses thereof
Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
1. 1873
                                                                                                     Variants of the gamma chain of ampk, dna sequences encoding the
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                                        Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
1 (bases 1 to 1873)
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/organism="Sus scrofa"
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1. .1395
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580 c 53
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Best Local Similarity 86.9%;
Matches 53; Conservative
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Sus scrofa
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VERSION
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                      REFERENCE
                                             AUTHORS
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PAT 27-MAY-2002

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/codon_start=1
/protein_id="cap2667.1"
/db_xref="G1:21261111"
/db_xref="G1:2126111"
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/db_
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AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 7 14 *MAR-2002,
IOWA State University Research Foundation, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                 Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 5 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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                                                                     linear
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                                        AX398335 1873 bp
Sequence 5 from Patent W00220850.
AX398335
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AX398337
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1. 1395

    1873
    /organism="Sus scrofa"

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1. .1395
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580 c 5
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Best Local Similarity 86.9
Matches 53; Conservative
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TDFILVLHRYKSPLVQYYBEDERIKTETWRETTYGGCFRFYSISPNDSLFEAYYALI
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KNRTHRLPVLDPGSGAVLHILTHKRLLKFLHFGTLLPRPSFLYSISPNDSLFEAYYALI
GEALRGRILCLEGYLLGGVTDRIVUNETGQVVGLSSRFDVHLDANY
GEALRGRILCLEGYLLGGVTLSTUNETVREQVHRLILVNDETQHLLGVVSLSDILQ
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Pred. No. 7.2e-06;
0; Mismatches 8; Indels
/note="unnamed protein product"
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Job time: 194.613 secs
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Human AMPK ganma s
Pig AMPK ganma sub
Pig AMPK ganma sub
Pig AMIC ganma sub
Pig wild-type PKKA
Pig PRKAG3 polymor
Pig PRKAG3 polymor
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PRKAG3 cDNA. Homo
                                                                                                                                      June 13, 2003, 01:37:39; Search time 22.1613 Seconds (without alignments) 6198.732 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                          2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                            Sequence:
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CDNA sequence enco
Mycobacterium tube
Mycobacterium tube
Aspergillus oryzae
Rhizobium species
                                                                                                             DNA encoding novel
DNA encoding novel
Human peptidase NA
Human peptidase NA
 Pig PRKAG3 polymor
Pig PRKAG3 polymor
Sus scrofa PRKAG3
                                                               DNA encoding novel
Human lung specifi
Drosophila melanog
                                                                               Phytase gene. Asp
A. terreus phytase
Drosophila melanog
                                                                                                   DNA encoding novel
Human protein enco
                                                                                                                                            Human peptidase NA
Human peptidase NA
Human peptidase NA
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C-C chemokin
                                                                                                                                                                                 Primate GPR2 seque
Human C-C chemokin
                                                Pseudomonas aerugi
Human polynucleoti
                                                                                               Drosophila melanog
                                                                                                                                   peptidase NA
peptidase NA
                                                           Human polynucleoti
                                                                                                                                                            DNA encoding novel
                                          Rhizobium species
                                                                                                                                                                                                                                                                        Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
                                                                                                                                   Human
                                                                                                                                                                       Human
                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                     /note= "3' portion of intron 2"
                                                                                                                                                                                                      ALIGNMENTS
                AAA64328
AAI99683
AAI99682
AAF12737
AAV30458
AAV30459
AAS54367
AAD36459
AAD36460
AAD03321
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AAS74015
AAS74014
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AAZ58305
AAZ58306
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AAZ58310
AAS74016
AAZ58307
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                                                                    AAD32338
ABL19505
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AAZ27414
ABL19504
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AAS74013
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AAZ58304
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                                                                                                                                                                           ABL40464
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946..989
/*tag= e
/number= "Intron 4"
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                                                                                                                                                                                                                                                                                                                 "Intron
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/number= "Intron
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 PRKAG3 intron 2 - intron 4.
                                                                                                                                                                                                                                                   21-JAN-2002 (first entry)
1873
1873
2022
5259
4403765
4411529
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                               534720
536165
                                              1473
7818
7818
7818
14533
14917
1406
2327
2327
2327
3406
3593
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Homo sapiens
                                                    225.88.2
225.88.2
225.88.2
225.88.2
255.88.2
255.88.2
255.88.2
                                                                                                                                                                                                                                         AAH43682;
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'note= "Causes P71A"

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61 G 61
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                                                                                                                              18-OCT-2001
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             variation
                                                     variation
                                                                                                                                                                                                                                                                                                  variant -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD03296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCCAGATCTACATGCGGCTTCATGCAGGA 60
                                                                                                                                                                     New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                          The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 61; DB 22; Length 989; 100.0%; Pred. No. 1.6e-12; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
 portion of intron 4"
                                                                                                                             Marklund S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "PRKAG3"
230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH43685 standard; cDNA; 1647 BP.
                                                                                                                                                                                                                         Example 1; Fig 2; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/label= "C230G"
                                                                                   07-APR-2000; 2000US-195665P.
                                                             06-APR-2001; 2001WO-SE00765
/note= "5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                             Luthman H,
                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 100.
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20..1489
                                                                                                                                                 WPI; 2001-657170/75.
                                                                                                       (AREX-) AREXIS AB
                    WO200177305-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 882 G 882
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                                                                                                                             Andersson L,
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                                          18-OCT-2001
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                                                                                                                                                                                                    variant -
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution of a G for a C at nucleotide 550; and in exon 0 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCCAGATCTACATGCGCCTTCATGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1647;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 61; DB 22;
100.0%; Pred. No. 1.7e-12;
tive 0; Mismatches 0;
                                                /note= "Silent variation"
1037
                                                                                                                                   /*tag= d
/label= "C1037T"
/note= "Causes R340W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marklund S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5; 25pp; English.
C "T559C" -
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                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2001; 2001WO-SE00765.
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                               /label=
   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersson L, Luthman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-657170/75.
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Human, gamma subunit; adenosine monophosphate-activated kinase; AMPK; FKKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.

Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.

AAD03320 standard; cDNA; 2115 BP.

G 489

489

13-JUN-2001 (first entry)

AAD03320;

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a sequence encoding the first cystathione beta synthase (CBS) domain PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRKAG3. Mutation in Prkag3 results in an altered regulation for carbohydrated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle- PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalm E, Milan D, Robic A, Rogel-Gaillard C;
I, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is a cDNA encoding human adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
                                                                                                                                                      /*tag= b
/product= "Human Prkag3 protein"
1390..2109
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                                                                                                                                                                                                                                                                                                                                                                                                      (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 2; 71pp; English.
                                                                                                                                                                                                                                                                                                                 11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                10-SEP-1999; 99EP-0402236.
18-MAX-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Looft C, Ka, Gellin J,
                                                                                                                       /*tag= a
472..1389
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                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                       ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-244810/25.
P-PSDB; AAE00221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KALM E.
                                                                                                                                                                                                                                              WO200120003-A2.
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                                                  Homo sapiens.
                                                                                                                                                                                                                                                                              22-MAR-2001.
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                                                                                     Key
5'UTR
                                                                                                                                                                                         3'UTR
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Iannuccelli N, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                             /product= "Human complete Prkag3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 65-68; 71pp; English.
                                                                                                                                                                                      Location/Qualifiers
1..1395
                                                                                                                                                                                                                                                                                                                                                              11-SEP-2000; 2000WO-EP09896.
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18-MAY-2000; 2000EP-0401388.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KALM/) KALM E.
                                                                                                                                                                                                                                                                                     WO200120003-A2.
                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                          22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myopathy
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such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a
cheterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                       Pig; gamma subunit; adenosine monophosphate-activated kinase; AMFK; prakkā3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbolydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sus scrofa complete Prkag3 protein"
                                                                                                                                                                                                                                                                                                      Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    Score 48.2; DB 22;
Pred. No. 7.6e-08;
0; Mismatches 8;
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD03319 standard; cDNA; 1873 BP.
                                                                                                                                                                                                                                                                                                                                      79.0%;
86.9%;
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18-MAY-2000; 2000EP-0401388.
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/product= "
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                                                                                                                                                                                                                                                                                                                                                     Local Similarity 86.9
tes 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200120003-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 G 61
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                                                                                                                                                                                                                                                                                                                                    Query Match
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AAD03319
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robic A, Rogel-Gaillard C;
                                                                                                             1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.
                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                             0
                                               Length 2115;
                                                                                                                                                                                                                                                                                                                                                                                   Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                                                             Indels
               Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sus scrofa PRKAG3 protein"
                                             Query Match 100.0%; Score 61; DB 22; Best Local Similarity 100.0%; Pred. No. 1.8e-12; Matches 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
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(ANDE), ANDERSSON L.
(LOOF/) LOOFT C.
(RALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                       AAD03295 standard; cDNA; 1867 BP.
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18-MAY-2000; 2000EP-0401388.
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/product= "s
1390..1867
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472..1389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-244810/25.
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Gaps

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Indels

Length 1867;

Robic A, Rogel-Gaillard C;

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1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                             /standard_name= "Single nucleotide polymorphism (SNP)"
   /standard_name= "Single nucleotide polymorphism (SNP)"
                                                          "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase requiatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger likely to The present sequence is pig wild-type PRRAG3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24; Length 1873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%; Score 48.2; DB 24;
86.9%; Pred. No. 7.6e-08;
Live 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                              Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
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                                                        /standard_name=
replace (599, A)
                   replace (595, A /*tag= d
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                                                                                                                                                                                                                                                              08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                                                                                                                            Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                                           10-SEP-2001; 2001WO-US28283.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 86.9
nes 53; Conservative
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                                                                                                                                                                                        14-MAR-2002
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                     variation
                                                                            variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD36457;
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                                                                                                                                                                                                The present sequence is a cDNA encoding pig adenosine monophosphate

(AMP)-activated kinase (AMEK) gamma subunit muscle-specific isoform,

complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome

15. Mutation in Prkag3 results in a altered regulation of carbohydrate

therapeutic for treating carbohydrate metabolism disorders such as

therapeutic for treating carbohydrate metabolism alsorders such as

clabetes, obesity, and disorders associated with muscle metabolism

such as myopathy and cardiovascular diseases, to modulate AMPK

cutivity, and for restoring a normal AMPK function. PRKAG3 sequence

and its functionally altered mutants are useful for the diagnostic

cardivity, and for restoring and prognosis of a metabolic disorder,

cardivity, and for restoring and prognosis of a metabolic disorder,

cardivity, and for sebonydrate metabolism disorder. Pinners that can detect

and its functionally altered mutants are useful for the diagnostic

evaluation, genetic testing and prognosis of a metabolism resulting

cuseful for detecting a dysfunction of carbohydrate metabolism resulting

Crow the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a

creening compounds able to modulate AMPK activity, Nucleic acid

consisting compounds able to modulate AMPK activity, Nucleic acid

consisting compounds able to modulate AMPK activity, Nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= "Single nucleotide polymorphism (SNP)"
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replace (89, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                            Claim 12; Page 62-64; 71pp; English.
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.98;
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                 2001-244810/25.
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Best Local Similarity
Matches 53; Conserv
                                     P-PSDB; AAE00222.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variation
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Gaps

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Indels

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The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein thase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-22).
                                                                                                                                                                                                                                                                                                                                                                                                    Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                  /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                   "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                          Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 34; Page 93-95; 109pp; English.
      Cocation/Qualifiers
                                                                replace (154, A)
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                                                   /product-
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                                                                                                                                                              14-MAR-2002
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                                                                  variation
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AAD36459
ID AAD36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGCTGGGATGACGAACTGCGGAAACCCGGGGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase requlatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                               Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                               /*tag= a
/product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
replace (89, C)
                                                                                           /standard_name= "Single nucleotide polymorphism (SNP)"
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                       Ciobanu DC, Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 89-91; 109pp; English.
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Location/Qualifiers
1..1395
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                                                                                                                                                                                                                     08-SEP-2000; 2000US-231045P. 08-JAN-2001; 2001US-260239P. 18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                       10-SEP-2001; 2001WO-US28283.
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Best Local Similarity 86.97
Matches 53; Conservative
                                                                             /*tag=
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                                                                                                                            WO200220850-A2
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                                                              variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; prakfa3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbolydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                        "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                    /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Malek M, Plastow G;
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Pred. No. 7.6e-08;
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             Location/Qualifiers
                                                                                        replace (599, A)
/*tag= b
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                                                                                                                                                                                                                                                                                                          08-SEP-2000; 2000US-231045P.
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18-JUN-2001; 2001US-299111P.
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/product= '
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Best Local Similarity 86.99
Matches 53; Conservative
                                                  /*tag=
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                                                                                               variation
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                                                     /product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)" replace (595, A) /*tag= b
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                                                                                                                                    /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48.2; DB 24;
Pred. No. 7.6e-08;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Malek M, Plastow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 98-100; 109pp; English.
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Location/Qualifiers
1..1395
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Best Local Similarity 86.9%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                                                                                                                     08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity, and for restoring a normal AMPK function. PRRAGS sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAGS, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAGS. Transgenic animal and host cell transformed with PRRAGS or a heterotrimeric AMPK consisting of PRRAGS or its mutant, are useful for screening compounds able to modulate AMPK activity, Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a sequence encoding the first cystathione beta synthase (CBS) domain PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                 New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
                                                                                                                                                                                                                                             Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMFK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Praga3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as such as such as a myopathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                              /product= "Sus scrofa Prkag3 splice variant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
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Chardon P;
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8
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                                                                                                                                                                                (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                            Milan
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F, Le Roy P,
        Location/Qualifiers
1..1545
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                                                                                                                     11-SEP-2000; 2000WO-EP09896.
                                                                                                                                             10-SEP-1999; 99EP-0402236
18-MAX-2000; 2000EP-0401388
                                                                                                                                                                                                                                           Looft C, Ka
Gellin J,
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....hes 53; Conservative
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                                                                       WO200120003-A2.
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designated SMAK. SMAK is a caspase activated protein kinase. SMAK activated SMAK activated protein kinase. SMAK activated SMAK activated protein kinase. SMAK activated 2 signalling pathways that are involved in mediating apoptosis. It also mediates activated stress fiber dissolution through caspase-3-cleavage and functions to activate the stress activated protein kinases (cjun-amino terminal kinase (JMK) signalling pathway). SMAK proteins and polynucleotides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate SMAK production of antibodies, and in assays to identify modulators (agonists and antagonists) of SMAK expression and activity. The SMAK protein is associated with apoptosis and may play a role in preventing neoplasia development, lymphoproliferative conditions, inflammation, ischemia or strokes and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding a Ste20-related protein kinase designated SWAK, useful for the prevention, diagnosis and treatment of neoplasia development, lymphoproliferative conditions, inflammation, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                caspase activated protein kinase; apoptosis; neoplasia development; actin stress fiber dissolution; lymphoproliferative condition; inflammation; ischemia; stroke; autolmmune disease; ss.
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                                                                cDNA sequence encoding a Ste20-related protein kinase called SMAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                   Mouse; Ste20-related protein kinase; SMAK; caspase-3-cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_except= (pos: 4..5, aa: Ser)
/transl_except= (pos: 1373..1376, aa: Xaa)
/product= "SMAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note- "Xaa is the termination codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 66..3674
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AA199683/c
ID AA199683 standard; DNA; 4403765 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strokes and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 1; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2000; 2000WO-CA00165.
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(first entry)
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P-PSDB; AAB08521.
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Les 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rudnicki MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-1999;
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variation; epidemiology; patient treatment; epidemic monitoring;
                                                                                                      24-JUN-1998;
                                                                                                                                24-JUN-1998;
                                                    US6294328-B1
                                                                              25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CCC 1551 (AN199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                    determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M, tuberculosis strains CDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGCTGGGATGACGAAACTGCGGAAACCCGGCGCCCAGATCTACATGCGTTCATGCAGGA
                                                                                                                                                                                                                                                                                                                                        Evaluating strain variation of Mycobacterium tuberculosis, comprises
                                                                                                     variation; epidemiology; patient treatment; epidemic monitoring; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
                                                                                         Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4403765;
                                                               Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                        Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25.8; DB Pred. No. 33; 0; Mismatches
                                                                                                                                                                                                                                                                                      Fleischmann RD, White OR, Fraser CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                               Mycobacterium tuberculosis
                                     (first entry)
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nes 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              1551 and H37Rv differ
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                                     15-JAN-2002
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                                                                                                                                                                                 25-SEP-2001.
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            AA199683;
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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AN199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37RV differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser CM, Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.3%; Score 25.8; Ilarity 63.9%; Pred. No. 33; Conservative 0; Mismatches
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                                                                   Mycobacterium tuberculosis.
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BJ005207 BJ005207 BJ0641446 RPCT93-BC BBJ11478 BBJ11478 AIG05158 VOL5C0.x BH140228 ZMMBBB000 BH140563 ZMMBBD000

AW024446 wu7d609.x BE19823 002819380 BE120119 601756421 BW006421 603515139 AA519383 TGESTEZ54 AL240746 TELTAGOON BW468546 ACBNCOURT W68459 CA36603.r1 BL616099 RH45605.5 BH537568 416137 NA ANB8804 U1.M-BH3-BL060200 BL060200 BF135856 601782168 BF73519 CMZ-ITO03 AW501053 UT-HF-BPO AV392022 AV392022 AM395150 zr34c12.r BL19961 1031046G1

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Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

1 (bases 1 to 444)
Smith, T.P. L. (Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291826 WARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF890374
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                                                       BH140228
BH140653
AW024410663
BH1961316
BH1961316
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CNS013ERS
BM468546
BH16537568
BH16160200
BH135856
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VERSION
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MEDLINE
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LOCUS
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AL212510 Tetraodon
AL233007 Tetraodon
BG394974 602457369
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6506.409 Million cell updates/sec
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                                                                                                  June 13, 2003, 02:37:44; Search time 151.839 Seconds
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             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                            16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
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BB630381
CNS02SYT
CNS038S6
BG394974
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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74.8
72.1
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44.9
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AG130442 Pan trog1 AV755229 AV753229 BG70079 602681675 BE394076 601312450 BM011144 603634858 BP033403 601457923 AL262954 Tetracodon BQ508350 EST615765 BM088002 501350 NA BG59496 EST504391 BE809466 21508 NA BE80946 21508

25-APR-2001

45.6 44 27.4 27.4 27.2

45. 45.

Score

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Mus musculus
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 548)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
v0.980904.e. Vector identified by cross_match with the -minscore 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 25-SEP-2001
                                                                                                                                                                                                                                                                                            /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.8%; Score 45.6; DB 12; Length 444;
85.0%; Pred. No. 3.2e-05;
Live 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI775360 548 bp mRNA linear 467815 MARC 2BOV Bos taurus cDNA 5', mRNA seguence.
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PO Box 166, Clay Center, NE 68933-0166, USA
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                                                                                                                                                                                                                                 /clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/clone_lib="MARC 2BOV"
                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 57 row: H column: 11
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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                    and -minmatch 12 options.
PCR PRimers
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BI775360
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fukuishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinaqawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P.. Shibata,Y., Hayatsu,W., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                                                                                                                                                                                                                                                                                                  2 GGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAG
                         Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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                                                                                                                                                                                   74.8%; Score 45.6; DB 13; Length 548; 85.0%; Pred. No. 3.4e-05; Live 0; Mismatches 9; Indels 0.
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CNS038S6 1010 bp DNA linear GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence T? end of clone 005N22 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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1 (bases 1 to 1010)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                         1. .910
/organism="Tetraodon nigroviridis"
/db.xref="taxon:99883"
/clone="163d17"
/clone_lib="6"
/note="Genoscope sequence ID : COAG163AD09LP1-end : T7"
a 263 c 305 g 160 t 3 others
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g 210 t l others
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/clone="notern"
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Location/Qualifiers
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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/clone_lib="G"
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                                                                         FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS02SYT 910 bp DNA linear GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 165017 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                           /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was chasacagadaadgancaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaadgacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagacaagaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 910)
Rosest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Bllault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the
                                                                                                                                        /clone_lib="RIKEN full-length enriched, 6 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 10;
Pred. No. 0.00012;
0; Mismatches 10
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                                                                                                                                                                                                                  /tissue_type="skin"
/dev_stage="6 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis DNA sequence
                               /organism="Mus musculus'
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 g
                                                                                                     /clone="A030014A04"
                                                                                                                                                                                                                                                                                            /lab_host="DH108
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AL212510.1 GI:7871329
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83.3%;
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VERSION SOURCE

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Trypanosoma.
I (bases 1 to 442)
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., MelVille,S., Donelson,J.,
Fraser,C. and Adams,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ641446 442 bp DNA linear GSS 08-JUL-1999
RPC193-ECORI-4113.TJ RPC193-ECORI Trypanosoma brucei genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
1 (bases 1 to 581)
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Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences search
page: http://www.tigr.org/tdb/mdb/tbdb/.
                                                                                                                                                                         Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. Medaka EST Project in Takeda's lab Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library for gene discovery and sequence-ready map construction Unpublished (1999)
Other_GSSs: RPC193-EcoRI-4113.TV
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                                                                                                                                                                                                                                                            Center For Genetic Resource Information
National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="segmentation stage 20
235 c 119 g 91 t 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="MF01SSA076B04"
/clone_lb="WR01SSA_cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryzias latipes"
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73.9%; Pred. No. 71;
tive 0; Mismatches
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Department of Eukaryotic Genomics
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                                                                                                                                                                                                                                                                                                                                                                        Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Hd-rR"
/db_xref="taxon:8090"
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Best Local Similarity 73.99
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei.
Trypanosoma brucei
                             Japanese medaka.
                                                 Oryzias latipes
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                       BG394974 112-MAR-2001 602457369F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4579696 5',
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                                                                                     /note="Organ: eye; Vector: porB7; Site_1: XhoI; Site_2: EcoRI: CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCRACGAGGG. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using &AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Stratagene) and M. MCC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 955)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M. A.G.B. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 717.
Location/Qualifiers
                                                               1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCCAGATCTACATGCGCTTCATGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 955;
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                           21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
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65.6%; Pred. No. 50; tive 0; Mismatches
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Pred. No. 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref-"taxon:9606"
/clone="IMAGE:4579696"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MGC_16"
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Best Local Similarity 67.99
Watches 38; Conservative
Best Local Similarity 65.6
Matches 40; Conservative
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Mon Jun 16 09:56:21 2003

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sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fwunnuishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI606158 349 bp mRNA linear EST 21-APR-1999 vol5c02.xl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1049954 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primer [5' GAGAGAGAGAGGACCAAGAGCTCTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 349)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person, F., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter, E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 GCTGGTAAAACAACAGAAAAAAGGGTACCCCATCCCCCATCTGAACAAGA 109
                                                                                                                                                        encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="B020024106"
/clone_lib="RIKEN full-length enriched, 2 cells egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="egg"
/dev_stage="2 cells"
/lab_host="DH10B"
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Fax: 314 286 1810
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                                                                                                              /clone="Replies Ecors."
/clone="Replies Ecors."
/clone="Neprol9-Ecors."
/clone="Neprol9-Ecors."
/note="Vector: pBACe3.6; Site_1: Eco RI; Site_2: Eco RI;
/note="Vector: pBACe3.6; Site_1: Eco RI; Site_2: Eco RI;
/constructed for The Institute for Genomic Research by
Robui Zhao in Pieter de Jong's laboratory (Roswell Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
bruce; TREU92/74 GUTat 10.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPC193-EcoRI segment) or Dpn II (RPC193-DpnII
segment). High molecular weight fragments were ligated in
pBACe3.6 vector digested with Eco RI or Bam H1,
respectively. The average insert size is 141 Kb. Total
coverage (Doth segments): > 90 X the haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare full-length copy. Ilbraries for rapper-selected cDNAs to genes. Genome Res. . 10 (10), 1617-1630 (2000) wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Marsuura S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 bp mRNA linear EST 11-OCT-2001
BB711478 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA
BB711478
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URL.http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., OkazaKı,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 248)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCAGCA 60
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.3%; Score 26.4; DB 17; Length 442; 65.0%; Pred. No. 90;
1ive 0; Mismatches 21; Indels 0
                          /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
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Fax: 81-45-503-9216
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Matches 39; Conservative
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BB711478
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SOURCE
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Tel: 864 656 7288
Fax: 864 656 4293
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BH140663.1
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BH140663/c
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AW024446
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ZMMBBb0001L18f Maize B73 Zea mays genomic clone ZMMBBb0001L18f, DNA
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                                                                                                                                                                                                                                                               Tomkins,J.P., Main,D., Goicoechea,J.L., Frisch,D.A. and Wing,R.A. A Deep-Coverage BAC Library for Maize Unpublished (2001)
                                 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
High quality sequence stop: 326.

Location/Qualifiers
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IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                        /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
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Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
Clemson University
                                                                                                              1. .349
/organism="Mus musculus"
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Class: BAC ends
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/clone="ZMMBBb0001L18f"
/clone_lib="Maize B73"
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                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:1049954"
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BH140228.1 GI:15099289
                                                                                                                                                     /strain="C3H"
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Matches 38; Conservative
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BH140663 593 bp DNA linear GSS 07-AUG-2001 AMMBBD0002118f Maize B73 Zea mays genomic clone ZMMBBD0002118f, DNA
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Eukaryotts, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae, Andropogoneae; Zea.
1 (bases 1 to 593)
1 (bases 1 to 593)
1 Tomkins, J. P., Main, D., Goicoechea, J. L., Filsch, D. A. and Wing, R. A.
Deep-Coverage BAC Library for Malze
Unpublished (2001)
                                                                                                                                            http://www.genome.clemson.edu/projects/stc/maize/ZMMBBb " 221 c 138 g 146 t l others
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/cultivar="873"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone="lambBb00021.8f"
/clone=lambBb00021.8f"
/clone=lambBb00021.8f"
/clone=lambBb00021.8f"
/clone=lambare B73"
/tissue_type="Young leaves"
/note="Vector: pcuGIBBC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation, ordering clones and sequence analysis see
                                                   /note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI; For more details on library preparation, ordering clones and sequence analysis see
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
/tissue_type="Young leaves"
/lab_host="E. coli"
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
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Location/Qualifiers
1. .593
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Best Local Similarity 65.54
Matches 38; Conservative
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Matches 38; Conservative
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mRNA sequence.
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JOURNAL
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BG918873
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AW024446 648 bp mRNA linear EST 09-MAR-2000 wu76d09.xl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2525969 3' similar to TR:043176 043176 PEPTIDASE HOWOLOG ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCL-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: Kidney; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source: 2 pooled kidneys. Library went through one round of normalization, Library constructed by Bento Soares and w Earling Industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 680) NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 648)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.3%; Score 25.8; DH 10; Length 648; larity 67.9%; Pred. No. 1.6e+02; Conservative 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at:
www.blo.l.lnl.gov/bbrp/imago/image.html
Insert Length: 878 Std Brror: 0.00
Seq primer: -40UP from Gibbo
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/lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2525969"
                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                    Emmert-Buck, M.D., Ph.D.
                                                              AW024446
AW024446.1 GI:5877976
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VERSION
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pT713D-Pac (Pharmacia) with a modified Polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dI) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), diseased with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 738)
                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:953633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: gapbs-rémail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="infiltrating ductal carcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25.8; DB 10;
Pred. No. 1.6e+02;
0; Mismatches 17;
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/clone_lib="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1548285"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                         Seq primer: -40RP from Gibco
High quality sequence stop: 472.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 715.
Location/Qualifiers
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                                                            Email: cgapbs-r@mail.nih.gov
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67.98;
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Matches 36; Conservative
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Sequence 7, R
Sequence 1, R
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Sequence 39,
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Sequence 1,
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/bark/1/seq:*
6: /cgn2_6/ptodata/1/ina/bark/1/seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-518-914-1
US-09-518-914-3
US-08-804-227C-7
US-08-804-198-1
US-08-993-358A-1
US-08-993-358A-1
US-08-993-55A-27
US-08-332-57GC-27
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US-08-3808-324-27
PCT-US94-14030A-27
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US-07-901-703-14
US-08-147-023-4
US-08-447-570-4
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US-07-679-451-1
US-07-989-847-1
US-07-721-847A-3
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US-08-713-556F-39
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Maximum Match 100%
Listing first 45 summaries
                                           - nucleic search, using sw model
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Maximum DB seq length: 200000000
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APPLICANT: WHITE, Owen R.
APPLICANT: WRITE, Owen R.
APPLICANT: PRASEN, Claire M.
APPLICANT: VENTEN, Claire M.
APPLICANT: VENTEN, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24566-20007,000
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFWARE: PATENTIN VET: 2.1
SEQ ID NO 2.
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Patent No. 6294328
GENERAL INFORMATION
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: VENER, Claire M.
APPLICANT: VENER, John C.
APPLICANT: 
            Sequence 1,
Sequence 3,
Patent No. 5
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US-08-925-779-3

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US-09-027-337-9

US-09-644-600-9

US-09-395-6748-5

US-08-943-731-20

US-08-943-731-5

US-08-774-0258-3

US-09-244-093-3

US-09-244-093-3

US-09-244-093-3

US-09-644-053-34

US-09-044-718-13

US-09-044-718-13

US-08-08-61-14

US-08-08-61-14

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Pred. No. 7.4;
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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Matches 39; Conserv
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US-09-103-840A-1/c
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US-09-103-840A-2/c
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       Best Local Similarity 73.8%; Pred. No. 5.2;
Matches 31; Conservative 0; Mismatches 11; Indels
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                                                                                                                                                                                                                               Sequence 1, Application US/08744231
Patent No. 638872
GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA 53
                                                                        12 ACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcharin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: Case Docket 9339 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ), NAME/KEY: CDS
; LOCATION: join(374..420, 469..1819)
US-08-744-231-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Nutley STATE: New Jersey COUNTRY: United States of America 21P: 07110
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US-09-518-914-1
; Sequence 1, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: BOTOWSKY, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhlani, Parul P.
; APPLICANT: Adham, Nika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2327 base pairs
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STRANDEDNESS: double
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                                                                                                                                                                                       RESULT 4
US-08-744-231-1
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                                                                                                                                                                                                                                                                                                                                                                     1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                         Query Match 42.3%; Score 25.8; DB 4; Length 4411529; Best Local Similarity 63.9%; Pred. No. 7.4; Matches 39; Conservative 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 24.4; DB 4; Length 2327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELEPOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEPRAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(374..420, 469..1819
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United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/868,435
                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/744,231
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08868435
; Patent No. 6291221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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LENGTH: 2327 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2322130 G 2322130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New COUNTRY: Un ZIP: 07110
                                                                                                                                        LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 G 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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US-08-868-435-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-08-868-435-1
                                                                                                                                                                    TYPE: DNA
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RESULT 8
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Sequence 3, Application US/09518914

Fatent No. 6413731

GENERAL INFORMATION:

APPLICANT: BOTOWSKY, Beth E.

APPLICANT: Lakhlani, Parul P.

APPLICANT: Lakhlani, Parul P.

APPLICANT: Lakhlani, Parul P.

APPLICANT: Lakhlani, Parul P.

APPLICANT: APPLICATION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS

FILE REFERENCE: 59138-A/JPW

CURRENT APPLICATION NUMBER: US/09/518,914

CURRENT FILING DATE: 2000-03-03

EARLIER PELING DATE: 1999-05-03

NUMBER OF SEQ ID NOS: 494

SOFWMARE: PATENTIN VET. 2.1
TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS FILE REFERENCE: 59138-A/JPW
CURRENT APPLICATION NUMBER: US/09/518,914
CURRENT FILING DAFE: 2000-03-03
EARLIER APPLICATION NUMBER: US 09/303,593
EARLIER FILING DAFE: 1999-05-03
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                    11 GACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.4%; Score 23.4; DB 4; Length 1541; Best Local Similarity 67.3%; Pred. No. 11; Matches 33; Conservative 0; Mismalches 16; Indels 0.
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Patent No. 587691
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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ZIP: 46285
                                                                                                                                                                                   SEQ ID NO 1
LENGTH: 1508
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Gaps
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Pred. No. 26;
0; Mismatches 13; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Burgett, Stanley G.
APPLICANT: Ruhstoss, Stuart A.
APPLICANT: Rac, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOTTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: Macintosh
COMPUTER: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ. ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/08804198
; Patent No. 5945320
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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70.5%;
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LENGTH: 44377 base pairs
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36155..41830
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Best Local Similarity 70.5%
Matches 31; Conservative
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14046..20036
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31329..36071
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20110..31284
                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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LOCATION:
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LOCATION:
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FEATURE:
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; LOCATION:
US-08-804-227C-7
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No. 60602980 No. 6060298disk of No. 6060298th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CIGGGAIGACGAACIGCGGAAACCCGGCGCCCAGAICIACAIGCGCIICA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 37.4%; Score 22.8; DB 3; Length 1 Best Local Similarity 66.0%; Pred. No. 18; Matches 33; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MELUNA TESTEM: COMPUTER: ISM COMPATIBLE OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:

PILING DATE: 12-DEC-1997

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101.200-US
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ostergaard, Peter
IIILE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 3
                                                                                                                                                                   5101.200-US
                                          FILING DATE: 07-MAY-1997,
APPLICATION WINBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08989358A Patent No. 6060298
                                                                                                                        NAME: Gregg, Valeta A
REGISTRATION NUMBER: 35,127
REPRENCE/DOCKET NUMBER: 5101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 405 Lexington Avenue CITY: New York
    12-DEC-1997
MMBER: 0529/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0529/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fuglsang, Claus
APPLICANT: Ohmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Ostergaard, Peter
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 09-MAY-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-DEC-1996
APPLICATION NUMBER: 0529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1997
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lassen, Soren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bech, Lisbeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12-DEC-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gregg, Valeta A REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
COUNTRY: U.S.A.
orp: 10174
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APPLICANT: Lassen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-989-358A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-221-654-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27492 GGGCAGCGGGTCGAACTGCCGGAGTCCGGTGACCGGATGTACA 27535
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SOFTWARE: FASTESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,654
FILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/989,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lassen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Fuglasng, Claus
APPLICANT: Ornan, Anders
APPLICANT: Ornan, Anders
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Periophora Phytase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/804,198
                         ELLIAN LALLE
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTATION UNDERR: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/09221654
; Patent No. 6054306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
COUNTRY: U.S.A.
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                            CDS
14046..20036
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20110..31284
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31329..36071
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350..14002
                                                                                                                                                                                                                                                                                         linear
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LOCATION:
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LOCATION:
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US-08-804-198-1
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135 GGGCTGGGATGAGGGGGGGCCCGACGCCGCCGCGCGAACTTCCTGCGGCCCA 83
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Pred. No. 21;
0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/362,670B
FILING DATE: December 22, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R:
REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding BMP2 propeptide/BMP-12 mature peptide
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APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Nell
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
                                                                                                                                                                                          APPLICANT: Melton, Douglas A. TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
                                                                                                                                                                                                                                                                                       ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive
  Sequence 27, Application US/08362670B Patent No. 5658882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 27, Application US/08333576C
; Patent No. 6027919
                                                                                          Wozney, John
Rosen, Vicki A.
Wolfman, Neil
Thomsen, Gerald H.
                                              GENERAL INFORMATION: APPLICANT: Celeste, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celeste, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
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64.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.2 Matches 34; Conservative
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847..1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..1233
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APPLICANT: Celeste,
APPLICANT: Worney,
APPLICANT: Rosen, V
APPLICANT: Wolfman,
APPLICANT: Thomsen,
APPLICANT: Melton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                      Cambridge
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CLONE: DNA ence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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LOCATION:
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; LOCATION:
US-08-362-670B-27
                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                          360 CGGGGCTAACCAATCGCACCAACCGGCACCGATATGTATACGCGCTACA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 CGGGGCTAACCAATCGCACCAAACCGGCACCGATATGTATACGCGCTACA 531
                                                                                                                                                                                                                                                                                                                                                            4 CTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CIGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA 53
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                                                                                                                                                                                                                                                                 DB 3; Length 1320;
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                                                                                                                                                                                                                                                            37.4%; Score 22.8; Di
66.0%; Pred. No. 18;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lassen, Soren F.
APPLICANT: Lassen, Soren F.
APPLICANT: Danain, Anders
APPLICANT: Domain, Anders
APPLICANT: Domain, Anders
APPLICANT: Puglsang, Claus C.
APPLICANT: Evglsang, Claus C.
APPLICANT: Sotergaard, Peter R.
TITLE OF INVENTION: Phytase Polypeptides
FILE REFERENCE: 5383.500-US
CURRENT APPLICATION NUMBER: US/08/993,359A
CURRENT APPLICATION NUMBER: 1480/96
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-05-07
EARLIER FILING DATE: 1997-05-09
NUMBER OF EQUID NOWHER: 1997-05-09
NUMBER OF EQUID NOWHER: 1997-05-09
NUMBER OF EQUID NOWHER: 1997-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08993359A Patent No. 6039942 GENERAL INFORMATION:
                      TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
IENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                  Best Local Similarity 66.03
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Peniophora lycii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (123)...(1439)
; NAME/KEY: sig_peptide
; LOCATION: (123)...(212)
; NAME/KEY: mat_peptide
; LOCATION: (213)...(1439)
US-08-993-359-23
TELEFAX: 212-878-9655
                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-08-362-670B-27/c
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                                                                                                                                                                                                                                                                 Query Match
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1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA 53
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tive 0; Mismatches 19; Indels 0
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PCT-USS4-14030A-27/C
Sequence 27, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
CLONE: peptide
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
                                                                           Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-WAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-N0Y-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LAZAL, Steven R.
REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: GENETICS INSTITUTE, INC. 87 CambridgePark Drive
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DX
SOFTWARE: PAtentin Release #1.
                                                                                                                                                                                                                                                                                                                                                           REFERENCE TO THE TOTAL T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 64.28 Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: mat_peptide
; LOCATION: 847..1233
US-08-808-324-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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FEATURE:
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Patent No. 6284872

GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: Celeste, Anthony J.

APPLICANT: Wozney, John

APPLICANT: Wozney, Vicki A.

APPLICANT: Thomsen, Gerald H.

APPLICANT: Thomsen, Gerald H.

APPLICANT: Thomsen, Gerald H.

APPLICANT: Melton, Douglas A.

TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT ADDITION TO LOGGING $1.25

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/333.576C

FILING DATE: No. 602/919ember 2, 1994

CLASSIFTCATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lazar, Steven R.

REGISTRATION NUMBER: 5202-B

TELECOMOUNICATION INFORMATION:

TELEPHONE: 617 498-826

TELEPHONE: 100: 27:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding BMP2 propeptide/BMP-12 mature peptide
                                  CORRESPONDENCE ADDRESS:
ADDRESSES:
STRET: GRWTICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: mat_peptide
LOCATION: 847..1233
   NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                         STATE: Massachusetts
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..1233
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STATE: Massachus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                               USA
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US-08-808-324-27/c
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                                                                                                                                                                                                                       COUNTRY:
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Page 1

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June 13, 2003, 04:39:50 ; Search time 19:2903 Seconds (without alignments) 4579:068 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                     US-09-826-581-5_COPx_529_589
61
1 gggctgggatgacgaactgc.....acatgcgcttcatgcaggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: // Grant-frame / John Jubpa / USO7_PUBCOMB.seq:*
2: // Grafe / // Pubpa / USO7_PUBCOMB.seq:*
3: // Grafe / // Pubpa / USO7_NEW_PUB.seq:*
4: // Grafe / // Pubpa / USO6_PUBCOMB.seq:*
5: // Grafe / // Pubpa / USO6_PUBCOMB.seq:*
6: // Grafe / // Pubpa / USO6_PUBCOMB.seq:*
7: // Grafe / // Pubpa / USO6_PUBCOMB.seq:*
7: // Grafe / // Pubpa / USO8_PUBCOMB.seq:*
8: // Grafe / // Pubpa / USO8_PUBCOMB.seq:*
9: // Grafe / // Pubpa / USO8_PUBCOMB.seq:*
10: // Grafe / // Pubpa / USO8_PUBCOMB.seq:*
11: // Grafe / // Pubpa / USO8_PUBCOMB.seq:*
11: // Crafe / USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seg:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seg:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1029858 seqs, 724030393 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY_NUC Gapox 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                         Run on:
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SUMMARIES

Description	Sequence 2, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 8004, Ap	Sequence 11, Appl	Sequence 19, Appl	Sequence 1, Appli	Sequence 17, Appl	Sequence 166, App	Sequence 84, Appl	Sequence 51, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 1694, Ap	Sequence 4, Appli	Sequence 23, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 12740, A
3 ID	.0 US-09-826-581-2	10 US-09-826-581-5	US-09-939-964-1	.0 US-09-815-242-8004	US-09-909-567B-11	10 US-09-931-381A-19	US-09-898-751A-1	10 US-09-931-381A-17	10 US-09-764-864-166	3 US-10-108-605-84	10 US-09-934-868-51	3 US-10-146-835-1	3 US-10-146-835-3	10 US-09-917-800A-1694	9 US-09-927-827-4	3 US-10-007-270-23	9 US-09-927-827-1	9 US-10-265-593-3	10 US-09-960-352-12740
Query Match Length DB	989	1647]	536165 9	1473 1	14917	1086	1089	1244	009	573	2760	1508	1541	1323	3627	4204	7356	27847	242
Query Match	100.0	100.0	41.6	41.0	40.7	39.3	39.3	39.3	39.0	38.7	38.7	38.4	38.4	38.0	38.0	38.0	38.0	38.0	37.7
Score	61	61	25.4	25	24.8	24	24	24	23.8	23.6	23.6	23.4	23.4	23.2	23.2	23.2	23.2	23.2	23
Result No.	H	7	3	C 4	S	و د	c 7	8	σ	10	c 11	12	13	14	c 15	16	c 17	c 18	19

Sequence 5, Application US/09826581; Patent No. US20020142310A1; GENERAL INFORMATION:
APPLICANT: Andersson, Leif appliCANT: Luthman, L. Holger

US-09-826-581-5

RESULT 2

61 G

ŏ g

Sequence 6224, App Sequence 6227, Appl Sequence 533, App Sequence 602, App Sequence 934, Appl Sequence 17, Appl Sequence 173, Appl Sequence 513, Appl Sequence 513, Appl Sequence 5146, Appl Sequence 330, Appl Sequence 786, Appl Sequence 786, Appl Sequence 786, Appl Sequence 7818, Appl Sequence 31548, Appl Seq	KINASE GAMMA 3 S	Gaps 0; TGCAGGA 60 TGCAGGA 881
	'S AMP-ACTIVATED PROTEIN	; Length 989; 4; Indels 0; ATCTACATGCGCTTCA ATCTACATGCGCTTCA
US-09-764-891-6224 US-09-764-891-6227 US-09-923-876-2303 US-09-923-876-2303 US-09-945-182-27 US-09-945-182-27 US-09-945-182-27 US-09-945-182-27 US-09-957-425-4 US-09-957-425-4 US-09-957-425-4 US-09-957-425-4 US-09-957-425-4 US-09-957-9143 US-09-988-955-360-1 US-09-988-955-360-1 US-09-988-955-360-1 US-09-988-956-3718 US-09-988-958-96 US-09-988-958-96 US-09-988-958-96 US-09-988-958-96 US-09-988-958-96 US-09-988-958-96 US-09-988-958-96 US-09-988-958-96 US-09-988-958-96 US-09-988-958-96 US-09-988-958-96 US-09-988-96-988-988-988-988-988-988-988-988	5 2 1 C	imilarity 100.0%; Score 61, DB 10; Length 989; ; Conservative 0; Mismatches 0; Indels 0; Gaps GGGCTGGGATGACGGAACCCGGCGCCCACATCTACATCCATC
416 9 5335 9 2335 9 2335 9 233 9 233 9 2 240 110 240 9 2 240 110 24 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1-2 ORAPLICATION US/09826 US20020142310A1 ORMATION: Andersson, Leif Luthman, L. Holger MARKLUNG, Stefan PPLICATION: VARIANTS OF PELICATION NUMBER: US/ LILNG DATE: 2001-04-0 LILNG DATE: 2001-04-0 LILNG DATE: 2000-04-07 SEQ ID NOS: 14 SEQ ID NOS: 14 SEQ ID NOS: 14 MANDERS US/ B89 HOMO Sapiens 1-2	100.0%; larity 100.0%; Conservative CTGGGATGACGAACTC
23 23 24 25 27 27 27 27 27 27 27 27 27 27	SULT 1 SULT 1 SQUE-581-2 SEQUENCE 2, APPLICATION US/09826581 PRATENT NO. US20020142310A1 APPLICANT: Andersson, Leif APPLICANT: Anderson, Leif APPLICANT: Luthman, L. Holger APPLICANT: Marklund, Stefan TILE OF INVENTION: VARIANTS OF THE HUMAN FILE REFERENCE: 11145-007001 CURRENT APPLICATION NUMBER: US 60/195,665 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 14 SEQ ID NO 2 LENGTH: 889 TYPE: DNA ORGANISM: Homo sapiens OOSGANISM: Homo sapiens	7 I 61.5
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-826-581 Sequence 2, Patent No. GENERAL INF APPLICANT: APPLICANT: APPLICANT: TITLE OF I FILE REFER CURRENT AP CURRENT	Query Matches Matches Qy Db 82

Sui

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APPLICANT: Macina, Roberto A.
APPLICANT: Macina, Roberto A.
APPLICANT: Main, Manoj
APPLICANT: Chen, Selyu
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT APPLICATION NUMBER: 05/09/909,567B
CURRENT FILING DATE: 2001-07-21
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2869 GAAGAGGACCTGCAGAACCTCTGTGACCCAGATGAGCTCCCAGCAGG 2920
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.0%; Score 25; DB 10; Length 1473; 64.9%; Pred. No. 2.7; ive 0; Mismatches 20; Indels
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: U$/09/815,242
CURRENT APPLICATION NUMBER: 60/10/8
PRIOR APPLICATION NUMBER: 60/20/6,848
PRIOR PILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: 60/20/7,727
PRIOR APPLICATION NUMBER: 60/20/7,727
PRIOR APPLICATION NUMBER: 60/20/8
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25/,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25/,931
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25/,931
PRIOR PILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/25/,931
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 64.9
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(1473)
US-09-815-242-8004
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-909-567B-11
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  APPLICANT: Marklund, Stefan
TITLE OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REPERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
PRIOR APPLICATION NUMBER: US/09/826,581
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NO 5
LENGTH: 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181656 GGATTCTATGACGTTCTGATGAATGCCGGCCGCACCTCTCGTGCGCAGCATCCGCGA 181598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Plasmid
FILE DF INVENTION: Plasmid
FILE REFERENCE: CARPOGGE
CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 1999-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 61; DB 10;
100.0%; Pred. No. 3.5e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25.4; DB 9;
Pred. No. 3.1;
0; Mismatches 21;
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/09939964; Publication No. US20030054522A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 41.6%;
Best Local Similarity 64.4%;
Matches 38; Conservative
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APPLICANT: Rosenthal, Andre
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5
                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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; ORGANISM: Rhizobium
US-09-939-964-1
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US-09-939-964-1/c
                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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TITLE OF INVENTION: Methof for Identifying Agents Which
TITLE OF INVENTION: Medulate Chemckine "MEC"-Induced Functions of CCR3 and/or
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
CURRENT ELER REFERENCE: 1855.2010-003
CURRENT FILING DATE: 2001-08-15
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1244
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                                                                                                                                                                                                       2 GGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGC 49
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 166

LENGTH: 600
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                                                                                                                                 15; Indels
                                                                  39.3%; Score 24; DB 9 68.8%; Pred. No. 6.5; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09931381A, Patent No. US20020137107A1; GENERAL INFORMATION: APPLICANT: Butcher, Eugene C. APPLICANT: Runkel, Eric J.; APPLICANT: Pan, Juniang APPLICANT: Soler-Ferran, Dulce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 166, Application US/09764864; Patent No. US20020132753A1; GENERAL INFORMATION:
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Best Local Similarity 68.89
Matches 33; Conservative
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Best Local Similarity 66.73
Matches 34; Conservative
                                                                  Query Match 39.33
Best Local Similarity 68.83
Matches 33; Conservative
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US-09-764-864-166
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ORGANISM: Homo sapiens
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; LOCATION: (5)...(1093)
US-09-931-381A-17
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US-09-898-751A-1
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APPLICANT: Kellerman, Sirid-Aimee
APPLICANT: McEvoy, Leslie M.
APPLICANT: Bowman, Edward P.
APPLICANT: Bowman, Edward P.
TITLE OF INVENTION: CHEMKINE AND RECEPTOR USES; COMPOSITIONS; METHODS
FILE REFERENCE: DX0882XR
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CURRENT APPLICATION NUMBER: US/09/898,751A
CURRENT FILING DATE: 2001-07-02
PRIOR PRICATION NUMBER: US60/471,549
PRIOR PILING DATE: 1999-05-27
PRIOR PILING DATE: 1999-05-27
PRIOR FILING DATE: 1999-05-27
PRIOR FILING DATE: 1998-05-27
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO
                                                                                                 ; Sequence 19, Application US/09931381A
; Patent No. US20020137107A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/09898751A
; Patent No. US20020160024A1
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APPLICANT: Oldham, Elizabeth R.
APPLICANT: Soto, Hortensia
APPLICANT: Liu, Ying
                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Butcher, Eugene C.
APPLICANT: Kunkel, Eric J.
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Homey, Bernhard
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US-09-931-381A-19
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OTHER INFORMATION:
                                                                  US-09-931-381A-19/C
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US-09-898-751A-1/C
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APPLICANT:
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Publication No. US20030073167A1
GENERAL INFORMATION:
APPLICANT: BOLOWSKY, Beth E.
APPLICANT: BOLOWSKY, Beth E.
APPLICANT: Adhani, Parul P.
APPLICANT: Adhani, Nika
TILLE OF INVENTION: DATE: US/10/146,835
CURRENT APPLICANTION NUMBER: US/10/146,835
CURRENT APPLICATION NUMBER: US/09/518,914
PRIOR FILING DATE: 2000-03-03
PRIOR PAPLICATION NUMBER: US/09/518,914
PRIOR PLING DATE: 12000-03-03
PRIOR PLING DATE: 1209-05-16
PRIOR APPLICATION NUMBER: US 09/303,593
PRIOR FILING DATE: 1999-05-03
PRIOR PLING DATE: 1999-05-03
SEQ ID NO 3
LENGTH: 1541
                                                                                     GENERAL INFORMATION:
APPLICANT: Borowsky, Beth E.
APPLICANT: Borowsky, Beth E.
APPLICANT: Ogozalek, Kristine L.
APPLICANT: Adham, Nika
APPLICANT: Adham, Nika
TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
FILE REFERENCE: 59138-A/JPW
CURRENT APPLICATION NUMBER: US/09/518,914
PRIOR PPLICATION NUMBER: US/09/518,914
PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US/09/303,593
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Pred. No. 11;
0; Mismatches 16; Indels 0
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Best Local Similarity 67.3%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 16;
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US-09-917-800A-1694
Sequence 1694, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
                            Sequence 1, Application US/10146835 Publication No. US20030073167A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.4%;
Best Local Similarity 67.3%;
Matches 33; Conservative (
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1508
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ORGANISM: Homo sapiens
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                                                                                                                                        ; Sequence 84, Application US/10108605
; Patent No. US20020160934a1
; GENERAL INFORMATION:
    APPLICANT: Broadus, Julie
    APPLICANT: Broadus, Julie
    APPLICANT: Broadus, Julie
    APPLICANT: Bachmann, Jane
    APPLICANT: Bachmann, Jane
    APPLICANT: Bachmann, Jane
    APPLICANT: Amadar, Kim
    APPLICANT: Bachmann, Jane
    APPLICANT: William Session and Ses
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Patent No. US20020137190A1

GENERAL INFORMATION:
APPLICANT: Offs. Mattheos
FILE REPERBENCE: C1.556 US NA
CURRENT APPLICATION NUMBER: 05/09/934,868
CURRENT FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-09-01
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCAT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B GATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAG 61
GGCGAGCGGCCCTACCACTGCGCCGAGTGCGGCAAGCGGCTTCACGCAGAAG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Best Local Similarity 64.8%; Pred. No. 10;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster US-10-108-605-84
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CTHER INFORMATION: nasA gene
US-09-934-868-51
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US-09-934-868-51/c
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LENGTH: 2760
                                                                                                                                US-10-108-605-84
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TITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas campestris FILE REFERENCE: 38-10(15824)8
CURRENT APPLICATION NUMBER: US/09/927,827
CURRENT FILING DATE: 2001-08-10
PRIOR PPLICATION NUMBER: US 60/279,493
NUMBER OF SEQ ID NOS: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_022220 US-09-917-800A-1694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 38.0%; Score 23.2; DB 9; Length 3627; Best Local Similarity 65.4%; Pred. No. 15;
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                                                                                                               APPLICANT: Endanolt, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038 US
CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/220,029
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-15
PRIOR PELICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR PLING DATE: 2001-05-22
PRIOR PLING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-06-19
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Publication No. US20030036176A1
GENERAL INFORMATION:
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                                                               Castle, Arthur
Elashoff, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Conservative
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LENGTH: 3627
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APPLICANT:
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Search completed: June 13, 2003, 09:00:41 Job time: 21.2903 secs

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Query
Match
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DEFINITION
ACCESSION
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                                                                Result
No.
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9216.782 Million cell updates/sec
                                                                                               13, 2003, 01:49:14; Search time 192.613 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                     2054640 seqs, 14551402878 residues
                                                                                                                                                                US-09-826-581-5_COPY_1007_1067
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Maximum Match 100%
Listing first 45 summaries
                                                                nucleic search, using sw model
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em_htgo_other:*
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em_htg_other:*
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em_htg_rod:*
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em_htg_vrt:*
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seq length: 2000000000
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em_pl:*
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Maximum DB :
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Pred. No. is the number of results predicted by chance to have a

AX099774 Sequence
AX099774 Sequence
AX099774 Sequence
AX099774 Sequence
AX099800 Sequence
AX39833 Sequence
AX281580 Sequence
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AX29833 Sequence
AX2983 Sequence
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AX3933 Sequence
AX2933 Rattus no
AX2933 Rattus no
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AX2933 Max muscu
AX2933 Homo sapien
AX29236 Homo sapien
AX29236 Homo sapien
AX29236 Homo sapien
AX20322 Homo sapien
AX20322 Mus muscu
AX20322 Homo sapien
AX20322 Mus muscu
AX20322 Homo sapien
AX203222 Homo sapien
AX20322 Homo sapien
AX203222 Homo sapien PAT 02-NOV-2001 Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 5 18-OCT-2001; Oryza sat Human DNA Homo sapi Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapi Homo sapi AX099776 Sequence AX099802 Sequence AX281582 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AC105743 O AL034548 H AC018818 H AC101452 1 AC023022 1 AC108872 0 AL078605 1 AC025266 1 linear DNA ALIGNMENTS Sequence 5 from Patent WO0177305. AX281582 SUMMARIES AX099802 AF214519 HSA249977 AC096427 AL663072 HSJ894D12 AF336381 AC129702 AF334948 AC112601 AC108872 AC019360 AX281582.1 GI:16608833 5102 DB 100.0 10 Length AUTHORS TITLE JOURNAL

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2115 bp mRNA linear PRI 03-JUN-2000 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3) mRNA, complete cds. AF214519
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/db_xref="GI:13538837"
/translation="MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG
EPPGGGEGPRSRPTAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAG
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KNRIHRLEVLDPVSGNVLHILTHKRLLKFLHIEGSLLPRPSFLYRTIQDLGIGTFRDL
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GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
                                                                                            PAT 02-APR-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              same, and uses thereof
Patent: WO 0120003-A 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variants of the gamma chain of ampk, dna sequences encoding the
                                                                       Gaps
                                       Gaps
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Length 2109;
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ilarity 100.0%; Pred. No. 9.4e-10;
Conservative 0; Mismatches 0;
Score 61; DB 6; Pred. No. 9.4e-10;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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ISPNDSLFEAVYLLIKNRIHRLPVLDPVSGNVLHILFHKRLLKFLHIFGSLLPRPSFL
YRIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNEGGQVVGLYSRFDVI
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TQHLLGVVSLSDILQALVLSPAGIDALGA"
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LSPQAPPRELGWDDELREPGAQIYMRPWGEHTCYDAMATSKLVIFDTHLEIKKAFFA
LLVANGVYRAPEWDSKKOSYVGLITPFILVLHRYRSPLVQIYEIEDGWHIETHWEIY
LQGCFRPLVSISPNSLEEAVYTLIKNRIHRLPVLDPYDPVGDWLHITHRERLLFFEHTF
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQV
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QVHRUVLVDETQHLLGVYSLSDTLGALVLSPAGIDALGA"
502 c 462 a 337 t
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SSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEATFPKTTPLAQA
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Patent: WO 0120003-A 3 22-MAR-2001;
INSTITU MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., Le Roy,P. and Chardon,P.
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                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
20. .1489
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Sequence 3 from Patent W00120003.
AX099776

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    /organism="Homo sapiens"
/db_xref="taxon:9606"

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/db_xref="G1:13538811"
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/protein_id="CAD10589.1"
/db_xref="G1:16608834"
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LLANGVERARALWISKRGSFVGALTITDFILVLHEYERSPUOTIETEDGIKLETEREIT
LQGCFKPLVSISPNDSLFEAVTLIKNIHELPVLDPVSGNVLHILTHKELLKFLHIF
GSLLERFSFLYTTODLGTGTFRDLAVULETREITMLEITHENLEVLHIF
GSLLERFSFLYTTODLGTGTFRDLAVULETREITMLEVENVSALPVVNEGGOV
VGLYSRFDVIHLAAQOTYNHLDMSVGSRLKRFLCLEGVLEGVLESCAFFSLGFVIDRIARE
QVHRUXLVBTQHLGTGVSLSTGLALVLSPAGIDPSGPEKI"

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SSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEEATFPKTTPLAQA
DPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., 1e Roy, P. and
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="CAB65117.1"
/db_xref="GI:6688201"
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Variants of the gamma chain of ampk, dna sequences encoding the
                                                                                                    Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding Biochem, J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                                                                                                           Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 ONN, UNITED KINGDOM Location/Qualifiers

Location/Qualifiers

| . . 2290
/organism="Homo sapiens"
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/gene="AMPK gamma
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Direct Submission
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EPPGGGEGPRSRPTAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDGTASAAG
SSTDDVBLATEFPATEAMECELGGLEERPALCLSPQAPFPKTGWDDELKFPGADYN
RFWGEHTCYDAMATSKVVIFDTMLEIKKAFFALVANGWRAAPLWDSKKQSFVGMLT
TDFILVLHYYYRSPLVQYTBIEGHK EFWREIYLQGCFRPLVSIGSNDSLFEAYTLL
KNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYTTIQDLGIGTFRDL
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GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
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                                                                                                                                                                                                                                                 A mutation in PRKAG3 associated with excess glycogen content in pig
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AJ249977.1 G1:6688200
AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
                                                                                                                                                                                                                                                                                                                                                          Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Reinsch, N., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L. Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., lannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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/protein_id="AAF73987.1"
/db_xref="G1:8215682"
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Science 288 (5469), 1248-1251 (2000)
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/db_xref="taxon:9606"
/chromosome="2"
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1. .2115
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GI:8215681
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                                                 Homo sapiens.
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Best Local S.
Matches 61
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PAT 02-APR-2001

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/translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVERG
GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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KNRIHHLPUDPVSGAVLHILTHRKLÄKFLHFGTLLERPSELLKRIDDGLGIGFREDL
AVVEETAPILTALDIFVDRAVSALPVNHETGOYNGIYSRFDYIHLAAQOTYNHLDMN
GBALRQRILCLEGVISCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGWVSLSDLIQ
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            same, and uses thereof
Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Pred. No. 3.5e-08;
0; Mismatches 3;
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/protein_id="CAC35800.1"
/db_xref="G1:13538835"
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                                                      /note="AMPKG3"
                                                                            /codon_start=1
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 /gene="PRKAG3"
                                     /gene="PRKAG3"
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nes 58; Conservative
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LWDSKKQSFVGMLIITDFILVLHRYIRSPLVQIYEIEEHKIETWREIXLQGCFKPLVS
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HLAAQQYTVHLDMNVGEDLRQRPLCLEGVLSCQPHETIGEVIDRIVREQVHRLVLVDE
TQELLGVVSLSDILGALVLSPAGIDALGA"
583 c 529 g 375 t
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gailard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
             Patent: Wo 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
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Pred. No. 3.5e-08;
0; Mismatches 3;
                                                                                                                                                                    /note="unnamed protein product"
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/tissue_type="skeletal muscle"
1. .1873
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                                                                                                                                                                                      /codon_start=1
/protein_id="CAC35798.1"
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/db_xref="taxon:9823"
/chromosome="15"
                                                                                                         /organism-"Sus scrofa"
/db_xref="taxon:9823"
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and uses thereof
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Best Local Similarity 95.1%;
Matches 58; Conservative
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gppgfregegorrpvassarggea/prfxpflegaplea/brbpfregulesbCAsAsa
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HPMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKGSFVGMLTI
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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220856-A 1 14-WAR-2002,
Iowa State University Research Foundation, Inc. (US)
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           Score 56.2; DB 6; Length 1873;
Pred. No. 3.5e-08;
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Pred. No. 3.5e-08;
0; Mismatches 3;
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/mote="unnamed protein product"
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                                         0; Mismatches
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/db_xref="G1:21261107"
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AX398333
AX398333.1 GI:21261108
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/organism="Sus scrofa"
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Best Local Similarity 95.1%;
Matches 58; Conservative
              92.1%;
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/translation-"MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 5 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
1. 1873
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                                                                     Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G. Novel prkag3 alleles and use of the same as genetic markers reproductive and meat quality traits Patent: WO 0220850-A 3 14-MAR-2002, Iowa State University Research Poundation, Inc. (US)
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Pred. No. 3.5e-08;
0; Mismatches 3
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Sequence 5 from Patent WO0220850.
AX398335
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Best Local Similarity 95.15
Matches 58; Conservative
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PAT 27-MAY-2002

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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDBTQHLLGVVSLSDILQ
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Mammalia, Eutheria, Cetartiodactyla, Suina; Suidae, Sus.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 2022)
                                                                                                                                                                                                         Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 9 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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Patent: WO 012003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Anderson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Pred. No. 3.5e-08;
0; Mismatches
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Sequence 31 from Patent WO0120003.
AX099804
          Sequence 9 from Patent W00220850.
AX398339
AX398339.1 GI:21261114
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/db_xref="taxon:9823"
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HPMQBHTCYDAMATSSR1.VIFDTMLE"RKAFFALVANGIRAAPLWDSKRQSFVQMLT
                                    AVVLETAP ILTALDI FVDRRVSALPVVNETIGOVGLI SRFDVI HLAAQQTYNHLDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRI VREQVHRLVLVDETQHLLGVVSLSDILQ
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KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 0177305-A 3 18-0c1-2001;
Arexis AB (SE)
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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a 504 c 534 g 363
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Search completed: June 13, 2003, 04:39:46 Job time: 194.613 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human AMP-activate	PRKAG3 CDNA. HOMO	Human AMPK gamma s	Human AMPK gamma s	Pig AMPK gamma sub	Pig AMPK gamma sub	Pig wild-type PRKA	Pig PRKAG3 polymor	Pig PRKAG3 polymor
SOUTHWINE			ID	ABA08485	AAH43685	AAD03296	AAD03320	AAD03295	AAD03319	AAD36456	AAD36457	AAD36458
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AAD36459 AAD36460 AAD03321 AAH43683	AAK81194 AAK76548	AAK81195 AAS05559 ABL08199 ABL08198	AAA07842 AAC64727 AAC64726	ABI97971 AAT38911	AAF20881 AAF20881 AAF20882	AAF20890 AAF20891	AAA34759	AAA34768 AAA34769	AAC98901	AAF208/9	AAA34757 AAA34766	AAF20880	AAA34758 AAA34767	AAF20874	ALIGNMENTS		ъ.			kinase su	4	issue gro	nesis; th	oid cell	on; proli	vascular	ealing; realing;	; haemost	lcer; ss.				
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                                                                                                                                                                                                                                   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. C antibodies against the polypeptides, methods of detecting the nucleotides of the invention. Although novel, many of the bind to polypeptides of the invention have homology to known proteins, thereby be polypeptides of the invention have homology to known proteins, thereby cylving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, stem cell growth factor activity. Thereby differentiation activities, stem cell growth factor activity, charactopicis regulatory activity; tissue growth activities, or may be immunomodulatory activity; tissue growth activities; charactories controlly activities; activities; and mander controlly activities; and mander controlly activities; activities, and activities of mander activities of activities and adminition activities; and activities, and adminities; and adminities; activities and activities; and adminities; activities and activities; and adminities; activities and activities; and adminities; activities and adminities; activities and adminities; and adminitie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                   Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
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                                                                                                                                                                                                                Claim 1; Page 429; 1963pp; English.
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                                                                          Liu C, Drmanac RT;
03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                     WPI; 2001-457740/49.
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                                            (HYSE-) HYSEQ INC.
                                                                                                                        P-PSDB; ABB11241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DRA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon in a subject. The variation of a G for a C at nucleotide 320, resulting in the amino acid substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in introm 6. The numbering of these
                                                                                                                Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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100.0%; Pred. No. 1.7e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= "T559C"
/note= "Silent variation"
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/label= "C1037T"
/note= "Causes R340W"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Causes P71A"
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20..1489
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/product= "PRKAG3"
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"C1037T"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "T559C"
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/label= "C230G"
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(first entry)
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21-JAN-2002
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                                                        PRKAG3 CDNA
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                                                                                                                                                                                                                                                                            PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalm E, Milan D, Robic A, Rogel-Gaillard C;
J, Le Roy P, Chardon P;
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                                                                                                                                                                                                                                                              gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                              Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA,
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472..1389
/*tag= b
/product- "Human Prkag3 protein"
1390..2109
/*tag= c
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                              AAD03296 standard; DNA; 2109 BP
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18-MAX-2000; 2000EP-0401388.
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Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleac acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; strKa3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
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                                                                                                                                                                                                                                                                                Length 2109;
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/product= "Human complete Prkag3 protein"
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                                                                                                                                                                                                                Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
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                                                                                                                                                                                                                                                                          100.0%; Score 61; DB 22; 100.0%; Pred. No. 1.8e-10;
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(ANDE/) ANDERSSON L.
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1..1395
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18-MAY-2000; 2000EP-0401388.
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                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 61; Conservative
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(KALM/) KALM E.

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complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primars that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. are ransgenic animal and host cell transformed with PRKAG3 or a neterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 and is useful for detecting mutations in a Prkag3 gene, or of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obseity; myopathy; cardiovascular disease, anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase. CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                            Length 2115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                             Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/product= "Sus scrofa PRKAG3 protein"
1390..1867
                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.8e-10;
                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 61; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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18-MAY-2000; 2000EP-0401388.
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472..1389
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5'UTR
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                                                                                                                                                   New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                    Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                      The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56.2; DB 22; Length 1867;
Pred. No. 6.2e-09;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
                                    ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD03319 standard; cDNA; 1873 BP.
                                                                                                                                                                                                                                                      Claim 12; Fig 2; 71pp; English.
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95.1%;
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                                      Looft C,
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                                                                                            WPI; 2001-244810/25.
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                                                                                                                  P-PSDB; AAE00220
                                                       Iannuccelli N,
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                                      Andersson L,
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us-09-826-581-5_copy_1007_1067.rng

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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name- "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                       AMP activated protein kinase regulatory gamma subunit, PRKAG3 gene, screening, meat quality, single nucleotide polymorphism; SNP; pig;
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/product= "Pig PRKAG3 wild-type protein"
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Pred. No. 6.2e-09;
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95.1%;
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                          Pig wild-type PRKAG3 gene.
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les 58; Conservative
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                                                                                                                                                                                Sus scrofa
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                                                                                                                              gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a cDNA encoding pig adenosine monophosphate (AMP) cativated Kinase (AMEK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome of the complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome of the complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome of the complete in the RN location of carbohydrate metabolism disorders such as the papertic for treating carbohydrate metabolism disorders such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence on the functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a creening compounds able to modulate AMPK activity. Nucleic activity or consisting compounds able to modulate AMPK activity. Nucleic activity or consisting to a present of the present of the present of the consisting of PRKAG3 or its mutant, are useful for a screening compounds able to modulate AMPK activity. Nucleic activity or consisting to the present of the presen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                           Rogel-Gaillard C;
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Pred. No. 6.2e-09;
0; Mismatches 3; Indels 0;
/product= "Sus scrofa complete Prkag3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                           Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                         Kalm E, Milan D, Robic J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                  (INRG ) INRA INST NAT RECH AGRONOMIQUE.
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95.1%;
                                                                                                                                                   11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                   10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
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Gellin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 95.1
hes 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                         (KALM/) KALM E.
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                                               WO200120003-A2
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Gaps

AAD36456;

AAD36456

Query Match

Best Loc Matches

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Best Loc
Matches
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 RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase requlatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant DNA (PRRAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                              /*tag= a
/product- "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
replace (89, C)
                                                                                                                                                                                                                                                                                                                             /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                     AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                                                                                                                        Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                  Cocation/Qualifiers
                             AAD36457 standard; DNA; 1873 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-2001; 2001US-260239P. 18-JUN-2001; 2001US-299111P.
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Matches 58; Conservative
                                                                                                                                                                                                                                                                 1395
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                                                                                                                                                                      screening; meat que gene; variant; ds.
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                                                                                       09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subunit gene
                                                                                                                                                                                                                   Sus scrofa.
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                                                          AAD36457;
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RESULT 8
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TICCIGCACATCITIGGCACCCIGCIGCCCGGCCCTCCTTCCTCTACCGCACCATCCAA 972
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                                                                                                                                                                                                                                  AMP activated protein kinase regulatory gamma subunit, PRKAG3 gene, screening, meat quality, single nucleotide polymorphism; SNP; pig;
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                                                                                                                                                                             Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
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                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/*tag= b
   BP
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/product= "Pig
AAD36458 standard; DNA; 1873
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95.18;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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                                                                                                                                                                                                                                                                                                gene; variant; ds.
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                                                       AAD36458;
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Sus scrofa

Key

AAD36459;

RESULT 10 AAD36459

variation

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The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase requiatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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                                                                                                                                                                                          AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malek M, Plastow G;
                                                                                                                                                        Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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Pred. No. 6.2e-09;
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                                    AAD36460 standard; DNA; 1873 BP.
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95.1%;
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/product= '
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les 58; Conservative
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                                                                             AAD36460;
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RESULT 11
AAD36460
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)"
replace (595, A)
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                                                                                                                                                                                        AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malek M, Plastow G;
                                                                                                                                                      Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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                                    AAD36459 standard; DNA; 1873 BP
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95.1%;
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                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rothschild MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200220850-A2
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                                                                                                                 09-AUG-2002
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Gaps

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24; Length 1873; Indels

Query Match

Matches

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Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3.
Transgenic animal and host cell transformed with PRKAG3 or a
heterotrineric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                   PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalm E, Milan D, Robic A, Rogel-Gaillard C;
J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                                                 Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Sus scrofa Prkag3 splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                      Sus scrofa PRKAG3 splice variant DNA
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 69; 71pp; English.
                                                                            AAD03321 standard; DNA; 2022 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2000; 2000WO-EP09896.
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18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                 (first entry)
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Gellin J,
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                                                                                                                                                              13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                        Sus scrofa
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                                            1 TICCIGCACAICTINGGITCCCIGCIGCCCCCCCCCCCTCCTCCICTACCGCACIAICCAA
                         Gaps
                                                                                                                                                                                                                                                         Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ds.
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  Length 2022;
                        Indels
  DB 22;
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                                                                                                                                                                                                                                                                                                                                              /number = "Intron 4"
/note= "3' portion of intron 4"
 Score 56.2; DB 22
Pred. No. 6.2e-09;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               c "Intron 5"
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r= "Intron 6"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/number= "Intron 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Intron 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Intron 9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Exon 6"
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                                                                                                                                                                                                                                                                                                                                                                                          "Exon 5"
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92.1%;
95.1%;
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           Local Similarity 95.1 tes 58; Conservative
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/*tag=
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 Query Match
Best Local S
Matches 58,
                                                                                                                                                                                         AAH43683;
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                                                                                                                                              RESULT 13
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2820 IGCIGCACCICACCGGITACGATCIGCCGATGCACTCCTTTTTGTGCCGCACTGCCCTG 2761
                                                                                                                                                                                                                                   polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) as useful in gene therapy techniques to restore normal activity of (II) as useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36006.
                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 8.6;
0; Mismatches 20; Indels
                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3238 BP; 926 A; 915 C; 858 G; 539 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                         Claim 1; SEQ ID No 13137; 103pp; English.
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2000US-0189874.
2000US-0190076.
2000US-019123.
2000US-020515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.9%;
ilarity 66.7%;
Conservative
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2000US-0184664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
  2001-639362/73.
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nes 40; Conserv
                        P-PSDB; ABG13146
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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16-MAR-2000;
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                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-2000;
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24-FEB-2000;
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                                                                                                                                                                                                                                                                                                    New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C t nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The variation may occur
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #13137.
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Pred. No. 1e-05;
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                                                                                                                                                                                                                      Marklund S;
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86.4%;
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2000US-0649167.
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                                                                                    06-APR-2001; 2001WO-SE00765.
                                                                                                                                 07-APR-2000; 2000US-195665P.
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                                                                                                                                                                                                                      Andersson L, Luthman H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
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                                                                                                                                                                                                                                                                WPI; 2001-657170/75
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WO200177305-A2
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in intron 6.
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SM; Ruben Barash SC, G, Rosen

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 36006; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased

Search completed: June 13, 2003, 03:00:00 Job time: 22.1613 secs

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June 13, 2003, 02:37:44; Search time 151.839 Seconds (without alignments) 6506.409 Million cell updates/sec
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Gaps

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                               AQ997354 1inear GSS 24-FEB-2000 RPCI-23-271P21.TV RPCI-23-271P21 GES 24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library availability, please contact Pieter de Jones Hore BACPAC Resources (http://bacpac.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea on Genetics (info@resqen.com). BAC end page: http://www.igr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 271 row: P column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 389)
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Moubulished (1999)
Other_CSS: RPCI-23-271P21.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 638                                                                                                                                          5 IGCACATCTITGGTTCCCTGCTGCCCGGCCCTCCTTCCTCTACCGCACTATCCA 59
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71.2%; Pred. No. 3.1e+02;
71.2%; Mismatches 15; Indels
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      70.9%; Pred. No. 1.5e+02;
live 0; Mismatches 16;
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AGENCOURT_6540753 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737918
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                       /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="Maxc 2PIG"
/tissue_Lype="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
a 190 c 151 g 124 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //issue_type="duodenal adenocarcinoma, cell line"
//isb.host="Duplum (phage_resistant)"
//note="Organ: small intestine; Vector: pCMV-SPORT6;
//isp.el. rough: Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
rechnologies. Note: this is a NIH_MGC Library."

4 400 c 377 g 175 t 3 others
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NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arged by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.1%; Score 56.2; DB 13; Length 572; 95.1%; Pred. No. 4.3e-06; Live 0; Mismatches 3; Indels 0
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http://image.llnl.gov
Plate: LLAM12748 row: m column: 23
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Location/Qualifiers
1. .1173
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/clone_lib="NIH_MGC_88"
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG.
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Matches 58; Conservative
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BM556730
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Cione—1bb-"Drosophila melanogaster adult testis library"

//sex="male"
//dev_stage="1-5 day adult"
//dab_host="SouR (Stratagene)"
//dab_host="SouR (Stratagene) (Stre="SouR (Stre="S
Bmail: oliver@helix.nih.gov,
http://www.niddk.nih.gov/intram/people/boliver.htm
trissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 73 row: g column: 07
Seq primer: Mi3RPI reverse primer (ABI).
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/strain="y[*] w[67c1]/Y"
/db_xref="taxon:7227"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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High quality sequence stop: 645.
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BE408262.1 GI:9344712
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BF528264 626 bp mRNA linear EST 11-DEC-2000 602043043F1 NCI_CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4180619
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Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm Bl-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLAMB492 row: f column: 12
High quality sequence start: 130
High quality sequence stort: 130
Location/Qualifiers
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Drosophila melanogaster

Bukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster testis expressed sequence tags
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:4180619"
/clone_lib="NCI_CGAP_Brn67"
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BE978092.1 GI:10609221
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                                                                       5', mRNA sequence.
BF528264
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Dissophila melanogaster

Bukaryota, Metazoa Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;

Bphydroidea; Drosophilae; Drosophilae;

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlsen, J., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, C., Miranda, A., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.
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/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: ADULT testes; Vector: pOTB7, Site_1: ECORI, Site_2: Xho1; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3
                                                                                                                                                                                                                              BF488250
715 bp mRNA linear EST 23-APR-200 AT0.3475.prime AT Drosophila melanogaster adult teetes pOTB7 Drosophila melanogaster cDNA clone AT0.3475 5 similar to CG4714:
EBan0004714 located on: 2R 49F15-50A1:: 04/09/2001, mRNA sequence.
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          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003819: arm:ZR [6082036,8314191]
estimated-cyto.49F2-50A3: 04/09/2001
Plate: AT.234 row: G column: 3
High quality sequence stop: 674.
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/lab_host="Plates Ar.10-Ar.120: DH5-alpha. Plates
Ar.121-Ar.319: DH5-alpha TonA"
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     11;
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
       Mismatches
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Unpublished (2000)
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     34; Conservative
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/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
                                                                                         /lab_host="DHIUB (phage-resistant)"
//lab_host="DHIUB (phage-resistant)"
//lab_host="Cogan: placenta; Vector: pOTB7; Site_1: XhoI;
//lab_host="Cogan: placenta; Vector: pOTB7; Site_1: XhoI;
//lab_host="Cogan" of the property of placental of the blacental of the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 706)
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Superscript II RT (Life Technologies). Note: this is a
NHLMGC Library."
1183 c 224 g 130 t
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consorthum/LLNL at:
http://image.llnl.gov
Plate: LLCM1689 row: i column: 02
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Pred. No. 5e+02;
0; Mismatches 11; Indels 0
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Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
                                               /clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_106"
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Location/Qualifiers
/db_xref="taxon:9606"
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75.6%;
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BG479057 757 bp mRNA linear BST 21-MAR-2001 602526134F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:4649792 5',
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 757)
                                                                                                                                                                                                                                               Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
melanogaster cDNA clone GH03085 5 similar to CG4714: FBan0004714 located on: 2R 49F15-50A1;: 04/10/2001, mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003819: arm:2R [8082036,8314191]
estimated-cyto:49F2-50A3: 04/10/2001
Plate: GH.30 row: H column: 1
High quality sequence stop: 754
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                                                                                                                                   Drosophija melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="GH Drosophila melanogaster head pOT2"
/sex=mahe and female"
/dex_stage="adult"
/lab_host="DH5 - alpha"
                                                                                                                                                                               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 754)
                                                                                                                                                                                                                                                                                                                                          On Jul 23, 1998 this sequence version replaced gi:3339282.
Other_ESTs: GH03085.3prime
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Pred. No. 5.1e+02;
0; Mismatches 16; Indels (
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/db_xref="taxon:7227"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence Berkeley National Lab
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Tissue Procurement: ATCC
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                                          AI063338.2 GI:13759449
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Matches 37; Conservative
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Fax: 510 486 6798
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/clone_Iib="NIH_MGC_21"
/clone_lib="NIH_MGC_21"
/tissue_type='choriocarcinoma"
/lab_host="DHOB (phage-resistant)"
/note="Organ: placenta; Vector: poTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/lab_host="bH10B" (phage=resistant)"
/note="organ: bladder; Vector: pCMV-SPORT6; site_1: NotI;
Site_2: Sali; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
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MNIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Close distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLAM10409 row: f column: 13
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at:
http://image.lll.gov
Plate: LLCM1430 row: c column: 09
High quality sequence stop: 757.
Location/Qualifiers
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                                                                                                                                                                                                                        /organism="Homo sapiens"
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/clone="IMAGE:4517004"
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/clone_lib="NIH_MGC_20"
/tissue_type="melanonic melanoma"
/lab_host="DHIOB (phage_resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
Coord: into EcoRI/XhoI sites using the following 5;
adaptor: GGCACAG(G): Size-selected >600bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 921)
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 5.2e+02;
0; Mismatches 11; Indels 0;
                                                                   Length 913;
                                                                                                                                                               1 INCCRECACATETTEGTTCCCTGCTGCCCCGGCCCTCCTTCCTC 45
                                                                 Score 27.4; DB 12; Length
Pred. No. 5.2e+02;
0; Mismatches 11; Indels
Note: this is a NIH_MGC Library." 254 c 287 g 146 t
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High quality sequence start: 5
High quality sequence stop: 742.
Location/Qualifiers
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BE275257.1 GI:9150210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                            SOURCE
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Contact: Robert Strausberg, Ph.D.
Email: agapbs.-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10406 row: p column: 19
High quality sequence stop: 648.
Location/Qualifiers
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                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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952021G01.y2 952 - BMS tissue from Walbot Lab (reduced rRNA) 2ea
                                                                                                                                                                                 NIH'MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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Pred. No. 5.2e+02;
0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 TICCIGCACCICCAIGGCIGGCIGCCAGAGCCCTGCTTGCTC 532
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/db_xref="taxon:9606"
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Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4516098"
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BQ048516
BG291149
BG291149.1 GI:13048809
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Best Local Similarity 75.6%;
Matches 34; Conservative
                                                                                                                                                             (bases 1 to 926)
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Search completed: June 13, 2003, 05:58:32
Job time: 155.839 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // note="Vector: put019; Site_1: EcoRI; Site_2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicallin-containing plates was used to recover positive clones.
                                                                                         /organism="Zea mays"
/cultiva="BMS (Black Mexican Sweet)"
/db.xref="tasms(Black Mexican Sweet)"
/db.xref="ta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mammary, Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammaliai; Butheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 887)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM10258 row: f column: 12
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/dev_stage="mixed logarithmic and stationary growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.6%; Score 27.2; DB 14; Length 569; 67.9%; Pred. No. 5.5e+02;
Live 0; Mismatches 18; Indels 0.
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/clone_lib="WGI_CGAP_Mam1"
/rissue_type="tumor, biopsy sample"
/dev_stage="10" months, virgin"
/lab_host="DH108"
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Location/Qualifiers
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Location/Qualifiers
1. .569
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BG174779
BG174779.1 GI:12681482
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Matches 38; Conservative
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Mus musculus
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BG174779/c
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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         FEATURES
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providing samples: Gilbert Smith, NIH"
249 a 199 c 219 g 220 t
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                                                            Score 27.2; DB 12;
Pred. No. 5.9e+02;
0; Mismatches 8;
                                                             44.6%;
80.0%;
                                                                            Best Local Similarity 80.0 Matches 32; Conservative
                                                               Query Match
                BASE COUNT
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Sequence 1, Appli
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Sequence 10, Ap
Sequence 3, Ap
Sequence 3, Ap
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                               Sequence 3, A
Sequence 3, A
Sequence 3, A
                                                                                                          Sequence 1, P. Sequence 7, P.
                                                                                                                                 Sequence 2,
                                                                                                                                                                                        Sequence
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Borkowski, Joseph B
Ransom, Richard W
TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-NO. 6407207-1993
CLASSIFICATION: <Unknown>
                                                                                                                              1 US-09-103-040A-2
1 US-09-103-840A-1
US-09-576-160B-10
US-09-576-160B-11
US-09-199-637A-164
US-08-200-016-4
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65.5%; Pred. No. 3.7;
          US-08-369-796-3

US-08-852-091-3

US-08-852-091-3

US-08-956-652-3

US-08-956-869-3

US-08-956-869-3

US-09-364-970-10

US-09-956-653A-3

US-08-087-465-1

US-08-087-465-1

US-08-814-095-7
                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 18713
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/860,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <Unknown>
ATTOREY/AGENT INFORMATION:
NAME: CATUSO, Charles M
REGISTRATION NUMBER: 30161
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                        Sequence 7, Application US/08148708; Patent No. 6407207; GENERAL INFORMATION: APPLICANT: Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
ULE TYPE: CDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 13
                                                                                                                  37.4 35060 3
37.4 4403765 37.4 4411529 36.7 960 4
36.7 1053 4
36.7 1161 4
                   CITY: Rahway
STATE: NJ
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Best Local Similarity
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US-08-148-708-7
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Patent No. 5171671
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                                                                                     (without alignments)
4027.262 Million cell updates/sec
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Sequence 9, 8
Sequence 3, 8
Sequence 2, 8
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Sequence 3,
Sequence 1,
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Sequence 1
Sequence 1
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                                                                       June 13, 2003, 02:39:09 ; Search time 4.64516 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                   Ltd.
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen
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US-08-466-906B-3
US-08-706-281A-3
US-09-201-746-3
US-09-201-746-3
US-08-592-383-7
US-08-592-383-7
US-08-592-383-3
PCT-US92-02320A-3
US-08-592-383-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-759-848-1
                                                                                                                                                                                               441362 seqs, 153338381 residues
                                                                                                       US-09-826-581-5_COPY_1007_1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    using sw model
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                                                                                                                                                              IDENTITY_NUC Gaport 1.0
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Maximum DB seq length: 2000000000
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3258 2
4403765
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                                                    - nucleic search,
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Match 1
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TITLE OF INVENTION: Cloned and Expressed Human Bradykinin BK-2 Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
OSCTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08 No. 6407207-1993
CLASSIFICATION: CURNOWN: CURNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08759848
Patent No. 5750826
GENERAL INFORMATION:
APPLICANT: Berweski, Joseph A.
APPLICANT: Strader, Catherine D.
APPLICANT: Chen, Howard V.
APPLICANT: Trumbauer, Myrna E.
TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/860,709
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Caruso, Charles M
REGISTRATION NUMBER: 30161
REFERENCE/DOCKET NUMBER: 18713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. BOX 2000
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4830
                                                                                                                                                                COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1179 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: John W. Wallen III
STREET: 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                           NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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0
                                                                                                                                                                                                                                                                  Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 42.6%; Score 26; DB 4; Length 909; Best Local Similarity 65.5%; Pred. No. 4.2; Matches 38; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-No. 6407207-1993
CLASSIFICATION CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: CATUSO, Charles M
REGISTRATION UNBER: 30161
REFERENCE/DOCKET NUMBER: 18713
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (908) 594-4830
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-08-148-708-3
Sequence 3, Application US/08148708
; Patent No. 6407207
; GENERAL INFORMATION:
                                                                                                                                                                                    Sequence 9, Application US/08148708
Patent No. 6407207
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hess, John W
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38; Conservative
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
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Matches
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Score 26; DB 4; Length 1378;
Pred. No. 4.5;
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BOrkowski, Joseph A.
APPLICANT: Strader, Catherine D.
APPLICANT: Hess, John W.
APPLICANT: Cheo, Howard Y.
APPLICANT: Trumbauer, Myrna E.
TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
TITLE OF INVENTION: NON-HUMAN ANIMALS
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                       20;
                                                                                                                                              Query Match 42.6%; Score 26; DB 4
Best Local Similarity 65.5%; Pred. No. 4.5;
Matches 38; Conservative 0; Mismatches
                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-148-708-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281,393
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9509383 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wallen III., John W.
REGIGTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 1923/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: John W. Marker empRET: 126 E. Lincoln Avenue
      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.6
Best Local Similarity 65.5
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rahway
New Jersey
                                                                                                                                                                                                                                                                                                                                                        PCT-US95-09383-2
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BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.6%; Score 26; DB 1; Length 1378; 65.5%; Pred. No. 4.5; tive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-NO. 6407207-1993
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 18713 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/860,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
                                    FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/281,393
FILING DATE: 27-JUL-1994
ATTORNEY/AGREW INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hess, John W
Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CATUSO, Charles M
REGISTRATION NUMBER: 30161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (908) 594-4830
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
                                                                                                                                                         NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19234
TELECOMMUNICATION INCOMMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08148708 Patent No. 6407207 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-759-848-2
                                                                                                                                                                                                                                            TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 65.3%,
".hog 38; Conservative
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: NJ
COUNTRY: US
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Query Match
Best Local Similarity 67.3*
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CORRESPONDENCE ADDRESS:
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15..959
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1..14
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       Chicago
                                        USA
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ZIP: 60606
                                                       90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-08-466-906B-3
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                                        COUNTRY:
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APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 8
                                                                    APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melancoyte Stimulating Hormone Receptor TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION VOMBER: US/07/866,979
FLING DATE: 19220410
CLASSIFICATION: 435
                                                                                                                                                                  ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: NO. 5532347nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154
TELEPHONE: 312-715-1000
TELEFAN: 312-715-124
TELEFAN: 912-715-124
TELEFAN: 912-715-124
TELEFAN: 912-715-124
TELEFAN: 910-221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                  Sequence 3, Application US/07866979
Patent No. 5532347
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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LOCATION:
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FEATURE:
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US-07-866-979-3
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APPLICANT: Cone, Roger D
APPLICANT: Fan, Wei
APPLICANT: Fan, Wei
APPLICANT: Boston, Bruce A
APPLICANT: Lu, Dongsi
APPLICANT: Chen, Wenbiao
TITLE OF INVENTION: Wethods and Reagents for Discovering and
TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagon
TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
NUMBER OF SEQUENCES: 19
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Pred. No. 11;
0; Mismatches 17; Indels 0
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
COMPUTER: TBM FC compatible
COMPUTER: TBM FC compatible
COMPUTER: TBM FC COMPATIBLE
COMPUTER: TBM FC FOOSYMS DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUBER: US/08/466,906B
FILING DATE: 06-JUN 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5849871nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10002
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STREET: 300 South Wacker Drive
CITY: Chicago
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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371 CGIGCTCATCTGTGGCTCCATGGTCCCAGTCTCTGCTTCCTGGGCATCATT 422
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TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                               40.7%; Score 24.8; DB 4; Length 1260; 67.3%; Pred. No. 11; tive 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,231
FILING DATE: 12-Jun-1998
CLASSIFICATION TONKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6278038nan, Kevin E
RESTERRATION NUMBER: 35,303
FEFERRENCE/DOCKET NUMBER: 96,886-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09097231
Patent No. 6278038
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
Chen, Wenbiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1260 base pairs
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                       INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1260 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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COMPUTER READABLE FORM:
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STATE: Illinois
        TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                    960..1260
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                                                                                                                                                                                                         NAME/KEY: 5'UTR
LOCATION: 1..14
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; LOCATION:
US-09-201-746-3
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 11;
0; Mismatches 17; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive
CITY: Chicago
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-DEC-1998
CLASSIFFCATION: 435
ATORNEY/AGENT INFORMATION:
NAME: NO. 626821nan, Kevin E
REGISTRATION NUMBER: 35,303
REPERBNUE/COCKET UNBER: 92,154-J
TELECOMMUNIC/DOCKET UNBER: 92,154-J
TELECOMMUNIC/DOCKET UNBER: 92,154-J
TELECOMMUNIC/DOCKET UNBER: 92,154-J
                                                          JMBER: US/08/706,281A
04-SEP-1996
                                                                             FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100048nan, Kevin E
REGISTRATION NUMBER: 35,303
REFRENCE/POCKET NUMBER: 96,886
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/201,746
FILING DATE: 01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6268221
                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                           LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 67.39
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                            APPLICATION NUMBER:
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US-09-201-746-3
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"Hematopoietic Cell Lines Bearing Altered Retinoic Acid Rec
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US-09-347-878-25/c

Sequence 25, Application US/09347878C

Patent No. Gardell

GENERAL INFORMATION:

APPLICANT: Yuan, Chong

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAVING ANALYTES

FILE REFERENCE: 25855-1651

CURRENT APPLICATION NUMBER: US/09/347,878C

CURRENT FILING DATE: 1999-07-06

NUMBER OF SEQ ID NOS: 75

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 25

LENGTH: 2561
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LOCATION: (1131)..(2399)
OTHER INFORMATION: Escherichia coli nucleic acid encoding
OTHER INFORMATION: folypolyglutamate synthetase-dihydrofolate
OTHER INFORMATION: synthetase
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: M32445/GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 2561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Christensen, O'Connor, Johnson and Kindness 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct) INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Competible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.7%; Score 24.2; D
62.3%; Pred. No. 19;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence 3, Application US/08592383; Sequence 3, Application US/08592383; Sequence 3, Application US/08592383; Sequence 3, Application: Sequence 3, TITLE OF INVENTION: "Hematopoietic Cell; NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Broderick, Thomas F.
RECISTRAILON NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FFCR-1-7190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATE: US/08/592,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,242
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 62.39
Matches 38; Conservative
                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tsai, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Recept
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: page 11, RAR-alpha N-terminal region; positions 103 to 363 of SEQ.
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Pred. No. 13;
                                                                                                                                                                                       Score 24.8; DB 4; Length 1; Pred. No. 11; 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31.332
REFERENCE/DOCKET NUMBER: PHCR-1-7190
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1.206.682-8100; 1-206-224-0709(direct)
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word for Windows 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/099,242
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08592383
Patent No. 5830760
GENERAL INFORMATION:
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APPLICATION NUMBER: 08/099,
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.7%;
66.0%;
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Best Local Similarity 67.3%;
Matches 35; Conservative
                                           15..959
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 66.0
Matches 35; Conservative
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                                                                                     NAME/KEY:
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                       NAME/KEY:
                                           LOCATION:
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    FEATURE:
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                                                                                                                                               US-09-097-231-3
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6 GCACATCTTTGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCC 58
Best Local Similarity 66.0%; Pred. No. 20;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                 Search completed: June 13, 2003, 06:01:18
Job time: 9.64516 secs
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                                                                                              MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: page 4, RAR-alpha403 dominant negative; deleted of 1311-1596 of SEQ.
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APPLICANT: DMITROVSKY, ETHAN
APPLICANT: MARRELL JR, RAYMOND P
APPLICANT: MILER JR, MILSON H
APPLICANT: MILER JR, MILSON H
APPLICANT: FRANKEL, STRALEY
TITLE OF INVENTION: METHODS FOR THE DETECTION AND
TITLE OF INVENTION: TRRATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                         6 GCACATCTTTGGTTCCCTGCTGCCCGGCCCTCCTTCCTCTACCGCACTATCC 58
                                                                                                                                                                                                                                            39.7%; Score 24.2; DB 2; Length 2658; 66.0%; Pred. No. 19; 18; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION NUMBER: US/08/095,728B
FLING DATE: 21-MT-1993
CLASSIFICATION A135
PRIOR APPLICATION NUMBER: US 07/673,838
FLICATION NUMBER: US 07/673,838
FLICATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION NUMBER: 38694-A
TELECOMMUNICATION NUMBER: 38694-A
TELECOMMUNICATION NUMBER: 38694-A
TELEFROM (212) 278-0400
TELEFROM (212) 278-0400
TELEFROM (212) 331-0525
INFORMATION FOR SEQ ID NO: 3:
ENGURNE CHARACTERISTICS:
LENGTH 2928 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3, Application US/08095728B; Patent No. 5843642
LENGTH: 2658 base pairs
                                                                                                                                                                                                                                              Query Match 39.7%
Best Local Similarity 66.0%
Matches 35; Conservative
                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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STRANDEDNESS: single
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; LOCATION; 103..1488
; OTHER INFORMATION:
US-08-095-728B-3
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                                                                                                                                                ; IMMEDIATE SOURCE:
; LIBRARY: cDNA
US-08-592-383-3
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39.7%; Score 24.2; DB 2; Length 2928;

Query Match

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Sequence 129, App
Sequence 1, Appli
Sequence 59, Appl
Sequence 2280, Ap
Sequence 6987, Ap
Sequence 21, Appl
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Sequence 7, Appli
Sequence 5, Appli
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4579.068 Million cell updates/sec
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Sequence 19,
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                                                                            June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMS.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMS.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-880-107-3428
2 US-10-044-090-92
US-10-269-353-21
0 US-09-750-264-21
US-10-269-353-11
0 US-09-790-264-11
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US-09-826-581-3

US-10-255-356-159

US-10-045-815-7

US-10-045-815-7

US-09-925-297-129

US-09-925-297-129

US-09-975-593-1

US-09-764-891-2280

US-09-764-891-6987
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US-10-288-160-3
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                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                  using sw model
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Gapop 10.0 , Gapext 1.0
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DB seq length: 2000000000
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APPLICANT: Luthman, L. Bolger
APPLICANT: Luthman, L. Bolger
APPLICANT: Marklund, Stefan
TITLE OF INVANION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 S
FILE REPERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
NUMBER OF SEQ ID NOS: 14
                                     Sequence 19, Appl Sequence 19, Appl Sequence 16, Appl Sequence 22, Appl Sequence 22, Appl Sequence 9, Appli Sequence 9, Appli Sequence 509, Appli Sequence 509, Appli
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Seguence 146, App
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US-09-764-898-74
US-10-073-865-52
US-09-764-898-146
US-10-269-33-191
US-10-269-333-19
US-10-269-333-16
US-10-269-333-16
US-10-269-333-16
US-10-269-333-16
US-10-269-333-16
US-09-790-264-16
US-09-790-264-22
US-09-790-264-29
US-09-978-128-509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 100.0%; Score 61; DB 10; Local Similarity 100.0%; Pred. No. 2.1e-12; nes 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                             ; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
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APPLICANT: Andersson, Lelf
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; LOCATION: (20)...(1486)
US-09-826-581-5
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1067 G 1067
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wadhwa, Renu
APPLICANT: Wadhwa, Renu
APPLICANT: SUGINATA, Takashi
ITILE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFRENCE: 05501-091001
FILE REFRENCE: 05501-091001
CURRENT FILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-10-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 15
SOFTHARE: FASTSEQ for Windows Version 4.0
SSOTHARE: FASTSEQ for Windows Version 4.0
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: JP 11/118806
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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GENERAL INFORMATION: APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COCATION: 2376
COTHER INFORMATION: n = A,T,C or G
US-10-045-815-5
                                                                                                                                                                                                                                                                                                                 ) LOCATION: 2282
) OTHER INFORMATION: n = A,T,C or G
US-10-045-815-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 5, Application US/10045815; Patent No. US20020160498A1
                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (12)...(1637)
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (12)...(2252) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
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                                                                                                                                                                                 ORGANISM: Mus musculus
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US-09-925-297-129
                                                                                                                                        LENGTH: 2322
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US-10-045-815-5
                                                                                                                                                               TYPE: DNA
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                                                                                  TITLE OF INVENTION: VARIANCE OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI FILE REPRENCE: 11145-007001
CURRENT APPLICATION NUMBER: US,09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 159, Application US/1025536

Publication No. US20030087807A1

GENREAL INPORMATION:

APPLICANT: Greenspan, Ralph J.

TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to TITLE OF INVENTION: Balance and the Perception of Gravity

FILE REPERBACE: P-NI 364

CURRENT APPLICATION UNMBER: US/10/255,536

CURRENT FILING DATE: 2002-09-25

PRIOR APPLICATION NUMBER: US 60/168,579

PRIOR FILING DATE: 1999-12-02

NUMBER OF SEQ ID NOS: 261

SOUTHWARE: PESESEQ for Windows Version 4.0

SEQ ID NO 159

LIENGTH: 566
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                                                                                                                                                                                                                                                                                                                                                                                                   75.7%; Score 46.2; DB 10; Length 1722; 86.4%; Pred. No. 3.1e-07; Live 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 566;
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44.9%; Score 27.4; DB 9;
Best Local Similarity 69.8%; Pred. No. 1.2;
Matches 37; Conservative 0; Mismatches 16;
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APPLICANT: Wadhwa, Renu
APPLICANT: Sugihara, Takashi
APPLICANT: Ohide, Akiko
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: 06501-091001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/045,815
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/JP00/02731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10045815 Patent No. US20020160498A1
                                             APPLICANT: Luthman, L. Holger APPLICANT: Marklund, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 86.49
Matches 51; Conservative
                             APPLICANT: Andersson, Leif
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Drosophila
US-10-255-536-159
    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                          LENGTH: 1722
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                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Score 25.8; DB 9; Length 12043; Pred. No. 4.4; 0; Mismatches 17; Indels 0;
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                                                                      APPLICANT: Lee, Helen H
APPLICANT: Nandabalan, Krishnan
TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2
TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2
CURRENT APPLICATION: NUMBER: US/09/979,593
CURRENT APPLICATION NUMBER: POT/11-14
PRIOR FILING DATE: 2001-05-07
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
SOFTWARE: PALENTING DATE: 2000-05-05
SOFTWARE: PALENTING DATE: 2000-05-05
INVERSE OF SEQ ID NOS: 83
SOFTWARE: PALENTIN Ver. 2.1
LENGTH: 12043
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OTHER INFORMATION: PS10: polymorphic base G or A
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CHER INFORMATION: PS12: polymorphic base G or A US-09-979-593-59
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LOCATION: (4141)
OTHER INFORMATION: PS3: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (3697)
OTHER INFORMATION: PS1: polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or
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LOCATION: (4110)
OTHER INFORMATION: PS2: polymorphic base C
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LOCATION: (7155)
OTHER INFORMATION: PS6: polymorphic base G
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OTHER INFORMATION: PS5: polymorphic base A
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OTHER INFORMATION: PS11: polymorphic base
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LOCATION: (7181)
OTHER INFORMATION: PS7: polymorphic base
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OTHER INFORMATION: PS8: polymorphic base
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OTHER INFORMATION: PS9: polymorphic base
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Best Local Similarity 67.9%;
Matches 36; Conservative (
       Choi, Julie Y
Denton, R. Rex
Kliem, Stefanie E
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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NAME/KEY: allele
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                                                     APPLICANT
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA105
CURRENT APPLICATION UNDER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NO 129
LENGTH: 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.6%; Score 26; DB 10; Length 1682; Best Local Similarity 64.4%; Pred. No. 3.7; Matches 38; Conservative 0; Mismatches 21; Indels
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APPLICANT: Kliem, Stefanie E
APPLICANT: Lee, Helen H
APPLICANT: Nandabalan, Krishnan
TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
FILE REPERENCE: MHH-0425 PCT ICAM2
CURRENT APPLICATION NUMBER: 05/09/979,593
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-05-07
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTIN Ver. 2.1
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Pred. No. 4.4;
0; Mismatches 17;
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Publication No. US20030082555A1
GENERAL INFORMATION:
APPLICANT: Genaissance Pharmaceuticals, Inc.
APPLICANT: Chew, Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Genaissance Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                    COCATION: (24)
COTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-129
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Publication No. US20030082555A1
GENERAL INFORMATION:
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Best Local Similarity 67.9%;
Matches 36; Conservative
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Choi, Julie Y
                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-1
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US-09-979-593-1/C
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APPLICANT: APPLICANT:

SEQ ID NO 1

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Query Match

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FEATURE:

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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper, NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                       Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.0%; Score 25; DB 9; Length 635; 64.9%; Pred. No. 8.2;
                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOGO.:
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Indels
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US-09-764-891-6987
                                                                                                                                   Sequence 2280, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
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Patent No. US20020038467A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
APPLICANT: Matthews, William
APPLICANT: Moore, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 64.9
Matches 37; Conservative
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US-09-764-891-2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                             RESULT 9
US-09-764-891-2280/c
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LOCATION: (9701)
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US-09-764-891-6987
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US-09-815-944-21
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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TITLE OF INVENTION: Methods and Reagents for Discovering and Using Manmalian Melanocortin Receptor Agonists and Antag To Modulate Feeding Behavior in Animals
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APPLICANT: Phillips, Russell TITLE OF INVENTION: TRANSGENIC MICE CONTAINING MELANOCYTE TITLE OF INVENTION: STIMULATING HORMONE RECEPTOR GENE DISRUPTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24.8; DB 10; Length 200;
Pred. No. 9.5;
0; Mismatches 17; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: ACCOUNCEL1 Boehnen Hulbert & Berghoff
ADDRESSEE: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/288,160
FILING DATE: 05-No. US20030105024A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/706,281
FILING DATE: 04-SEP-1996
ATTORNEY INFORMATION:
NAME: No. US20030105024Alnan, Kevin E
                                                                    FILE REFERENCE: R-654

CURRENT APPLICATION NUMBER: US/09/815,944

CURRENT FILING DATE: 2001-03-22

PRIOR PELLING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: US 60/191,236

PRIOR PELLING DATE: 2000-06-29

PRIOR PELLING DATE: 2000-06-29

PRIOR PELLING DATE: 2000-06-29

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/218,075

PRIOR PELLING DATE: 2000-07-19

PRIOR PILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 21

SOFTHARE: RASESEQ for Windows Version 4.0
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REFERENCE/DOCKET NUMBER: 96,886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kesterton, Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Targeting vector US-09-815-944-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/10288160; Publication No. US20030105024A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boston, Bruce A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cone, Roger D
Fan, Wei
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Best Local Similarity 67.3%;
Matches 35; Conservative (
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Chen, Wenbiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 21
LENGIH: 200
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US-10-288-160-3
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Search completed: June 13, 2003, 09:00:42 Job time: 20.2903 secs
SENERAL INFORMATION:
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APPLICANT: Allen, Keith D.
APPLICANT: Antichews, William
APPLICANT: Matthews, William
APPLICANT: Mocre, Mark William
APPLICANT: Mocre, Mark Mews, William
APPLICANT: Mocre, Mark Mewsell
TITLE OF INVEWION: STIMULATING HORMONE RECEPTOR GENE DISRUPTIONS
TITLE OF INVEWION: STIMULATING HORMONE RECEPTOR GENE DISRUPTIONS
FILE REFERENCE: Re 654
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/191,236
PRIOR APPLICATION NUMBER: US 60/215,214
PRIOR APPLICATION NUMBER: US 60/215,214
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FESTSEQ for Windows Version 4.0
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Pred. No. 9.7;
0; Mismatches 17; Indels 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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; Patent No. US20020142981A1
                 TELEX: <UNKnown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
TELEFAX: 312-913-0002
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Best Local Similarity 67.3%;
Matches 35; Conservative
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LOCATION:
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GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVANTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REPERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
SEQ ID NO 92
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Pred. No. 10;
0; Mismatches 17; Indels 0;
GENERAL INCOMPATION:
APPLICANT: Workley, Joseph G.
APPLICANT: Schorf, Uwe.
APPLICANT: Schorf, Uwe.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-W0
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR PILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SED ID NOS: 3950
SOFTWARE: PATENTIN VER. 2.1
SEQ ID NO 3428
LENGTH: 99014
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
US-09-880-107-3428
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Pred. No. 13;
0; Mismatches 21; Indels 0
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 416842.32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure

1 LOCATION: 665, 690, 698

7 OTHER INFORMATION: a, t, c, g, or other

US-10-044-090-92
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Patent No. US20020137081A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 67.3%;
Matches 35; Conservative C
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Best Local Similarity 63.8%;
Matches 37; Conservative (
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ORGANISM: Homo sapiens
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June 14, 2003, 11:14:11; Search time 4487 Seconds (Without alignments) 11168.939 Million cell updates/sec
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1722
I cctggcccctcagatcaaga......gatgagaggctcgggctgga 1722
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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4: gb_on:*

5: gb_ov:*

6: gb_pt:*

10: gb_pt:*

10: gb_ro:*

11: gb_st:*

11: gb_st:*

12: gb_vi:*

13: gb_ui:*

14: gb_vi:*

15: gb_vi:*

16: em_loi:*

17: em_loi:*

18: em_loi:*

18: em_loi:*

19: em_loi:*

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em_htgo_other:*
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mon

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CATCCTGACTGCACTTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAA 1680
                                                                                    CATCCTGACTGCACTGGACATCTTGTGGACCGGCGTGTCTCTGCACTGCCTGTGGTCAA 1680
                                                                                                                                                                                                     CTCCCTAGGCTGCCCCGAGGCTCACTGCTCCCATCTGCAGCCTGTTTGAAGCTGTCTA 1260
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                                                                                                                                                                                                                                                                                                  1381 CCCAGGTGGGAGGAAGGGGGAGACCTGGGCAGGTGATCAGAGGGCCTGAGGAGTCTTCAG
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AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, W., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Cardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Ille, Y., Lamazares, R., Janders, T., Leboczky, J., Klein, J., Lakocque, K., Lanazares, R., Landers, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McCarthy, M., McBwan, P., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C., H., O'Connor, T., O'Connorll, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, M., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Ray, A., Santos, R., Sothauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Vely, W., V., Wyman, D., Ye, W., Vely, W., V., Wann, D., Vely, W.,	Nessargn, 7, 200 charies Street, Cambridge, MA 02141, USA On Jun 7, 2000 this sequence version replaced gi:7342115. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatWasker.html	oortig of 1321 bp in of 100 bp contig of 1321 bp in of 100 bp contig of 1041 bp in of 100 bp contig of 1286 bp in of 100 bp contig of 2473 bp in of 100 bp contig of 2473 bp in of 100 bp contig of 2473 bp in of 100 bp

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Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                    TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACC
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Homo sapiens BAC clone RPl1-459119 from 2, complete sequence.
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459I19
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.H.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis WO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanase, J.J. and de Jong, P.J. (1988) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute
[http://Dacpac.med.buffalo.edu]
VBCTOR: pBACe3.6

The clone sequenced to the left is RP11-1077K22; the clone

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206864 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

JRES Location/qualifiers
Source 1. .206854
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/organism="Homo sapiens"
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/map="2"
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/clone_lib="RPCI-11"

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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

tz39c01.y1"
(NID:g11061273)" (NID:g11251653)"
(NID:913409904)" (NID:914467240)"
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Length 206854;

DB 9;

Score 1697;

98.58;

Query Match

GGGGATCTGACCCTCAACCTGCCTTCCACCCAAAGGCCCCGGGCTGACCTCCTCCCCGCC 166158 ä CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGTGAGGAGGAGGCTGGGGAGGTGAAG 120 AGGGGAGTCCTCCTGGAGCCTGGTGCCCTAGAAGCCCACGTCTTTCTGACTTCTGGAGTC CTCCATCTCTCTAATGATAGGTGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCC GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT CCTCCCCTGCAGGGATGCTGACCATCACTGACTTCATCCTGGTGCTGCATCGCTACTACA CTGTCGATGTCTCTAGGTCCAGATCTATGAGATTGAACAACATAAGATTGAGACCTGGAG CCTGGCCCCTCAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC ACTGTCCTGTTCCCACAGTCCCCACTGTCTCAGCACAAGGACACTGGCAGGGTGGGGA GGGTGAGTGGGGAAGCCCGGAAAGGGGCTGTTGGTGATGGTGGCCCAGGGCTTAAG GGTGCCTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTGACCGGCTCCCC **ACCACAGGTTGGCTTCAGGCCAAGCCCAGGGGCCCAGGGTGGAGGAAAGTCCATCC** GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG AGCAAATGGGGGGAGGCAGGAGAGAAAAAGAGCCCCAACTTCTCAGGCCTGGGGGGTGCCCC Gaps Indels ö Pred. No. 0; 0; Mismatches llarity 99.9%; Conservative l Similarity 719; Conserv ž

us-09-826-581-3.rge

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jóin(<1. .154,515. .918,1809. .1890,2349. .2407,2509. .2554,
2771. .2825,3027. .3153,3286. .3451,4578. .4615,4791. .4937,
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                                                                                                                                                                                                                                                                                               /product="AMPK gamma subunit"
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5294. 5410)
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DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGMDDELQKPGAQVYM
HFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLMDSKKQSFVGMLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDFILVLHRYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSIFBAYALI
KNRIHELPVLDPVSGAVALHITHREKLÄFLHFEGTLLEPREPERTYRTUGDLGIGTFRDL
AVVLETAPILTALDIFVDRAVSALPVNETGQVVGLYSRFDVIHLAAQQYTWHLDMY
GEALRORTLCLEGGVLSCQPHETLGEVIDRIVREQVHRAVLVDGTQHLGVVSISDILQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCTGGTGGCCAGCTGGGAGA-------TCTCAACTGTAGGAGAGCTGTGA 2080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1800 GGCGCTCAGATCAAGAAGGCCTTCTTTGCCCTGGTGGCCAACGGCGTCCGAGCGGCACCT 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1860 TTGTGGGACAGCAAGAAGCAGAGCTTCGTGGGTGAGGAGGGGCTGGGGAGG-CAGAGGTG 1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGCTTGGCTTCAGGCCAAGCCCAGGGCCAGGGTGGAGGAAAGTCCATCCGGAG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 TCTGCATGGCCAGCTGGGAGACCCTGGGGGCTCAATTTCCCCCATCTGTGGAGCCGCTATGA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCA-----TAGGTGCTAG 358
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Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swe
University of Agricultural Sciences, BWC Box 597, Uppsala 751
Sweden
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Pred. No. 1.9e-140;
0; Mismatches 484;
                                                                                                                                                                                                                                                                                                                                                                                                                /product="AMPK gamma subunit"
/protein_id="AAF73989.1"
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                                                            Location/Qualifiers
1. .5888
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                                                                                                                                                                                                                                                                               /gene="PRKAG3"
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                                                                                                                                                                                                  /gene="PRKAG3"
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Best Local Similarity 66.3%;
Matches 1155; Conservative C
                                                                                                                                                             /map="15q'
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalin,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1081 ACAGTCCCCTTCCCCAGTCCCACTCAGCTCTGAACTCACCTCTTCATCCTAGGCGGCACA
                                                              CAGACAAGGGAGCCTTGGTGCCCTGCCCTCTTTTTAGGGGCCTGGGATGGAGGTTGTCT
                                                                                                                                                                                                                      CACCCTCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGT
                                                                                                                                                                                                                                                                                                 ACTCCACATCCTCACACACACGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCAGGTGGGAGGAAGGGGGAGACCTGGGCAGGTGATCAGAGGGCCTGAGGAGTCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165319 CCCAGGTGGGAGGAAGGGGAGACCTGGGCAGGTGATCAGAGGGCCTGAGGAGTCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTAGCAGTCGTGGGGAAGAGCTGGGAGCCTCTTGAAGCTGCTGGATCCCTGATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1501 ACCIGGICCCCAICCIAACCAGGITCCCIGCIGCCCCGGCCCICCTICCICTACCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa AMPK gamma subunit (PRKAG3) gene, complete cds. AF214521.
AF214521.1 GI:8215685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Andersson, L.
A mutation in PRKAG3 associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 288 (5469), 1248-1251 (2000)
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Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus clone CH230-262H11, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5585
                                                                                                                                                                                                                                                                                                                                                                                                                                 1459 AGAGCTGGGAGCCCTCTTGAAGCTGCTGGATCCCTGATCTCCACCTGGTCCCAATCCTAA 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CTAGATCAAGTGTCTTGATCTGATGAGATCACTACCATGTCCCATCTA 5536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1519 CCAGGGTTCCCTGCTGCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCAT 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1579 CGCCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGA 1638
GATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACA 1338
                                                                                                                                       1339 CAAACGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGGCCCAGGTGGGAGGAAGGG 1398
                                                                                                                                                                                GGAGACCTGGGCAGGTGATCAGAGGCCTGAGGAGTCTTCAGCCCTAGCAGTCGTGGGGA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordala; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5475 CGCCACATTCCGAGATTTGGCTGTAGTTCTGGAAACAGCTCCTGTCCTGACTGCGCTGGA
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KEYWORDS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pleces is not known and their order in this sequence record is
Peters, L., Pickens, R., Primus, E., Pu, L.L., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, K., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Mang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wulliamson, A., Wieczyk, R., Wooden, S., Worley, K., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid;
Chemistry: DPe-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 72428 bases at least Q40
Consensus quality: 76114 bases at least Q30
Consensus quality: 79522 bases at least Q30
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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of 1072 }
unknown ]
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Center project name: GZRR
Center clone name: CH230-262H11
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TAGATCCAGTGTCT
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gap of unknown length
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contig of 4259 b
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HTG; HTGS PHASE1.
Norway rat.
Rattus norvegicus
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Best Local Simi
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REFERENCE

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ANIBRIA, D. Marie., Metzker, M. Lee., Abramzon, S., Addams, C., Allen, H., Abbrooks, S., Adin, A., Angulano, D., Anyalebechi, Y., Angupia, A., Angubia, A., Angubiano, D., Anyalebechi, Y., Angupia, A., Ayodeji, M., Baca, E., Baden, H., Balardiano, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Barden, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bayant, M., angupia, S., Carcia, S., Carcia, M., Creen, D., Charez, D., Chare, D., Charez, D., Charez, D., Charez, D., Chen, S., Chen, R., Chen, Y., Chen, Z., Charez, D., Charez, D., Chen, S., Chen, R., Chen, Y., Chen, Z., Charez, D., Davis, C., Coyle, M., Cree, D., D'Soura, L., Davila, M., L., Davis, C., Coyle, M., Cree, D., D'Soura, L., Davila, M., L., Davis, C., Davis, C., Coyle, M., Cree, D., Davis, K., Davis, C., Lau, C
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On Aug 3, 2002 this sequence version replaced gi:22038439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.

Direct Submission

Submitted (01-A0G-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of M, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequences soon as it is available and the accession number will
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 141109 bases at least Q40 consensus quality: 148891 bases at least Q30 consensus quality: 155675 bases at least Q20
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ILVANOYRAARALWDSKTGSYGWLTTIPDFILVLHRYYRSPLYVOIYEIEDRIKIETWREIT
LQGCFKPLYSISPHDSIFEAVYTLIKRRIHRLPVLDPVGDYBUHTTHRKLIKELHIF
GSLLPRPSFLYRTIODLGIGIFRRLAVULFRAPILTALDIFVDRNSALEVVNBCGQV
VGLYSRFDYIHLAAQOTYNHLDMSVGERLROFTLCIEGVLSCQPHESLGEVIDRIARE
OVHENLVLOFTQHLLGYVSLSOILQALVISPAGIDALGA"

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/db_xref==[0:1.16608834"
/translation="MEPGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSMPSPAVTS
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Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: NO 0177305-A 5 18-OCT-2001;
Arexis AB (SE)
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Primates; Catarrhini; Hominidae; Homo.
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AX281582
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Best Local Similarity 68.1
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AF214519 2115 bp mRNA linear PRI 03-JUN-2000
Homo sapiens AMP-activated protein kinase gamma subunit (PRRAG3)
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EPPPGGGERSRPTAESTGLEATPRYTPLAGADPAGVGFPTGWDCLESCTASAAG
SSTDDVELATERPATEAMPC.ELEGLLEERPALCLSPQAPPEKLGWDDELKRPRQIYN
RFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKGSFVGMLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A mutation in PRKAG3 associated with excess glycogen content in pig
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1 (bases 1 to 2115)
Milan, Jeon, Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. and Andersson, L.
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Chardon, P. Variants of the gamma chain of ampk, dna sequences encoding the
                                 Patent: WO 0120003-A 29 22-MAR-2001;
Patent: WO 0120003-A 29 E2-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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/note="unnamed protein product"
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Pred. No. 1e-30;
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Science 288 (5469), 1248-1251 (2000)
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/db_xref="G1:13538837"
                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                         Location/Qualifiers 1. 2115
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lspnscleavylliknihklevldprsgwlhtlitrknikfliffelifesllerpsft
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                                       PAT 02-APR-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                same, and uses thereof
Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                 Variants of the gamma chain of ampk, dna sequences encoding the
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
                                                                                                                                                                                                                        Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 168.2; DB 6; Length 2109;
Pred. No. 1e-30;
0; Mismatches 8; Indels 0;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAC35799.1"
/db_xref="GI:13538811"
                         AX099776 2109 bp
Sequence 3 from Patent Wo0120003.
AX099776
                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
472. .1389
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                                                                                         AX099776.1 GI:13538810
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Best Local Similarity 95.6
Matches 173; Conservative
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SOURCE
RESULT 9
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Length 2115; Indels

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LOGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIF
GSLLPRPSFLXRIJODLGIGTFRDLAVLETAPILTALDIFVDRRVSALPVVNECGOV
VGLYSRYDVIHLAAQOTVHLDMSVGEALRKRTLCLEGVLSCQPHESLGEVIDRIARE
OVHRLVLVDFTGHLGYVSLSDILQALVLSPAGIDPSGPEKI"
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LVANGVRAAPLWDSKRQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIY
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                         /evidence=experimental
/product="Amb-activated protein kinase gamma 3 subunit"
/protein_id="CAMES117.1"
/db_xref="GI:6688201"
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                                                                    Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Harmersmith Hospital, DuCane Road, London, W12 ONN, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                            /function="AMP-activated protein kinase regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.8%; Score 168.2; DB 9; Length 2290; 95.6%; Pred. No. 1e-30;
tive 0; Mismatches 8; Indels 0;
                                                                                                                                                              1. .2290
/organism="Homo sapiens"
/db_xref="taxon:9606"
22. .1500
                                                                                                                                                                                                                                                   /gene="AMPK gamma 3"
22. .1500
                                                                                                                                                                                                                                                                                                  gamma 3"
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HTG; HTGS_PHASE1.
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Rattus norvegicus
                                                   Direct Submission
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AC127107/c
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/transletion-"MSFLEQENSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG
/transletion-"MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG
SPPGGGGGPRSRPTAESTGLEATFPKTTPLAQADPAGGTPPTGWDCLFSDCTASAAG
SSTDOVELATFFPATEAWECELGGLEBRPALCLSPDAPFPRLGWDDELKRPGAQIYM
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KNRTHHELPVLDPVSGVVLHILTHREKLÄKFLHFGSLLDFRSETLRFTQDLGIGFFBDL
AVVLETAPILTALDIFVDRRVAALPVVNECQOVGIYSRFDYIHLAAQQTYNLDMSV
GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDFTQHILGVYSLSDILQ
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HOMO Sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
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Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2290)

Cheung, P. C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding Biochem. J. 346 pt 3, 659-669 (2000)

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/protein_id="AAF73987.1"
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                                                                                                                                                                                                                                                   /tissue_type="skeletal muscle"
1. .2115
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    .2115
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                           /chromosome="2"
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                                                                                                                                                                                                                                                                                                    /gene="PRKAG3"
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Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Coyle, M.D., Dathorne, S.R., David, R., David, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Plags, N., Ford, J., Ester, P., Frantz, P., Garzal, M., Gallsi, A., Gao, J., Garcal, Garzal, M., Gill, R., Gao, J., Garcia, A., Garner, T., Garzal, N., Gill, R., Garzis, R., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, K., Hart, M., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Hallyk, S., Hume, J., Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kartovic, J., Kurschi, A., Landry, M., Leal, B., Lewis, L.C., Lewis, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Ju, Martinez, E., Karlson, E., Kelly, S., Khan, U., Kinde, R., Martin, R., Svatek, A., Rojubokan, L., Paylor, S., Martin, R., Svatek, A., Rojubokan, P., Tanerisa, R., Tanerisa, R., Martin, R., M
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 74 contisg. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 1170 bp in length
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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1029 CGCACTGGACATCTTCGTGGACCGGCGTGTCTGCGCTGCCTGTGGTCAACGAAACTGG 1088
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                                                                                                                                                                                                                                                                                                                                            A mutation in PRKAG3 associated with excess glycogen content in pig
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10 DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Chardon, P.

Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof

Baren; and uses thereof

Batent: WO 0120003-A 1 22-MAR-2001;

INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);

Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)

Location/Qualifiers
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Falm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
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0; Mismatches 20; Indels
                                                                                                                                    /note="unnamed protein product"
/codon_start=1
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                                                                                            /organism="Sus scrofa"
/db_xref="taxon:9823"
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/translation="MSFLEQGESRSWPSRAVTYSSERSHGDGGNKASRWTRQEDVEEG
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KNRTHRLPYLDPGAYTIETERHK IETWRETYLQGCFKFLVSISPUNSLERAYALI
AVVLETAFILTALDIFVDRYSALPVVNETGQVVGLYSRPOYIHLDNNY
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                                                                                                                                                                                                                                            /product="AMP-activated protein kinase gamma subunit"
/protein_id="AAF73988.1"
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/db_xref="taxon:9823"
/chromosome="15"
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		PRKAG3 intron 4 -	Human breast cell	Human foetal liver	Probe #3373 for ge	Human brain expres	Human bone marrow	Probe #3398 for ge	Probe #3507 used t	Probe #3335 used t
SUMMARIES			ID		AAH43683	ABA44706	ABA55162	ABA24907	AAK03423	AAK28874	AAI13465	AA134821	AA 103344
			B	: 6	77	22	22	22	22	22	22	22	22
			Match Length DB I		77/7	378	378	378	378	378	378	378	378
	æ	Query	Match		100.0	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4
			Score	1777	77/1	351	351	351	351	351	351	351	351
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Human genome-deriv	Human AMP-activate	PRKAG3 CDNA, HOMO	dam	an AMPK gamm	AMPK qa	AMPK gamma	wild-type F	Pig PRKAG3 polymor	Pig PRKAG3 polymor	PRKAG3	PRKAG3	scrofa	inmun un	Human colon cancer	Human cDNA differe	Human pancreatic c		Mammalian AMPK-qam	Drosophila melanog	Drosophila melanog	Human breast cell	foetal		exbre	Human bone marrow	Probe #12625 for g	#16674 used	Probe #8345 used t	Human genome-deriv	Disease associated	DNA encoding novel	Human cDNA sequenc		Human cDNA clone (DNA encoding novel	
ABS0340	ABA0848	AAH4368	AAD0329	AAD0332	AAD0329	AAD0331	AAD3645		AAD3645	AAD3645	AAD3646		AAK7330	AAH3520	ABK8432		ABL3975	AAT8592						AAK1618			AA14798		ABS1595	AAX0688	AAS8426	AAH1483	AAC0166	AAH075	AAS84267	ALIGNMENTS
24	22	22	22	22	52	22	24	24	24	24	24	22	22	22	24	21	24	18	23	23	22	22	22	22	22	22	22	22	74	50	23	22	21	22	23	
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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
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/number = "Intron 4"
/note= "3' portion of intron 4"
14..95
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                        /number= "Intron 6"
                                                                                                                                                                                           "Intron 5"
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             AAH43683 standard; DNA; 1722 BP.
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Exon f
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/number= "Exon
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612..736
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                                          CTGTCGATGTCTCTAGGTCCAGATCTATGAGATTGAACAACATAAGATTGAGACCTGGAG
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                                                                                    ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGGTGGAAGGTCCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAH43681-84 represents genomic fragments encoding the buman AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A, in exon 4 variation may be a substitution of a for a C at uncleotide 50; and in exon 10 variation may be a substitution of a T for a C at uncleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
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/note= "5' portion of intron 10"
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Pred. No. 0;
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ص
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/number= "Intron 7"
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                                                                                                                                                                                                                                                                                           "Exon 10"
                                        7
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                                                                                                                          "Exon 8"
                                                                                                                                                                     "Intron
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                                       "Exon
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100.0%;
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737..782
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                           CACCCTCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New spatially-addressable set of single exon nucleic acid probes,
                                                                                                                                                                                                                                                                                                                                   microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                            CGAATGTGGTACCCACCCCCAGGATGAGAGGCTCGGGCTGGA 1722
                                                                                                                                                                                                                                   Human breast cell single exon nucleic acid probe #3401.
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nucleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label cound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for edetermining predisposition and/or prognosing breast disease. Gene determining predisposition and/or prognosing the toxicity of chemical agents on calls. The microarray of this invention presents a far greater capturessity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The resent sequence data for this patent did not form part of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGGCTGGGGGAGGTGAAG 120
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                                                                                                                                                                          relates to a spatially-addressable set of single
for measuring gene expression in sample derived from comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83;
                                                                                                   Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English.
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ID ABA55162 standard; DNA; 378
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample detrived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGGAGGCTGGGGAGGTGAAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human hearts
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                                                                                        Probe #3373 for gene expression analysis in human heart cell sample.
                                                                                                                          Human, gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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conqenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
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0; Mismatches 0; Indels
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03-AUG-2000;
21-SEP-2000;
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                                                                    30-JAN-2001;
                                                                                                                                                                                                   27-SEP-2000;
04-OCT-2000;
                                                                                                         04-FEB-2000;
                                    09-AUG-2001
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                                                                                                                                                                                                                                                                                              Penn SG,
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ABA24907/c
ID ABA249
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Gaps

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Length 378; Indels

us-09-826-581-3.rng

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240

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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
242 GGAGATGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCCTGATCTCTGATAT 183
                                                                   GGAGATGGAGGAGGTGAGGGGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT 180
                                                                                                                                                                              ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG 360
                                                                                                                                                                                                                                                                      ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGCCAGGGTGGAGGAAAGTCCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 3431; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bone marrow expressed single exon probe SEQ ID NO: 3431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR;
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XX
AXX28874,C
XX
AXX28874;
XX
C AAX28874;
XX
DT 06-NOV-2001 (first entry)
XX
Human bone marrow expressed single
XX
Human; bone marrow expressed exon;
XX
Homo sapiens.
XX
Homo sapiens.
XX
Homo sapiens.
XX
PN
O9-AUG-2001; 2001WO-US00668.
XX
PR
A0-JAN-2000; 2000US-010312.
PR
30-JAN-2000; 2000US-0180312.
PR
30-JAN-2000; 2000US-0236359.
PR
A1-SEP-2000; 2000US-03336.
PR
ANDLE-) MOLECULAR DYNAMICS INC.
XX
PP
Human Genome-derived single exon IP
T Hanan genome-derived from gence
C probes which are derived from gence
C probes which are derived from gence
C c probes which may enable the impurence
C c probes which may enable the impurence
C c probes which may enable the impurence
C c such as lymphoma, leukaemia and mix
C c the probes of the invention.
XX
SQUENCE 378 BP; 80 A; 128 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C; 97 C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CCCTCTATGGGACAGCAAGAAGCAGGCTTTGTGGGTGAGGAGGCCTGGGGAGGTGAAG 120
                                                                                     ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGCCCTGTGCCATAGGTGCTAGGG 360
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GGAGTCTGCATGGCCAGCTGGGAGCCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
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                                                                                                          62 ATGACCAGCTGACACTTTCACCTCTGCTACTGCATGCCCTGTG-CATAGGTGCTAGGGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 3414; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe SEQ ID NO: 3414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 20.4%; Score 351; DB 22.
Il Similarity 99.7%; Pred. No. 9e-83;
362; Conservative 0; Mismatches
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ID AAK03423 standard; DNA; 378 BP.
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2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483446/52.
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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Local Similarity ....
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                   gene expression analysis in human cervical cell sample.
                                           CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGGGCTGGGGAGGTGAAG
                                                                                                        121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT
                                                                                                                   242 GGAGATIGGAGGAGGTGAGGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT
                                                                                                                                                                             GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT
                                                                                                                                                                                     1 CCTGGCCCCTCAGATCAAGACGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \ensuremath{\mathsf{Human}} gene expression in human cervical epithelial cells -
20.4%; Score 351; DB 22; Length 378; 99.7%; Pred. No. 9e-83;
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0
         Pred. No. 9e-8
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID No 3398; 487pp; English
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; 2000US-0207456.
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; 2000US-0234687.
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2000GB-0024263.
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                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer; ss.
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                                                                                                                                                                                                                                                                                                                AAI13465 standard;
         Similarity
                                                                                                                                                                                                                                                   361 AGC 363
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26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                     Probe #3398
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The present invention relates to human single exon nucleic acid probes (SENF). The present sequence is one such probe. The SENFS are derived from human Hela cells. The SENPS can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CCCTCTATGGGACAGCAAGAAGCAGCTTTGTGGGTGAGGAGGAGGCTGGGGAGGTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAAG
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                                                                                                                                                                                                                                                                                                         Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                          20.4%; Score 351; DB 22
99.7%; Pred. No. 9e-83;
Live 0; Mismatches
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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2001WO-US00661
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 29-JAN-2001;
                             26-MAY-2000;
30-JUN-2000;
                    04-FEB-2000;
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Best Local S
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                                                                                                                                                                                                                                                                   303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; human; breast disease; breast cancer; development disorder; ss;
inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                           GGAGTCTGCATGGCCAGCTGGGAGCCCTGGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT
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                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #3335 used to measure gene expression in human breast sample.
                                                                                                                                                                                                                               ij
                                                                              Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                          Match 20.4%; Score 351; DB 22; Length 378; Local Similarity 99.7%; Pred. No. 9e-83;
                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                      Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                         analyzing gene expression in human placenta
                                                                                                                                                                                                                              0; Mismatches
                                                                                                          Claim 25; SEQ ID No 3507; 654pp; English.
                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                    (MOLE-) MOLECULAR DYNAMICS INC
                                       Chen W,
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                              Matches 362; Conservative
                                       Hanzel DK,
                                                           WPI; 2001-488897/53.
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                                       Penn SG,
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                                                                                                                                                                                                          Query Match
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polyagenic actiology. The diseases of the breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, prollferative breast disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                 Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 351; DB 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID No 3335; 322pp; English.
                                                                                                                                                                                                                                                                   Chen W, Rank DR;
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ID ABS03407 standard; DNA; 378 BP.
                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
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99.78;
                                                       20000S-0632366.
20000S-0234687.
20000S-0236359.
2000US-0207456.
2000US-0608408.
                                                                                                                                                  2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                in a human breast
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                                                          03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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WO200186003-A2.
                  Homo sapiens.
                          04-FEB-2000;
   19-AUG-2002
                      15-NOV-2001
                                     Penn SG,
ABS03407;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived concleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 sprobes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising the novel set of probes which hybridise at high stringency to a nucleic acid expression in the human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung cample detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, comprising (a) identifying exons from genomic sequence by the method a fragment identical to the predicted exon, the probe is included. In the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method in the above mentioned microarray; assigning exons to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene common pattern of the exons should be assigned to a single gene; a peptide comprising one common nums derived mRNA and for the study of lung diseases cusing human lung derived mRNA and for the study of lung diseases cusing human lung derived mRNA and for the study of lung diseases cusing human lung derived human continum disease (ILD), familial idiopathic publications are used f
                                                                                                                                                                                                                                                                                                                   Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicocytosis; lymphangiolejomyonicosis, Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                  Human, ds, single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                               Human genome-derived single exon probe from lung SEQ ID No 3398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                measure gene expression in human lung samples
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30-JUN-2000; 2000US-0608408.
03-MG-2000; 2000US-053266.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-23559P.
04-OCT-2000; 2000GB-0024263.
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                                                                                     (first entry)
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metasasis; cancer; tumour; haematopoleric disorder; mayeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CCCTCTATGGGACAGCAAGCAGGAGCTTTGTGGGTGAGGAGAGGCTGGGGAGGGTGAAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ATGACCAGCTGACACTTTCACCTCGCTACTGCATGGCCTGTG-CATAGGTGCTAGGG 4
                                                                     haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from RIPO at
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                                        sarcoidosis, pulmonary
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fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA08485 standard; cDNA; 547 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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hes 362; Conservative
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1630 TGCACTGGACATCTTTGTGGACCGGCGTGTCTGCACTGCCTGTGGTCAACGAATGTGG 1689
                                     392 TGCACTGGACATCTTTGTGGACCGGCGTGTGTGTCTGCACTGGCTGTGGTCAATGTGG 451
                                                                                                                                                                                                                                                                                                                                        Human; AMP-activated protein Kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                    1690 TACCCACCCCCAGGATGAGAGGCTCGGGCTGG 1721
                                                                                                         /*tag= c
/label= "T559C"
/note= "Silent variation"
1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= d
/label= "C1037T"
/note= "Causes R340W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= "C230G"
/note= "Causes P71A"
                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "PRKAG3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C "T559C"
                                                                                                                                                                                                         AAH43685 standard; cDNA; 1647 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "C230G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2001; 2001WO-SE00765.
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                                                                                                                                                                                                                                                                            (first entry)
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P-PSDB; QQB47679.
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                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                            PRKAG3 CDNA
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                                                                                                                                                                                                                                          AAH43685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell afferentiation activities; stem cell growth factor activity; hammatopolesis regulatory activity; tissue growth activity; immunomodulatory activity; tissue growth activity; chemotactic or chemokinetic activities; haemostatic, thrombolytic activities; receptor or liquid activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nuclecties of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclensis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth, polypeptides involved with tissue reqeneration and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1510 CCATCCTAACCAGGGTTCCCTGCCCGGCCCTCCTTCCTCCTCACCACTATCCAAGA 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                 Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          );
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Pred. No. 9.6e-42;
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                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 429; 1963pp; English.
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95.3%;
                                                                                                                                                                                       rang YT, Liu C, Drmanac RT;
                                                                 05-FEB-2001; 2001WO-US03800.
                                                                                                  03-FEB-2000; 2000US-0496914
27-APR-2000; 2000US-0560875
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                                                                                                                                                      (HYSE-) HYSEQ INC.
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WO200157188-A2.
                                 09-AUG-2001
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New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon resulting in the amino acid substitution Plat; in exon 4 variation may be a substitution of a G for a C at nucleotide 320, be a substitution of a T for a C at nucleotide 550; and in exon IV variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the full length cDNA encoding the human
Andersson L, Luthman H, Marklund S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1630 TGCACTGGACATCTTTGTGGACCGGCGTGTCTGCCACTGCCTGTGGTCAACGAATGTGG 1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; perkKA3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrare metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Iannuccelli N, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                  Gaps
resulting in the amino acid substitution R340W. There may also be notleotide variation in intron 6. The numbering of these variations is based on the full length CDNA as given, rather than on position 1 of the open reading frame.
                                                                                                                                                                                                           9.8%; Score 168.2; DB 22; Length 1647; 95.6%; Pred. No. 3.3e-34; Live 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                                                                                                                                    Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human Prkag3 protein"
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1..471
/*tag= a
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18-MAY-2000; 2000EP-0401388
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472..1389
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/product= "1
1390..2109
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Matches 173; Conservative
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                                                                                                                                                                                                                                              Similarity
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5'UTR
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in PrkAg3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as suppathy and cardovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing an oprognosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or the dranspring compounds able to modulate AMPK activity. Nucleic acid for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrkAG3 gene, or the a sequence encoding the first cystathione beta synthase (CBS) domain compounds and some therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bunnan AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                 New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCACCCTCCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 2109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.8%; Score 168.2; DB 22; Length Best Local Similarity 95.6%; Pred. No. 3.6e-34; Matches 173; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Human complete Prkag3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
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                                                                                                                  Claim 12; Fig 2; 71pp; English.
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                                                                               myopathy
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AAD03295 standard; cDNA; 1867

AAD03295;

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AAD03295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a cDNA encoding human adenosine monophosphate

(AMP)-activated kinase (AMEK) gamma subunit muscle-specific isoform,

complete PRKAG3. Mutation in Prkag3 results in an altered regulation of

carbobydrate metabolism, particularly in skeletal muscle. PRKAG3 is

useful as therapeutic for treating carbobydrate metabolism disorders such

as diabetes, obesity, and disorders associated with muscle metabolism

sy diabetes, obesity, and disorders associated with muscle metabolism

cutvity, and for restoring a normal AMFK function. PRKAG3 sequence

and its functionally altered mutants are useful for the diagnostic

evaluation, genetic testing and prognosis of a metabolic disorder,

preferably a carbobydrate metabolism disorder. Primers that can detect

a genetic polymorphic marker linked to a sequence encoding PRKAG3. are

useful for detecting a dysfunction of carbobydrate metabolism resulting

from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or are

neconing PRKAG3 and is useful for detecting mutations in a prkag3 gene, or

cencoding PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 2115;
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0; Mismatches 8; Indels
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95.6%; Pred. No. 3.60
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J, Le Roy P,
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                                                                                                                                             .1-SEP-2000; 2000WO-EP09896
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18-MAY-2000; 2000EP-0401388
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Gellin J,
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LOOFT C.
KALM E.
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Tannuccelli N,
                         WO200120003-A2.
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMFK) gamma subunit muscle-specific isoform, prkAg3 brkag3 gene is located in the RN locus of chromosome 15.

Mutation in prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3 or a heterotinaric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid cenceding PRKAG3 is useful for detecting mutations in a PrkAg3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                                                        gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                     Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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/product= "Sus scrofa PRKAG3 protein"
1390..1867
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18-MAY-2000; 2000EP-0401388.
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472..1389
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                                                                                                                                                               chromosome 15; ss.
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Iannuccelli N,
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                                                          0; Gaps
                                    Query Match 8.6%; Score 148; DB 22; Length 1867; Best Local Similarity 88.9%; Pred. No. 7.5e-29; Matches 160; Conservative 0; Mismatches 20; Indels 0
                   Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
of PRKAG3 and is useful in gene therapy.
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Search completed: June 14, 2003, 16:23:08 Job time: 426 secs

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
FORMARD: AGGAAACAGCTATGACCAT
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 572)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TP.
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Fai: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI344527 572 bp mRNA linear 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. BI344527
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AL047390
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COMMENT
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AUTHORS
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BI344527
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10885.491 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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132.4 116.8 88.8 84.6 82.6

Score

Result ş

EST 30-JUL-2001

BM48765 pgm2n.pk0
BM487789 pgm2n.pk0
BM440762 pgm2n.pk0
BM440762 pgm2n.pk0
BM440762 pgm2n.pk0
BM440762 pgm2n.pk0
BM395115 AJ395115
AJ395115 AJ395115
AJ451523 AJ451523
AJ451523 AJ451523
AJ451623 AJ451523
AJ4516335 AK60335
AV608257 AK608257
B1833269 603087144
AA558845 n156b09.s
BE166881 CM4-HT050
BM74390 RKZ-P586A
BE166881 CM4-HT050
BM74390 RKZ-P586A
BM765123 K-EST0046
BM765123 K-EST0046
BM765123 K-EST0046
BM761048 BCA530747
BG705895 602569366
BM782063 K-EST0058
BM764134 K-EST0058
BM764134 R-EST0046
BM78338 K-EST0058
BM764134 R-EST0046
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BM764148 K-EST0058
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BM78338 K-EST0058
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BM76418 R-EST0046
BM78383 K-EST0058
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BM78383 K-EST0058
BM764189 603034761
BM7685947 603386088
BM191312 603037761
BM313138 603038457
BM311288 BM313188 603038457

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Total number

Searched:

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Database

Title: Perfect score:

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1; Gaps

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Direct Submission Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                              1543 CTCCTTCCTCACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGT 1602
                                                                                                                                                                                                                                                                                                                                                                                                                      1603 GGTGCTGGAGACACCCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTC 1662
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGTGCTGGAGACA-NNCCAATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinopterygii, Metazoa Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Adanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 1042)
Roset-Crollins, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Barrot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                      1 CTCCTTCCTCTACCGCACTATCCAAGAITTGGGCATCGGCACATTCCGAGACTTGGCTGT 60
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2 (bases 1 to 1042)

Roset-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,

Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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/note="Genoscope sequence ID : C0BG033CF07LP1-end : T7"
1 282 c 241 g 271 t 6 others
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                                                                                                                                                                                                                                 Score 132.4; DB 9; Length 413;
Pred. No. 5e-21;
0; Mismatches 3; Indels 1.
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/db_xref="taxon:99883"
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GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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                                                                                                                                                                                                                                 Query Match 7.7%;
Best Local Similarity 97.3%;
Matches 144; Conservative
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CNS03KJ0
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1 (bases 1 to 413)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R., Theising, B., WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 CGCACTGGACATCTTCGTGGACCGGCGTGTCTGCGCTGCCTGTGGTCGACGAAACTGG 350
                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalmus, pituitary, and placenta."
190 c 151 g 124 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1280 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA178898 413 bp mRNA linear EST 09-MAR-
298410, L.1 Stratagene muscle 937209 Homo sapiens cDNA clone
IMAGE:611731 5' similar to SW:RAKG_RRT P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ; MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
TTE1: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                         Score 148; DB 13; Length 572;
Pred. No. 1.1e-24;
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/tissue_type="muscle"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 255.
Location/Qualifiers
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0; Mismatches
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/db_xref="GDB:4643570"
                                                                                                                                       /db_xref="taxon:9823"
/clone_lib="MARC_2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                      /organism="Sus scrofa"
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       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG.
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                                                                         Location/Qualifiers
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AA178898.1 GI:1760259
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 88.9
Matches 160; Conservative
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AA178898
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                                                                                                                                                                                                                                    1358 CIGCACATCTTTGTAAG------CCTGGGCCCAGGTGGGAGGAAGGGGAGAACCTGG 1408
                                                                                                                                                                                                                                                                                                                1409 GCAGGTGATCAGAGGCCTGAGGAGTCTTCAGCCCTAGCAGTCGTGGGGAAGAGCTGGGA 1468
                                                                                                                                                                                                                                                                                                                                                                                           1469 GCCCTCTTGAAGCTGCTG-----GAICCCTGATCTCCACCTGGTCCCCATCCTAACC 1520
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                                                                              255
                                                                                                                                                                           316 CICCAGCIGITIGIGAGIGCGACACAICCCCAICAGIGIGACAAAGGCGCCGIIGAAI 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 AGATGTGTGAGAAGCCAAAAGCCCGCTTTCATGAAGCAGACCCTGAGGGAGCTGGGCATTG 555
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       556 GTACATACCGGGACATIGCTTICATTCACCCCGACACGCCCATCATCAAAGCGCTCAACA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. Medaka EST Project in Takeda's lab Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 TGCAGCCTGTTTGATGCTGTACACGCTCATCAAAAACAAAATTCACCGCCTGCTTGTC
                                          17; Gaps
    DB 17; Length 1042;
                  Pred. No. 3.9e-17;
0; Mismatches 192; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="fry stage 40"

    591
    /organism="Oryzias latipes"

      Score 116.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MF01FSA040J15"
/clone_lib="MF01FSA cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:8090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ495978.1 GI:22147904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="d-rR
tch 6.8%;
al Similarity 56.3%;
269; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Japanese medaka.
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      Query Match
                      Best Local
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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JOURNAL
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KEYWORDS
SOURCE
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BJ495978
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BJ504184 728 bp mRNA linear EST 08-AUG-2002 BJ504184 MF01FSA CDNA Oryzias latipes cDNA clone MF01FSA006A14 3',
                                                                                                                               1228 CTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCG 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1241 AGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGCCTGCTTCTT 1300
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                                                                                                                                                   Orgrias latipes
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Orgziinae; Orgzias.

1 (bases 1 to 728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 TCTGCCCGTCATCGACCCGACGTCAGGAAACGTCCTCCACATCACCTCACACAGGCGT
                                                                                                 Gaps
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                                                         Length 591;
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   1 others
                                                                                             Indels
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National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                    1348 GCICAAGTICCIGCACAICTIIGIAAGCCIGGGCCC 1383
                                                     Score 88.8; DB 13;
Pred. No. 1.5e-10;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                          male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.9%; Score 84.6; DB 13;
Best Local Similarity 77.9%; Pred. No. 1.6e-09;
Matches 102; Conservative 0; Mismatches 29;
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/dev_stage="fry stage 40"
161 c 174 g 210 t
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 133
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/clone_lib="MF01FSA cDNA"
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   þŋ
130
                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BJ504184
BJ504184.1 GI:22156146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="d-rR
                                                       5.2%;
177 c
                                                     Query Match
Best Local Similarity 73.18
Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 CAACTGTTTAT 226
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150
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BASE COUNT
ORIGIN
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us-09-826-581-3.rst

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1599 CIGIGGIGCIGGAGACAGCACCCAICCIGACIGCACIGGACAICITIGIGGACCGGCGIG 1658
                                                                                                                                                                                                                                                                           BJ072114 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL096j16 5', mRNA sequence.
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                                                                Xenopodinae; Xenopus.
1 (bases 1 to 633)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="stage 25"
/note="vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oliqo-dr primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute).

(Wellcome/CRC Institute).
306 AGCCGGAATTCATGTCTAAGTCTCTCCCAAGAGCTGCAGATTGGCACCTATGCCAATATTG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIBB Mochii normalized Xenopus tailbud
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Conteat: Tadabasu Shin-1
Contear For Genetic Resource Information
National Institute of Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL096j16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed genes in X. laevis embryo
                                                                                                                            1659 IGTCTGCACTGCCTGTGGTCAACGA 1683
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                                                                                                                                                                  426 TCTCCGCCTTACCTGTAGTGGATGA 450
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                             BJ072114
BJ072114.1 GI:17502303
                                                                                                                                                                                                                                                                                                                                                                                                       African clawed frog.
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Best Local $
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ORIGIN
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COMMENT
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SOURCE
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BM488662
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                                                                                BG919314 100-2001 933 bp mRNA linear EST 05-JUN-2001 602817782F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4946661 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGGGCCTGAGGAGTCTTCAGCCCTAGCAGTCGTGGGGAAGAGCTGGGAGCCCTCTTGA 1478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally, Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH" 292 c 238 9 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 AGAGCGGTTGGGCACAGAGGAGCGGTGTTGGTGATGATGATGATGAGCGTAGCACCTCCATG 246
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                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 GTCCGGTTGATGCTCTTCTTCATTAATTCGAAATAAGATCCACAGGCTCCCAGTTATCG
                                                                                                                                                                                                                                                                                          1 (bases 1 to 933)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"

Strain="FVB/N"

/db_xref="texton:10090"

/clone="IMAGE:4946661"

/clone=lib="NCI_CGAP_Mam6"

/sex="female, virgin"

/tissue_type="infiltrating ductal carcinoma"

/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.8%; Score 82.6; DB 13; Length 933; 52.1%; Pred. No. 5.5e-09; ative 0; Mismatches 209; Indels 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .933
                                                                                                                                                                  BG919314.1 GI:14299790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232; Conservative
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                                                                                                                          mRNA sequence.
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/strain="Commercial broiler strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
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BG713637.1 GI:14007587
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Best Local Similarity 69.4%
Matches 109; Conservative
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                                                                                                                        Gallus gallus
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/lab_nost="E. coll EMDHIOS
/lab_nost="E. coll EMDHIOS
/note="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue (embryonic
muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
plate 33.3% of the final RNA pool). Single pass sequencing
from 5'-end"
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pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate Chicken library (pgm2n) Gallus gallus cDNA clone pgm2n.pk005.j24 5' similar to gb|AAC52580.1 (U4413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus], mRNA sequence.
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Strains 90 & 21"
/db_xrefe="taxon:901"
/clone="pgm2n.pk008.g21"
/clone="pgm2n.pk008.g21"
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1 (bases 1 to 536)

1 (bases 1 to 536)

ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate CDNA library, USDA/IFAFS Animal Genome
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Pred. No. 6.7e-09;
0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cogburn@udel.edu, www.chickest.udel.edu
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1348 GCTCAAGTTCCTGCACATCTTTGTAAGCCTGGGCCCA 1384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Larry A. Cogburn
University of Delaware
Universed Hall, Newark, DE 19717, USA
Tel: 302-831-2822
Fax: 302-831-2822
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/organism="Gallus gallus"
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BM488662.1 GI:18609593
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                                                                                                                           , mRNA sequence.
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Gallus gallus
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/dev_stage="Breast, leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,1)lab_host="E. coli EmDH10B"
/lab_host="Re. coli EmDH10B"
/note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth flom 5'-end"
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                                                                                                           pg110.pk008.c13 Normalized Liver Library Gallus gallus connactore pg110.pk008.c13 5' similar to gi|4506061 ref|NP 003724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gemma-1 [Homo sapiens] gi|12737489 ref|XP_006778.2| protein kinase, AMP-activated, gamca in kinase, AMP-a
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/clone=lb="kormalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
/tissue_type="Breast muscle, leg muscle and epiphyseal
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Cogburn, L.A. and Monsonego-Ornan, E.
ESTS from Normalized Chicken Breast Wuscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFARS Animal Genome
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Pred. No. 1.7e-08;
0; Mismatches 48; Indels 0
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Location/Qualifiers
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/clone_lib="Normalized Chicken Reproductive Tract cDNA Library (pgrln)"
/sex="Wale and Female" /tissue_type="Testis, ovary and oviduct" /tissue_type="Testis, ovary and oviduct" /dev_stage="Various stages;embryonic, post-hatch, immature and sexually-mature" /lab_host="E. coli EMDHIOB" /note="Vector: pcMvSPORT6; Library made from three total RNA pools from each tissue (testis 25%, ovary 25%, and oviduct 50% of final RNA pool); Single pass sequencing from 5'-end" a 222 c 160 g 128 t
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Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal BSTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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0
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                                                                 /strain="Commercial broller and layer"
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/clone_lib="dkfz426"
/tissue_ype="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dew_stage="2-3 weeks old"
127 c 155 g 137 t
                                          /organism="Gallus gallus"
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                                                                                     /db_xref="taxon:9031"
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BM440762
BM440762
BM5002.19 Normalized Chicken Reproductive Tract CDNB Library (pgrln) Gallus gallus CDNa clone pgrln.pk002.19 5' similar to gil4506061 ref|NP_002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subbnit; AMP gamma 1; Protein kinase, AMP-activated, noncatalytic, gemma 1 | Homo sapiens| gil12737489 ref|xP_006778.2| protein kinase, AMP-activated, gamma 1, mRNA sequence.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Patabaninae; Gallus.

1 (bases 1 to 636)

Burnside,J., Morgan,R.W. and Cogburn,L.A.
Chicken ESTs from a normalized liver library
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Cogburn, L.A. and Nys, Y.
Cost from Normalized Chicken Reproductive Tract cDNA library-
University of Delware and INRA, Tours-Poultry Unit Project
Unpublished (2002)
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/db_refe^*rexon:901"
/clone="polln.pk008.cd3"
/clone_lib="Normalized Liver Library"
/sex="Wale and Female"
/tissue_type="liver"
/lab_host="E.coli EMDH108"
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                                                                                                                                                                                                                                                                                                 Email: joan@UDel.Edu, www.chickest.udel.edu.
Location/Qualifiers
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                                                                                                                                                                                        Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
TEA: 302 831-1345
Fax: 302-831-3411
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215 c 167 g 119 t
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Tel: 302-831-1335
Fax: 302-831-2822
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University of Delaware
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                                                                                                                                                                        Contact: Joan Burnside
                                                                                                                                                  Unpublished (2001)
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AV603335 576 bp mRNA linear EST 27-NOV-2001
AV603335 Bos taurus kidney fetus Bos taurus cDNA clone ELKI015F02
5', mRNA sequence.
AV603335 GI:9725661
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Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11111 | 11111 | 11111 | 1111 | 1111 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 
                                                                                                                                                                                   1 (bases 1 to 758)
Abdrakhmanov.I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae<u>;</u> Bos.
                                             chicken.
Gallus gallus
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                   Cellular Immunology
Beinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks 01d"
238 c 186 g 166 t
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Best Local Similarity 68.8%; Pred. No. 4.5e-08;
Matches 108; Conservative 0; Mismatches 49;
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Animal Genetics Division
Shirakawa Institute of Animal Genetics

    758
    /organism="Gallus gallus"

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/clone="25f16r1"
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Contact: Buerstedde JM
GI:7127728
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AJ396118.1
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (bases 1 to 687)
Buerstedde, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ451523 687 bp mRNA linear EST 22-APR-
AJ451523 rikenl Gallus gallus cDNA clone 29a6r1, mRNA sequence.
AJ451523 1 GI:20261619
                                                                                                                                                                  0; Gaps
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                            Length 649;
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                      Score 80.2; DB 9;
Pred. No. 1.8e-08;
0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
228 c 191 q 125 t
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/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="29a6r1"

/clone_lib="riken]"
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Unpublished (2002)
Contact: Buerstedde JM
                            4.78;
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                            Query Match
Best Local Similarity 69.44
Matches 109; Conservative
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us-09-826-581-3.rst

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Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5755
Email: kazusugiecoca.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
1. 576
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

g	63, Appl		14, Appl	14, Appl	14, Appl		17, Appl	2, Appli	1, Appli	7, Appli	14, Appl	8, Appli				8, Appli					161, App		16, Appl	3, Appli	3, Appli	3, Appli	3, Appli
Description	Seguence	Sednence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-09-101-146-63	US-08-232-463-14	US-08-878-989-14	US-09-272-796-14	US-08-232-463-14	US-09-007-005-17	US-09-244-796-17	US-08-658-136-2	US-08-658-136-1	US-09-165-264-7	US-09-165-264-14	US-09-165-264-8	US-09-165-264-13	US-09-165-264-11	-959-94	US-07-959-943-8	8-56	US-09-165-264-12	US-09-215-966-21	7.	US-09-641-638-161	-41	US-09-128-155-16	-39	US-08-470-950-3	US-08-467-781-3	US-08-195-487-3
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Score	68.8	67.6	63.8	63.8	61	39.4	39.4	39	39	38.6	38.6	37.4	36.2	36	36	36	35.8	35.4	35.2	34.6	34.6	34.4	4	34.2	34.2	34.2	34.2
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	Ulication US/0911 Arrion: Medical Research Medical Research Medical Research Medical Research Medical Research Medical Research DIBMESS: 64 Jane Massey Li. E. Main Street Lton DISKETE, 3.: DISKETE, 3.: IBM PC CATION DAYA: MORDPERECT 6.0 CATION DAYA: I. October 7, 11 TION DAYA: I. October 7, 11 TION DAYA: MANMER: PN745; I. October 7, 11 TION DAYA: MANMER: PN745; I. October 7, 11 TION DAYA: MASSEY LICATA NAUMBER: PN745; MAS	ty serv	CTGTTTGAAGCTGTCT
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	1-63 FOR AND IN TABLE TO THE PART TO THE P	imi.	CAGC(
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ммм	T 1 -101-146- uence 63- uence 63- uence 63- NERAL INI APPLICAN APPLICAN TITLE CAN TITL	Mat Loca	17
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                                                                                           1146 AAGGGAGCCTTGGTGCCCTGCCTTTTTAGGGGCCTGGGATGGAGGTTGTCTCCC 1205
                                                                                                                                                               1206 TAGGCTGCCCCGAGGCTCACTGCTCCCATCTGCAGCCTGTTTGAAGCTGTCTACACCC 1265
                                                                                                                                                                                                                                        1266 TCATCAAGAACCGGATCCATCGCCTGCTGTTCTTGACCC 1305
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KIRASES
THERE OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DAPS:
APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 14, Application US/08878989
; Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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; CLONE: 1452972
US-08-878-989-14
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IMMEDIATE SOURCE:
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US-08-878-989-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1026 TCTCTCCTAATGATAGGTGGGTGTCTCTCCTCATTCACCTGAGCCTCCTCCTCCTCCACAGT 1085
                                                               906 CTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAAGGTGACCGGCTCCCCTGGCC 965
501 CAGCTTGTTTGATGCTGTCTTTCATTAATTCGCAACAAGATCCACAGGCTGCCAGTTAT 560
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MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/M9-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
DAPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.9%; Score 67.6; DB 1;
Best Local Similarity 6.2%; Pred. No. 1.9e-08;
Matches 25; Conservative 223; Mismatches 152;
                                                                                                                                                                                                                                                Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: PALKNER, F. G.
APLICANT: PALKNER, F. G.
APLICANT: RALKNER, F. G.
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                1360 GCACATCTTTGTAAGCCTGGGCCC 1383
                                                                                                                                                    621 CAAATTGTTTATCACTGAGTTCCC 644
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (703)836-9300
(703)683-4109
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ADDRESSEE: Foley & L
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ZIP: 22313-0299
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP 22313-029

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATEMENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F.
APPLICANT: SCHETELINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149.
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE: CHARACTERISTICS:
LENGTH: 7218 base pairs
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(703)683-4109
                                                                                                                                                                          1361 CACATCTTTGT 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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US-08-232-463-14
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    Length 1435;
Query Match 3.7%; Score 63.8; DB 2; Length 1 Best Local Similarity 67.9%; Pred. No. 1e-07; Matches 89; Conservative 0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09272796
Patent No. 6207148
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Golj, Surya K.
APPLICANT: Shah, Purya K.
TITLE OF INVENTION: KINASES
TITLE OF INVENTION: KINASES
MUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARES: RealFISED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0321 US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BILLINGS, LUCY J J
RECISTRATION NUMBER: 36,749
REFERENCE/COCKET NUMBER: PF-
FELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                1361 CACATCTTTGT 1371
                                                                                                                                                                                                                                                      629 CAGCTTTTAT 639
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TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: PENITUT01
CLONE: 1452972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
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FEATURE:
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187 GTGGGGAGAGGAACCCGGAAAGGGGCTGTTGGTGATGGTGGGGCCAGGGCTTAAGGTGGAG 846
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                             731 CTCTAGGTCCAGATCTATGAGATTGAACAAAAAAGATTGAGACCTGGAGGGGTGAGTGG 790
                                                                                        791 GGAGAGGAACCCGGAAAGGGGCCTGTTGGTGATGGTGGGCCCAGGGCTTAAAGGTGGAGGATG 850
                                                                                                                                                     851 GGCAGTGGGGATGTCCTGGAGTGAACAGGGGAGGGACAATAGGAGCCTCGGGTGCCTGAC 910
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                                                                                                                                                                                                                                    1102 RARRARRARRARRARRARRARRARRARRARRARRARARGCAGCCCCCCGGACCTG 1046
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                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09007005B Patent No. 6258558
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LOCATION: (1)...(289)

/ OTHER INFORMATION: n = A,T,C or

US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                              -09-007-005-17
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RESULT 7 US-09-244-796-17

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787 GIGGGGAGAGGAACCCGGAAAGGGGCTGITGGIGATGGTGGGGGCCAGGGCTTAAGGIGGAG 846
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                                    Partent No. 288344.

STREAL INFORMATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: SZOSTAK, Jack W.
APPLICANT: SZOSTAK, Jack W.
APPLICANT: ROBERTE, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVERTION: SELECTION OF PROTEINS USING RNA-PROPEIN
TITLE OF INVERTION: PISSONS;
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: 05/09/244,796
CURRENT APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1999-02-05
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-66
EARLIER FILING DATE: 1997-01-67
EARLIER FILING DATE: 1997-01-67
EARLIER FILING DATE: 1997-01-67
EARLIER FILING DATE: 1997-01-67
EARLIER FILING DATE: 1997-01-67
EARLIER FILING DATE: 1988-01-14
SANDHARE: FASTEGG FOR WINGOWS VERSION 4.0
SOFTWARE: FASTEGG FOR WINGOWS VERSION 4.0
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APPLICANT: CANONSK, TIMOTHY D
APPLICANT: GERAINO, GREGORY
APPLICANT: GERAINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
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STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
Sequence 17, Application US/09244796 Patent No. 6281344
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: LOCATION: (1)...(289)

: OTHER INFORMATION: n = A,T,C or G

US-09-244-796-17
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APPLICANT: KLINGER, KATHERINE APPLICANT: LANDES, GREGORY MAPPLICANT: BURN, TIMOTHY C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA ORGANISM: Artificial Sequence
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COUNTRY: USA
ZIP: 01701
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCORACTION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY W
APPLICANT: BURN, TIMOTHY C
APPLICANT: BONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GREMINO, GREGORY
APPLICANT: GINNENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/658,136
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CNORENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.3%; Score 39; DB :
Best Local Similarity 52.1%; Pred. No. 2;
Matches 87; Conservative 0; Mismatches
                                                                                                                                                                                                                       GEN4-17.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSES: GENEYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
                                                                                                                                        CLASSIFICATION: 435
ATORNEY/ACENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFRENCE/DOCKET NUMBER: GEN4-
TELECHAUNICATION INFORMATION:
TELEPHANE: 508-872-8410
TELEPHAX: 508-872-8415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08658136
Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 53526 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 01701
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777 GGAGGGGTGAGTGGGGAAGGGAACCCGGAAAGGGGCTGTTGGTGGTGGTGGCCCAGGGCT 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.2%; Score 38.6; DB 4; Length 320; Best Local Similarity 50.3%; Pred. No. 0.33; Matches 95; Conservative 0; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09165264
| Batent No. 6197510
| GENERAL INFORMATION:
| TITLE OF INVENTION: Multi-Loci Genomic Analysis
| TITLE OF INVENTION: Multi-Loci Genomic Analysis
| CURRENT APPLICATION NUMBER: US/09/165,264
| CURRENT PILING DATE: 1998-10-01
| NUMBER OF SEQ ID NOS: 14
| SEQ ID NO 7
| LENGTH: 320
                                                 GEN4-17.8
                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-840
TELEPHONE: 508-872-8415
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN
                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuralayah
APPLICANT: Vinayagamoorthy, Thuralayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44/47
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT APPLICATION NUMBER: US/09/165,264
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Vinayagamcorthy, Thuraiayah TITLE OF INVENTON: Milti-Loci Genomic Analysis CURRENT OF 14747 CURRENT APPLICATION NUMBER: US/09/165,264 CURRENT FILING DAMPE: 1998-10-01 SOFTHARRE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
                                                                                                                                                                                                          Sequence 13, Application US/09165264
Patent No. 6197510
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Best Local Similarity
Matches 87; Conserv
                                                                            CCC 929
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SEQ ID NO 13
LENGTH: 320
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LENGTH: 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-8
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.2%; Score 38.6; DB 4; Length 320; Best Local Similarity 48.8%; Pred. No. 0.33; Matches 104; Conservative 0; Mismatches 109; Indels
                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44/47
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 198-10-01
NUMBER OF SOC 10 NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 GCGGGGGGGGGTGTGCATGTACACAGAGA 320
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                            // Sequence 14, Application US/09165264
// Patent No. 6197510
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; Sequence 8, Application US/09165264
; Patent No. 6197510
                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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            US-09-165-264-14
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                                                                                                                                                                                                                                              LENGTH: 320
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LENGIH: 31
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                                                                                                                                                                                                                                                                777 GGAGGGGTGAGTGGGGAGAGAACCCGGAAAGGGGCTGTTGGTGATGGTGGGCCCAGGGCT 836
                                                                                                                                                                                    897 CTCGGGTGCCTGACGGAAGGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGTGACCG 953
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-13
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0
                                                                Length 320;
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                                                            Query Match 2.1%; Score 36.2; DB 4; Length 35 Best Local Similarity 50.3%; Pred. No. 1.4; Matches 89; Conservative 0; Mismatches 88; Indels
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837 TAAGGTGGAGGATGGGCAGTGGGGATGTCCTGGAGTGAACAGGGGAGGAGAATAGGAGC 896
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                             0; Gaps
                                                                    897 CICGGGTGCCTGACGGAAGGAAGCTGCCTGGGACTGCAAGGTGAGGCAGGT 948
                                                                                             Score 36; DB 1; Length 2278;
Pred. No. 3.6;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,943
FTI.ING DATE: 19921014
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             731 CTCTAGGTCCAGATCTATGAGATTGAACAACATAAG 766
                                                                                                                                                                                                                                                  APPLICANT: Blakely, Randy D.
APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Caron, Marc G.
ITLE OF INVENTION: Serotonin Transporter CDNA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31,665
ER: 5405.38a
                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Post Office Drawer 31107
CITY: Raleigh
STATE: No. 5418162th Carolina
COUNTRY: U.S.A.
ZIP: 27622
                                                                                                                                                                                               Sequence 6, Application US/07959943
Patent No. 5418162
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2278 base pairs
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51.9%;
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Best Local Similarity 51.9%
Matches 81, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: CDNA
POSITION IN GENOME:
UNITS: 2278 basepairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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48..1868
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: and
ADDRESSEE: Glbson
                                                                                                                                                                               us-07-959-943-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-07-959-943-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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1823 ITCAGGAGTGATACTITITAATAATGCGCTCCTTAAG 1788
g
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Search completed: June 14, 2003, 16:24:53 Job time: 93 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 14, 2003, 16:16:05; Search time 288 Seconds (without alignments) 8658.197 Million cell updates/sec Run on:

US-09-826-581-3

1722 1 cctggcccctcagatcaaga......gatgagaggctcgggctgga 1722 Perfect score: Sequence:

IDENTITY_NUC Scoring table:

Gapop 10.0 , Gapext 1.0

1029858 segs, 724030393 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1. /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2. /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/NE07_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
Published_Applications_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

## SUMMARIES

Description	Sequence 3, Appli	Sequence 3373, Ap	Sequence 5, Appli	Sequence 2, Appli	~4	럿	Sequence 29, Appl	Sequence 112, App	Sequence 346, App	Sequence 346, App	18,	Sequence 346, App	346	Sequence 394, App	Sequence 47, Appl	Sequence 8, Appli	Sequence 15, Appl	Sequence 9, Appli	Sequence 2, Appli
B (D	10 US-09-826-581-3	10 US-09-864-761-3373	10 US-09-826-581-5	10 US-09-925-297-2	9 US-10-108-605-70	10 US-09-864-761-20146	10 US-09-804-682-29	9 US-10-123-155-112	9 US-10-184-644-346	9 US-10-184-634-346	9 US-09-984-271-18	9 US-10-184-644-346	9 US-10-184-634-346	9 US-10-123-155-394	9 US-10-032-393-47	9 US-10-032-393-8	10 US-09-827-998-15	10 US-09-827-998-9	10 US-09-827-998-2
* Query Match Length DB	1722		1647	1691	11527	92	1064	910	671	671	1512				. ,		4158		5376
% Query Match	100.0	20.4	8.6	4.1	3.9	3.8	2.6	2.5	2.5	2.5	2.4	2.4	2.4	2.3	2.3	2.3	2	2.3	2.3
Score	1722	351	168.2	70.4	68	65	44.2	43	42.4	42.4	40.8	40.6	40.6	40.2	40	40	39.8	39.8	39.8
Result No.	ч	0	æ	4	ß	9	c 2	∞	<u>ი</u>	c 10	c 11	12	13	c 14	15	16	17	18	19

Sequence 8, Appli	Sequence 1, Appl1	Sequence 3, Appli		Sequence 574, App	Sequence 574, App	Sequence 8585, Ap	Sequence 49, Appl	Sequence 49, Appl	Sequence 348, App	Sequence 348, App	Sequence 10, Appl	Sequence 5509, Ap	Sequence 22281. A	Sequence 2835. Ap	Sequence 20, Appl	Sequence 6, Appli	Sequence 202, App	Sequence 202, App		Ap	Sequence 28, Appl	Sequence 312, App	312,	
US-09-827-998-8	US-US-82/-996-1 US-10-123-155-10	US-09-820-004-3	US-09-904-968A-1	US-10-184-644-574	US-10-184-634-574	US-10-198-846-8585	US-10-125-540-49	US-09-764-870-49	US-10-184-644-348	US-10-184-634-348	US-10-123-155-10	US-09-864-761-5509	US-09-864-761-22281	US-09-764-877-2835	US-09-771-208-20	US-10-026-188-6	US-10-184-644-202	US-10-184-634-202	US-09-804-682-33	US-10-017-724-3	US-10-123-155-28	US-10-184-644-312	US-10-184-634-312	US-09-804-682-20
10	2 6	10	σ	0	σ	σ	σ	10	6	6	σ	10	10	10	S	6	6	σ	10	6	σ	σ	6	10
5461	594	40090	53522	882	882	931	2531	2531	777	777	594	463	531	21423	659158	155074	440	440	1065	98829	765	802	802	987
2.3	. c.	2.3	2.3	2.3	2.3	2.5	2.5	2.5	2.5	2.3	2.5	2.5	2.5	2.5	2.5	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1
39.8	39.2	39.2	39	38.8	38.8	38.4	38.2	38.2	37.6	37.6	37.4	37.2	37.2	37.2	37.2	37	36.8	36.8	36.8	36.6	36.4	36.4	36.4	36.4
20	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45
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Sequence 3, Application US/09826581
Factor No. US20020142310A1
FAPPLICANT: Andersson, Leif
APPLICANT: Markind, Stefan
FILLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 S
FILLE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US/0195,665
FRIOR APPLICATION NUMBER: US/0195,665
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
STEWNOR APPLICATION NO. 3
SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGAIGGAGGAGGIGAGGGGGAGAICTIGIACGGIIGITCIGGGGGCTGAICTCTGGATAI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCCAACGGTGTGCGGGCAGC 60
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1722; Best Local Similarity 100.0%; Pred. No. 0; Matches 1722; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                        TYPE: DNA; ORGANISM: Homo sapiens
US-09-826-581-3
RESULT 1
US-09-826-581-3
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1009 CCIGCACATCITIGGTICCCCGCCCCGCCCTCCTCCTCCTCCACCGCACTATCCAAGA 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1570 TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1630 TGCACTGGACATCTTTGTGGACCGGCGTGTCTGCACTGCCTGTGGTCAACGAATGTGG 1689
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                                                                                                                                                                                                                 Score 168.2; DB 10; Length 1647;
Pred. No. 2.7e-39;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 70.4; DB 10
Pred. No. 1.3e-10;
0; Mismatches 46
            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COTHER INFORMATION: n equals a,t,g, or c US-09-925-297-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 GCACATCTTTGTAAGCCTGGGCCC 1383
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Best Local Similarity 68.1%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                 Query Match
Best Local Similarity 95.65
Matches 173; Conservative
                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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                                                 LENGTH: 1647
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US-09-925-297-2
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FILE REFERENCE: 11145-007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGCGAGGGCCAGGGTGGAGGAAAGTCCATCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 AIGACCAGCIGACACCITICACCICCGCIACTGCAIGGCCCIGIGCCAIAGGIGCIAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CCCTCTATGGGACAGCAAGAAGCAGTTTGTGGGTGAGGAGAGGCTGGGGGAGGTGAAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.4%; Score 351; DB 10; Length 378; 99.7%; Pred. No. 4.6e-93; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                       N: MAP TO AC009974.3

N: EXPRESSED IN HELA, SIGNAL = 4

N: EXPRESSED IN HEART, SIGNAL = 4.1

N: EXPRESSED IN PLACENTA, SIGNAL = 3.9

N: EXPRESSED IN ABULIO, SIGNAL = 3.9

N: EXPRESSED IN BR144, SIGNAL = 3.9

N: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3

N: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3

N: EXPRESSED IN PORM MARROW, SIGNAL = 4.8

N: EXPRESSED IN BUNC, SIGNAL = 4.8

N: EXPRESSED IN BRAIN, SIGNAL = 4.4
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-6-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NOS: 49117
SEQ ID NO 3373
LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/826,581 CURRENT FILING DATE: 2001-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09826581
Patent No. US20020142310A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Luthman, L. Holger APPLICANT: Marklund, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.79 Matches 362; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Andersson, Leif
                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                       CTHER INFORMATION: MACTHER INFORMATION: EX OTHER INFORMATION: EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-826-581-5
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                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGGGGCCAACGGTGTGCGGGGCAGC 60
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Patent No. US20020106765A1
GENERAL INFORMATION:
APPLICANT: Kinders, Robert
APPLICANT: Corey, Michael J.
TITLE OF INVENTION: BAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR SCREENING FOR OR
TITLE OF INVENTION: ENCODING THE SAME
FILE REFERENCE: 130001.406
CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT FILING DATE: 2001.03-12
NUMBER OF SEQ ID NOS: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4

OTHER INFORMATION: EXPRESSED IN HERA, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN HEALING, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HELLIOD, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HELLIOD, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BULLIVER, SIGNAL = 5.3

OTHER INFORMATION: EXPRESSED IN BULLIVER, SIGNAL = 5.3

OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4

OTHER INFORMATION: EXTREMENT BRAIN, SIGNAL = 4.4
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APLICATION NUMBER: PCT/US01/00665
PRIOR APLICATION NUMBER: PCT/US01/00665
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-06-31
PRIOR PILING DATE: 2000-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 65; Conservative
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ORGANISM: Homo sapiens
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5 CCCTC 1
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Sequence 20146, Application US/09864761

Sequence 20146, Application US/09864761

Sequence 20146, Application US/09864761

Sexement No. US2002004876341

Sexement No. US2002004876341

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: BUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: BUMAN GENOME-DERIVED SINGLE EXON MALYSIS BY MICROARRY FILE REPRENUE: 2001-05-23

CURRENT APPLICATION NUMBER: US 60/20/312

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-27

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APPLICANT: Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Ramdar, Kimm
APPLICANT: Ramdar, Kimm
APPLICANT: Ramdar, Kimm
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT APPLICATION NUMBER: US 09/761,142
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 361
SOSTWARE: PALEALING VET. 2.1
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                 Sequence 70, Application US/10108605
Patent No. US20020160934A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORCANISM: Drosophila melanogaster US-10-108-605-70
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APPLICANT: Broadus, Julie
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US-09-864-761-20146/c
                                                          RESULT 5
JS-10-108-605-70
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Query Match 2.5%
Best Local Similarity 13.2%
Matches 48; Conservative
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Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Homo Sapien
US-10-184-644-346
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us-10-123-155-112
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                                                                                        209, 214, 231, 232, 292, 297, 306, 319, 363, 372, 376, 378, 459, 468, 470
                                                                                                                                                                                                LOCATION: 485, 487, 488, 494, 496, 499, 511, 524, 527, 552, 557, 562, 100CATION: 583, 600, 611, 613, 623, 624, 652, 654, 664, 681, 687, 691, 691, 100CATION: 694, 701, 713, 713, 716, 725, 731, 734, 735, 739, 743, 100CATION: 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852, 743, 100CATION: 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852, 891, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948, 100CATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948, 100CATION: 1043, 1047, 1049, 1051, 1054, 1056, 1011, 1018, 0THER INFORMATION: n = A,T,C or 6
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.6%; Score 44.2; DB 10; Length 1064; Best Local Similarity 47.8%; Pred. No. 0.0058; Matches 85; Conservative 0; Mismatches 93; Indels 0;
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CURRENT FILING DATE: 2002-04-15
                                                                                        5, 6, 16, 21, 24, 25, 33, 39, 325, 235, 237, 238, 244, 245, 246, 321, 435, 430, 437, 454, 455,
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Publication No. US20030068794A1
GENERAL INFORMATION:
                                                                                                                                                                 OTHER INFORMATION: n = A, T, C or G
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Tumas, Daniel
Watanabe, Colin K
Wood, William
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 112
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                                                                                                                                                                                     misc_feature
                                    ORGANISM: Homo sapiens
                                                                           misc_feature
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TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: n
US-09-804-682-29
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LOCATION:
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APPLICANT:
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984 CAGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCATCTCTCTAATGATAGGT 1043
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                                                                                                                                                              191 TGGCTTCAGGCCAAGCCCAGGCCAGGGCCAGGGTGGAGGAAAGTCCATCCGGAGTCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFRENCE: P3430R1C27.

CURRENT APPLICATION NUMBER: US/10/184,644

CURRENT FILING DATE: 2002-06-28
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2.5%; Score 43; DB 9; Length 910;
13.2%; Pred. No. 0.013;
Live 93; Mismatches 224; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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APPLICANT: Baker, Kevin P.
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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1224 ACTGCTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCC 1283
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                                              275 Y..MABSBHSHSSSSSSSSSTSYTKTB...MTCHSHTMSHSHSTS.TMMMMYCC..CYY 216
                                                                                                                         386 AAGAGCCCCACTTCTCAGGCCTGGGGGGCTGCCCCACTGTCCTGTTCCCACAGTCCCCAC 445
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49.1%; Pred. No. 0.062;
tive 1; Mismatches 108; Indels 0
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APPLICANT TROSEN et al.

TITLE OF INVERTION: 71 Human Secreted Proteins
FILE REFERENCE: P10309D1

CURRENT APPLICATION UNBER: U5/09/984,271

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: 09/482,273

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 1990-07-14

PRIOR APPLICATION NUMBER: 60/092,921

PRIOR APPLICATION NUMBER: 60/092,921

PRIOR APPLICATION NUMBER: 60/092,925

PRIOR FILING DATE: 1998-07-15

PRIOR PILING DATE: 1998-07-15
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-984-271-18
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; Publication No. US20030040088A1
                                                                                                                                                                                            1284 ATCGCCTGCCTGTTCTT 1300
                                                                                                                                                                                                                             155 .CSNHSSMHSHSHS.KY 139
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Best Local Similarity
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OTHER INFORMATION:
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                                                                     1044 GGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCCACAGTCCCCTTCCCCAGTCCCAC 1103
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                                                                                                                                                                                                 335 ..YYYYT...YYYT.HYYMW.S.YHB.HSHSHSSSSS..Y..M.MYCY.M...M.T.MYC 276
                                                                                                                                                                                                                                                                                                   275 Y. MAGSBHSHSSSSSSSSSSTSTYKTB...MTCHSHTMSHSHSTS.TMAMMYCC..CYY 216
                                                                                                                                                                                                                                                                                                                                                                                             215 .TYBTTMM..A.H.HSAM.S.SSS.SN...S.SBST.H.HSSTWYTMSBSKM.T.AMYM 156
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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9 HASYSAPPPVSSSDSEAPEANPADGSDADEDDEDRGWAAVTAVTATAASDRMESDSDK 148
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFRENCE: P3430R1217 CURRENT APPLICATION NUMBER: US/10/184,634 CURRENT FILING DATE: 2002-06-28
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                      Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 346
LENGH: 671
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CURRENT FILING DATE: 2002-04-15
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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Publication No. US20030068794A1
GENERAL INFORMATION:
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Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
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DeForge, Laura
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Filvaroff, Ellen
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                                                                                                                                                                                                                                          ; ORGANISM: Homo Sapien
US-10-184-634-346
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US-10-123-155-394/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 ITCIGACTICIGGAGICCIGTCGAIGTCICTAGGICCAGAICTAIGAGAITGAACAACAI 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       824 GTGGGCCAGGGCTTAAGGTGGAGGATGGGCAGTGGGGATGTCCTGGAGTGAACAGGGGAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 SVKKPPRGRKPAEKPLEKPRGRKPKPERPPSSSSSDSDEVDRISEWKRRDEARRRELE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   884 GGACAATAGGAGCCTCGGGTGCCTGACGGAAGGTAGCTGCCTGGGACTGCAAGGTGAGG 943
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                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P343041C27.
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
PTIOT APPLICATION TEMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
PTIOT APPLICATION FILENCE: 2002-06-28
PTIOT APPLICATION FILENCE: 2002-06-28
PTIOT APPLICATION NUMBER: US/10/184,644
SEQ ID NO 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 RGRGPPSSSDSEPEAELEREAKKSAKKPOSSST 421
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                   Sequence 346, Application US/10184644
Publication No. US20030044930Al
GENERAL INFORMATION:
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Publication No. US20030068684A1
GENERAL INFORMATION:
                                                                                                                                                             APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
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Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Gurney, Austin L.
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                                                                                           APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                     Zhang, Zemin
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                                                              Length 1184;
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Publication No. US2030027286A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
CURRENT FAPPLICATION NUMBER: US/10/032,393
CURRENT PELLING DATE: 2001-12-21
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR SEQ ID NOS: 68
NUMBER: OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1620 CCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTG 1664
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                                                                              Best Local Similarity 8.8%; Pred. No. 0.089;
Matches 57; Conservative 175; Mismatches 412; Indels
                                                            2.3%; Score 40.2; DB 9;
8.8%; Pred. No. 0.089;
ORGANISM: Homo Sapien
                      US-10-123-155-394
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Pred, No. 0.18;
0; Mismatches 105; Indels
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                                                                                        ; OTHER INFORMATION: Vector pEPEF14
US-10-032-393-47
                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                          Query Match 2.3%;
Best Local Similarity 49.5%;
Matches 103; Conservative
SEQ ID NO 47
LENGTH: 12
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June 13, 2003, 01:49:14 ; Search time 192.613 Seconds (without alignments) 9216.782 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AX281580 Sequence	AC009974 Homo sapi	AC106524 Rattus no	AC118404 Rattus no	AJ276505 Mus muscu	AC126076 Rattus no	AC094964 Rattus no	G75185 MARC 11245- G74939 MARC 11245-	AF354168 Ovis arie	AC128911 Rattus no	AC111983 Rattus no	AC109982 Rattus no	AL138688 Human DNA	AC094543 Rattus no	AC091776 Chlamydom	AC0904335 Chlamydom	AC106670 Rattus no	ACLLYOOL KALTUS NO	AP004862 Oryza sat	AC115443 Rattus no	ALS83/22 Human Chr AC103544 Rattus no	AC098460 Rattus no	AC103128 Rattus no	AC117323 Rattus no	AC013606 Homo sapi	AA411543 Sequence AC010758 Homo sani	AC021669 Homo sapi	AC096454 Rattus no	ACTU3081 Kattus no	AC109908 Rattus no	AC011747 Homo sapi	APUUZ893 Homo sapi	AC096340 Rattus no			DNA linear PAT 03-NOV-2001				Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	+ 0.00 1.00 0.00	TIDOTO S
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Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 8, 2001 this sequence version replaced gi:13431203.
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Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
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The sequence of Homo sapiens BAC clone RP11-459I19
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donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J., and de Jong, P.J., (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer institute (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute (http://pacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between AC03323 am unresolved tandem in the HERV SVA exists between 184390-185163.
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEIGHBOAING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-1077K22; the clone
sequenced to the right is RP11-64705. Actual start of this clone
is at base position 1 of RP11-459119; actual end is at base
position 206854 of RP11-459119.
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/note="match to EST A1670836 (NID:94850567) wa04910.x1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mapping information for this clone was provided by Dr. John D. McPherson. Department of Genetics, Washington University, St. I. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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/note="match to EST BG477625 (NID:913409904)"
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    37
    /note="similar to Homo sapiens EST BI114348
(NID:914565249)"

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/db_xref="taxon:9606"
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Stren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Bruna, N., Burkett, G., Bouslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzflugh, M., Gaqe, D., Galaqan, J., Gardyna, S., Glidde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illew, I., Johnson, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Maylor, J., Minrand, C., Mengay, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Pisani, C., Pollara, T., Raynon, G., Pierre, N., Pisani, C., Pollara, T., Raynow, P., Rody, P., Rothman, D., Pisani, C., Pollara, T., Raynon, G., Pierre, P., Pollara, T., Rody, P., Rothman, D., P., Rothman, D., Pierre, R., Rody, P., Rothman, D., P., Rody, P., Rothman, C., Palan, R., P., Rothman, P., Rothman, R., Rody, P., Rothman, R., Rothman, R
                                                                                                                                                                                                                                                                                          homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROY, A., Santos, R., Schauer, S., Severy, P., Spencer, P., Stones, S., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Fyman, D., Ye, W.J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 7, 2000 this sequence version replaced gi:7342115. All repeats were identified using RepeatMasker: Smit, A.R.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 152129) Birren, B., Linton,L., Nusbaum,C. and Lander,E. Homo. Sapiens, clone RP11-504G11
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                                                                                                                                                                                                                                                               ch 100.0%; Score 61; DB 9; Length 206854; Similarity 100.0%; Pred. No. 2e-09; 61; Conservative 0; Mismatches 0; Indels 0;
  967. .1090
/note="similar to Homo sapiens EST BI114348
(MID:914565249)"
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Center clone name: 504_c_11
------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
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Web site: http://www-seq.wi.mit.edu
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AC027416.2 GI:8317289
HTG; HTGS_PHASE1; HTGS_DRAFT.
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AUTHORS
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/note="match to EST AA481361 (NID:92210913) zv44e01.rl"
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/note="match to EST AA043371 (NID:91521226) zk53e10.r1"
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Thote="match to EST BE047599 (NID:98364652) tz39c01.yl"
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/note...match to EST BI059713 (NID:g14467240)"
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                                                                                /note="match to EST BG470047 (NID:g13402322)"
281. .344
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//OCte="match to EST AL567345 (NID:g12920610)"
281. 344
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complement(557. .558)
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/note="match to EST AL567345 (NID:g12920610)"
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281. .344
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281. .344
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note="similar to Homo sapiens EST BI114348
NID:9145652499"
164. .662
/note="match to EST C05773 (NID:g1502549)"
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Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 135376 bases at least Q40 Consensus quality: 142264 bases at least Q40 Consensus quality: 146503 bases at least Q20 Insert size: 161000; agarose-fp Insert size: 161002; sum-of-contigs Quality coverage: 3.1 in Q20 bases; agarose-fp Quality coverage: 3.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                      22028: gap of 100 bp 24319: contig of 2291 bp in length 24419: gap of 100 bp 27559: contig of 2640 bp in length 27159: gap of 100 bp 30170: contig of 3011 bp in length
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10084 12556: contig of 2473 bp in length
1255 12656: gap of 100 bp
15043: contig of 2387 bp in length
15044 15143: gap of 100 bp
15144 17123: contig of 1980 bp in length
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55871; contig of 4486 bp in length
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60595: contig of 4624 bp in length
955: gap of 100 bp
66595: contig of 5900 bp in length
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85022: contig of 7807 bp in length
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27060 27159; gap of
27160 30170; conti
30171 30270; gap of
30271 333968; conti
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46466 51285: cont
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55972 60595: conf
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101194 101293: gap of 100 bp
101294 113090: config of 11797 bp in length
113191 123496: config of 10306 bp in length
113191 123496: config of 10306 bp in length
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## L (Dasses 1 to 91424) By Muzny, D. M., Adams, C., Are, J. B., Ali-osman, F. R., Allen, C., Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbaria, J., Benton, J. Binmage, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J. Binmage, K., Blankenburg, K., Bonnin, D., Burbaria, J., Burde, B., Burkelt, C., Burrell, K. L., Brid, N. C., Chavez, D., Chen, G., Chen, R., Chave, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Cayle, M. D., Dathores, R., David, R., Davila, M. L., Davis, C., Davy-Carroll, L., Daderich, D. A., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Day-Carroll, L., Dederich, D. A., Davis, C., Edaga, D., Edaga, D., Edaga, C. C., Elbaj, C., Escotto, M., Faris, C., Earrhatt, C., Edarguto, D., Flagy, M., Ford, J., Foster, P., Frantz, P., Falls, T., Ferrandez, C., Carroll, J. Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Haris, R., Har % SEQUENCING IN PROGRESS #**, 52 unordered pieces. #**, 52 unordered pieces. #** ó 9 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 0; Gaps Length 152129; 1; Indels Score 59.4; DB 2; Pred. No. 6.7e-09; 0; Mismatches 1; /note="assembly_fragment" AC106624.2 GI:21734702 1 (bases 1 to 91247) Direct Submission Unpublished 2 (bases 1 to 91247) ch 97.4%; 1 Similarity 98.4%; 60; Conservative HTG; HTGS_PHASE1. Norway rat. Rattus norvegicus 35947 C 35947 61 C 61 Query Match Best Local 9 RESULT 4 AC106624/c DEFINITION ORGANISM TITLE JOURNAL ACCESSION Matches REFERENCE AUTHORS KEYWORDS VERSION SOURCE LOCUS

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgs.bcm.tmc.edu/docs/denbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                             Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced gi:18139148.
                     Department
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Departmen Submitted (12-JAN-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 91247)
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 46677 bases at least Q40 Consensus quality: 50328 bases at least Q30 Consensus quality: 53862 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s: contig of 1038 bp in length

s: gap of unknown length

contig of 1175 bp in length

s: gap of unknown length

s: contig of 1182 bp in length

s: contig of 1182 bp in length

contig of 1182 bp in length

s: contig of 1102 bp in length

s: gap of unknown length

s: gap of unknown length

s: contig of 1147 bp in length

s: contig of 1179 bp in length

s: contig of 1188 bp in length

s: contig of 1188 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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Worley, K.C.

REFERENCE AUTHORS φ

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Ratury, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alabaratung, H.C., Are, J.R., Ayele, M., Banks, T., Barbarta, J., Bencho., Blankenburg, K., Bonnin, D., Blabarta, J., Bencho., J. Biankenburg, K., Bonnin, D., Bubarata, J., Bencho., J. Briwett, C., Blankenburg, K., Bonnin, D., Bubarata, J., Bencho., J. Briwett, C., Burrell, K., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Charlet, C., Durrell, K., Byrd, N.C., Chen, R., Charlet, C., Coyel, M.D., Dathorne, S.R., David, R., Davis, C., Chan, R., Charlet, C., David, R., Delyado, C., Coyel, M.D., Dathorne, S.R., David, R., Davis, C., Coyel, M.D., Dathorne, S.R., David, R., Delyado, C., Den, A.L., Ding, Y. Dinh, H.H., Delyado, C., Den, A.L., Ding, Y., Dinh, H.H., Delyado, C., Berner, C., Blah, C., Bscortto, M., Earniste, C., Edgar, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Garis, A., Garner, T., Garza, N., Gill, R., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hatt, M., Havlak, P., Hales, S., Hamilton, K., Harris, C., Harris, K., Hatt, M., Hallak, P., Hawes, A., Henner, C., Edwis, L., L., Jockson, L.E., Jacobson, B., Jia, Y., Johnson, R., Willyer, S., Joudh, S., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., C., Lewis, L., Li, J., Li, Lichtarge, C., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Li, Z., Liu, X., Lucier, A., Lucier, R., Luns, M., Mayuen, M., Maheshwari, M., Mapua, P., Martin, R., Wattingle, K., Martin, S., Savery, G., Mawhiney, E., Martin, R., Wattinger, R., Wankiney, E., Martin, S., Savery, G., Scher, P., Wosen, M., Ren, Y., Hawes, M., Ren, Y., Rusek, A., Tabor, P., Tamerisa, A., T
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Submitted (17-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
3 (bases 1 to 127181)
Worley,K.C.
Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                  16; Indels
   Best Local Similarity 71.4%; Pred. No. 8.8; Matches 40; Conservative 0; Mismatches
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Query Match

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JOURNAL. Submitted (18-JUL-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA COMMENT Data, Houston, TX 77030, USA COMMENT On Jul 14, 2002 this sequence version replaced gi:20162777. Center: Baylor College of Medicine Center: Conter: Baylor College of Medicine Center code: BCM Web Site: http://www.hgsc.bcm.tmc.edu/ Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc.bcm.tmc.edu Contact: http://www.hgsc	imated insert size may differ from sequence length tips//www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html). s is a 'working draft' sequence it currently of 56 contigs. The true order of the pieces nown and their order in this sequence record is cons and their order in this sequence record is s for contigs. The true order of the pieces i, but the exact sizes of the gaps are unknown and will be updated with the finished sequence is it is available and the accession number will sit is available and sit is available and season sit is available and season sit is available and season sit is available and season sit is available sit is sport unknown length sit is available sit is sport unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length sit is sport of unknown length s	of 1060 bp in length unknown length of 1412 bp in length of 2158 bp in length of 2009 bp in length of 2009 bp in length

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cars gene; Cdknlc gene; cyclin-dependent kinase inhibitor 1C;
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receptor p60 homologue 1; tumor necrosis factor receptor p60
homologue 2; tumor suppressing subtransferable candidate 5.
western European house mouse.
                                                                                                            ROD 06-MAR-2002
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Submitted (17-MAR-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Innestrasse 73, 14195
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Max-Planck-Institut fuer Molekulare Genetik, Innestrasse 73, 14195
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Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Engemann, S., Strodicke, M., Paulsen, M., Franck, O., Reinhardt, R.,
Lane, N., Reik, W. and Walter, J.
Sequence and functional comparison in the Beckwith-Wiedemann
region: implications for a novel imprinting centre and extended
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On Jan 27, 2001 this sequence version replaced g1:11191799, related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.
Location/Qualifiers
                                                                                                        MMU276505 281000 bp DNA linear ROD
Mus musculus genomic fragment, 281000 bp, chromosome 7.
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/organism="Mus musculus domesticus"
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/sub_species="domesticus"
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/chromosome="7"
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Revised by author 22-MAY-2000
3 (bases 1 to 281000)
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/gene="Obph1"
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MMU276505
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Rattus norvegicus clone CH230-143P6, *** SEQUENCING IN PROGRESS ***, 63 unordered pieces.
AC126076. G1:21699142
HTG; HTGS PHASE1.
Rattus norvegicus.
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McPhezson, JD. and Waterston, R.H.
Direct Submission
Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louls, MO 63108, USA
3 (bases 1 to 140819)
McPherson, J.D. and Waterston, R.H.
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Submitted (16-101.2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jul 16, 2002 this sequence version replaced gi:21040003.
                                                             Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Best Local Similarity 77.8%; Pred. No. 23;
Matches 35; Conservative 0; Mismatches
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MCPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
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/organism="Mus musculus"
/db_xref="taxon:10090"
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                                   house mouse.
                                                                                                                                                                                                                                              Unpublished
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47068. .47141,48531. .48627)
/gene="Tnfrhl"
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48531. .48580)
/gene="Infinl"
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77140. .77213,77826. .77868,78677. .78828)
/gene="Tnfrh2"
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/protein_id="CAC7352.1"
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/db_xref="GP12583597"
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KCHPGTFTGKDDALLGSFCDKDQNWADCSATSDRKCECGIGLXYYDPKFPESC
RPCTKCPQGIPVLQBCNSTANTVCSSSVSNPRNWLFLLMLIVPCII
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Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
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Williams, G., Williamson, A., Weison, D.,
Williams, G., Williamson, A., Weison, D.,
Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pleces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 117082) Worley,K.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 5, 2002 this sequence version replaced gi:21686820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 55139 bases at least Q40
Consensus quality: 61060 bases at least Q30
Consensus quality: 64630 bases at least Q20
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1155: gap of unknown length
2165: contig of 1010 bp in length
2265: gap of unknown length
3314: contig of 1049 bp in length
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Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center project name: GZTG
Center clone name: CH230-143P6
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Worley, K.C.
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TITLE JOURNAL REFERENCE TITLE JOURNAL

AUTHORS

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Lebow, H., Levan, J., Lewis, L., Liu, J., Liu, M., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Manindartne, M., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Manjoy, K., Manjoy, M., Morris, S., Mcleod, M., Mcnell, T., Meenen, E., Milosavijevic, A., Minner, G., Mindasa, M., Mcnell, T., Meenen, E., Milosavijevic, A., Morris, S., Mundasa, M., Mcris, S., Nwaokelemeh, O., Okwuon, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannok, C., Plopper, F., Poindexter, A., Perez, A., Perez, L., Pfannok, C., Plopper, F., Poindexter, A., Redier, M., Rogier, M., Rogier, M., Richards, S., Riyas, F., Rives, C., Rodkey, T., Rodies, A., Sont, G., Sharama, S., Shen, H., Shetty, J., Shvartsbeyn, A., Staten, Y., Sharama, S., Shen, H., Shetty, J., Shvartsbeyn, R., Staten, S., Statek, A., Taebor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., State, M., Taejos, Z., Wang, J., Lao, J., Zhou, J., Zhao, J., Zhao, J., Zhao, J., Zhao, J., Zhao, J., Zhao, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhao, J.,
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NOTE: This is a 'working draft' sequence. It currently consists of 79 conting. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 15564).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Hug 23, 2002 this sequence version replaced g1:21716685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: plasmid;
Sequencing vector: plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality; 96145 bases at least Q40
Consensus quality: 110750 bases at least Q30
Consensus quality: 111678 bases at least Q20
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1171: gap of unknown length
2288: contig of 1118 bp in length
2389: gap of unknown length
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Center code: BCM
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------ Project Information
Center project name: GBUZ
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Rattus norvegicus clone CH230-6L21, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.
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Best Local Similarity
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899 bp DNA linear STS 14-MAY-2002
MARC 11245-11246:999628105:1 Sheep WBC Ov1s aries STS genomic,
sequence tagged site.
975185
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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Freking, B.A., Leymaster, K.A., Keele, J.W. and Smith, T.P.L. Identification of a mutation apparently causing the polar overdominance callipyge phenotype in sheep
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                                                                                                                                                                                                                                                                                          DB 2; Length 155645;
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each 20 pmoles
each 88 uM
0.25 units (Qlagen Hotstar)
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bp in length
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Commercially supplied Qiagen HotStar buffer
             in length
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95 degrees for 30 seconds
54 - 60 degrees for 30 seconds
68 degrees for 2 minutes
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bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
Email: freking@email.marc.usda.gov
Primer A: AGTCTCACCCTTCCTGGAC
Primer B: TGGAGACCCACTGGAAATT
PCR Profile:
                          Length
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Best Local Similarity 69.6
Matches 39; Conservative
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TITLE
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KEYWORDS
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sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence does not necessarily represent the entire amplicon. Sequence derived from Polyphred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G74939 945 bp DNA linear STS 14-WAY-2002
MARC 11247-11248:1020442896:1 Sheep WBC Ovis aries STS genomic,
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                                                                                                                                                                          /organism="Ovis aries"
/strain="Dorset, Romanov, and Dorset-Romanov crossbreds"
/db_xref="taxon:9940"
/dor_stage="sheep WBC"
/dev_stage="adult"
/note="organ: blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The STS is derived from PCR amplicons generated from genomic DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [ (bases 1 to 945)
Freking, B.A., Leymaster, K.A., Keele, J.W. and Smith, T.P.L. Identification of a mutation apparently causing the polar overdominance callipyge phenotype in sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequenced from each end using the amplification primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
NO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                      لد
                                                                                                                                                                                                                                                                                                                                                                           Score 28.6; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: freking@email.marc.usda.gov
Primer A: ATCTGGCAGCTCCTCCTCTA
Primer B: GAACTTGCCCTTGGAAGTGA
                                                                                                                                       Location/Qualifiers
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δ qq

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sequence does not necessarily represent the entire amplicon. Sequence derived from Polyphred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater.
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Submitted (22-FEB-2001) Department of Genetics, B43, University of
Liege, 20, Bd de Colonster, Liege 4000, Belgium
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Georges, M.
Human-ovine comparative sequencing of a 250-kb imprinted domain encompassing the callippyed (clpg) locus and identification of six imprinted transcripts; DAXI, DAY, GTL2, PEG11, antiPEG11, and MEG8 Genome Res. 11 (5), 850-862 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidea; Caprinae; Ovis.

1 (bases 1 to 215046)
Charlier,C., Segers,K., Wagenaar,D., Karim,L., Berghmans,S.,
Jaillon,O., Shay,T., Weissenbach,J., Cockett,N., Gyapay,G. and
                                                                                                                                                                 1. 945 | Appainsm="Ovis aries" | Appainsm="Ovis aries" | Appainsm="Oviset, Romanov, and Dorset-Romanov crossbreds" | Ab_xref="taxon:9940" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 12054: contig of 12054 bp in length

* 12055 27921: contig of 1847 bp in length

* 27922 27941: gap of unknown length

* 27942 29846: contig of 1805 bp in length

* 27942 29846: contig of 1805 bp in length

* 28847 29848: contig of 1806 bp in length

* 33483 33502: gap of unknown length
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Pred. No. 59;
0; Mismatches
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                                                                                                                                                                                                                                                             /clone_lib="Sheep WBC"
/dev_stage="adult"
/note="Organ: blood"
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Owis aries.
                                                                                                                                       Location/Qualifiers
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AF354168.1 GI:13926066
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Best Local Similarity 67.8%;
Matches 40; Conservative (
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid;
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Worley, K.C.
Direct Submission
                                                                     Rattus norvegicus.
Rattus norvegicus
                                                       HTG; HTGS_PHASE1
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 DEFINITION
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ORGANISM
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KEYWORDS
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contig of 4748 bp in length
gap of unknown length
contig of 1748 bp in length
gap of unknown length
gap of unknown length
contig of 953 bp in length
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                         contig of 1665 bp in length
gap of unknown length
contig of 2884 bp in length
gap of unknown length
contig of 9899 bp in length
gap of unknown length
                                                                                                                                                         unknown length
of 4078 bp in length
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of 1746 bp in length
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/organism="Ovis aries"
/db_xref="taxon:9940"
/chromosome="18"
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RE MURDAY D. M. Addms. C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C., Amany, D. M., Adams. C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C., Amary, D. M., Adams. C., Adio-Oduola, B., Ali-Osman, F. R., Bunks, T., Bardok, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burch, P., Burket, C., Burch, E., Brown, E., Bryad, N. C., Carter, M., Cavazco, S. R., Chack, J. Charez, D., Chowdhry, I., Christopuolos, C., Carton, R., Chen, Z., Chowdhry, I., Christopuolos, C., Carton, R., Chen, Z., Chowdhry, I., Christopuolos, C., Carton, E., Chan, C., Coyle, M. D., Dathorne, S. R., Datok, S., Dathi, H. H., Datlam, M. L., Daig, Y., Dilin, H. H., Datlamey, K. R., Delgado, O., Denn, A. L., Ding, Y., Dilin, H. H., Douthwaite, K. J., Draper, H., Dugar, Rocha, S., Durbin, K. J., Barnhart, C., Edgar, D., Edwards, C., C., Elhaj, C., Escotto, M., Falls, T., Ferraquto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, R., Hart, M., Harlak, P., Hale, S., Hamlton, K., Harris, C., Harri
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                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus norvegicus clone CH230-326J5, *** SEQUENCING IN PROGRESS AC128911.1 GI:21953455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990339
Consensus quality: 156726 bases at least Q40
Consensus quality: 144728 bases at least Q30
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164800 bp DNA linear HTG 17-JUL-2002 Rattus norvegicus clone CH230-195D20, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.
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                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 1025 b
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gap of unknown 1
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of 1065
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Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced gi:19525921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 164800)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 96892 bases at least Q40 consensus quality: 103381 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: GSES
Center clone name: CH230-195D20
----- Summary Statistics
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 79 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Bouck, J., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N. P.,
Buhay, C., Burch, P., Burketl, C., Burrell, K.L., Byrd, N. C.
Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, R., Chen, R., Chen, Z., Choyle, M. D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D. A.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D. A.,
Bouthwaite, K.J., Drager, H., Dugan Roccha, S., Durbin, K.J.,
Falls, T., Ferraguto, D., Elagy, N., Ford, J., Foster, P. Frantz, P.,
Garris, A., Gao, J., Garcia, A., Ganer, T., Garca, N., Gill, R.,
Gorrell, J.H., Guevard, W., Gunarthe, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Hallsk, P., Hawes, A., Hernandez, J.,
Harris, C., Harris, K., Hart, M., Hallsk, P., Hawes, A., Hernandez, J.,
Harris, C., Harris, K., Hart, M., Hallsk, P., Hawes, A., Hollins, B.,
Jacobson, B., Jia, Y., Johnson, R., Johlee, J., Jodkson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Johlee, J., Jodkson, L.E.,
Jacobson, B., Jia, Y., Jan, M., Hallyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Jan, M., Marinez, M., Marinez, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Marth, R., Marth, R., Ma, J.,
Manssey, B., Marthney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Man, M., Nagua, P., Marth, R., Marth, R., Marth, M., Mory, M., Moryen, N.,
Nguyen, N., Nickerson, E., Norkenwo, S., Oguh, M., Okwaou, G.,
Oragunyen, N., Nickerson, E., Norkenwo, S., Oguh, M., Okwaou, G.,
Scherre, S., Sontaiker, P., Frimus, E., Pu, L., Oulies, M., Rang, G.,
Scherre, S., Sontaiker, P., Primes, P., Pu, L., Oulies, M., Naguez, L., Peters, L., Vera, Y., Villaion, D., Vinson, R., Man, M.,
Sutton, A., Svatek, A., Tahor, P., Tamerisa, A., Tamerisa, K., Tanag, G.,
Wang, S., Ward, Mark, M., Washington, C., Warlington, S.,
Williams, G., Williams, G., Walliams, G., Walliams, G., Walliams, G.,
Wang, S., Ward, M., Washing, M., Wallished,
Dipublished
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 94 conligs. The true order of the pieces

* Is not known and their order in this sequence record is
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Direct Submission
Submission
Submission
Molecular and Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 170476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission Submission Submission Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2002 this sequence version replaced gi:18701729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 103990 bases at least Q40 Consensus quality: 112822 bases at least Q30 Consensus quality: 119677 bases at least Q20
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Center code: BCM
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AUTHORS
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Rattus norvegicus clone CH230-26L15, *** SEQUENCING IN PROGRESS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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MuznyD.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratung,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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Search completed: June 13, 2003, 04:39:36 Job time: 197.613 secs

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Genomic sequence e
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Listing first 45 summaries
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ATFx coding

Human

Human CDNA sequence # Human p53ArP1 asso Gene #2926 used to CNA encoding a hu Human secreted pro DNA of APP related Rat metastatic tum DNA encoding novel Human brast cell Probe #4800 for ge Human brain expres Human brain expres Human brain expres Human brain expres Human penome-deriv Probe #5017 used t Human penome-deriv Probe #1468 for g Human brain expres	Human Rb-interacti Human Rb-interacti Human RIZ allele D Human RIZ allele E Human RIZ allele E Human mutant RIZ a DNA sequence encod Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Human foctal liver Probe #17409 for g Human brain expres Human brain expres Human bone marrow		<pre>ramma 3 subunit; PRKAG3; variant; substitution; ds. intron 4"</pre>	
AAH18673 ABK42266 ABK42266 ABH5428 AAA14998 AAA37383 AAX37383 AAX37383 AAX37383 AAX37383 AAX37383 AAX37383 AAX37383 AAX37383 AAX3738374 AAX36323 AAX363374 AAX363374 AAX363374 AAX363374 AAX363374 AAX363374 AAX363374 AAX363374 AAX363374 AAX363374 AAX363374 AAX363374 AAX363374	ABS17483 ABK17335 AAA10020 AAA60123 AAA60123 AAA60124 AAA6112 AA116645 AA116646 ABA38943 AAS2202 AAK48368 AAI26223	ALIGNM BP.	ty; s of	"Exon 5" "Intron 5" "Exon 6" "Intron 6"
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AAL38336 standard; DNA; 143899 BP.

RESULT 2 AAL38336

(first entry)

15-AUG-2002

AAL38336;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PKRAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A, in exon 4 variation may be a substitution of a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
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Pred. No. 5.1e-10;
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                                                                                                                                                                                                                                                                          'number= "Intron 10"
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The invention relates to a Nogo receptor homologue polypeptide, NgR2 or NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRCT sequence, or a 420, 461 or 392 amino acid Sequence, all given in the sequence. The NgR3 protein or its binding antibody is useful for secreasing inhibition of axonal growth of a central nervous system (CNS) neuron, by contacting the neuron NgR3 or its antibody, and for treating corebral injury, NgR3 or a vector comprising NgR3 is useful for treating cerebral injury, spinal cord injury, stroke, demyelinating diseases, e.g. multiple sclerosis, monophasic of demyelinating diseases, e.g. multiple sclerosis, monophasic of demyelinating diseases, e.g. multiple sclerosis, monophasic of demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchidava-Bignami disease, Spongy degeneration, alexander's disease, Canavan's disease, metachromatic leukodystrophy and Krabbe's disease, Canavan's disease, metachromatic leukodystrophy and Krabbe's disease, NGR3 is useful for identification, characterisation and purification of interacting, regulatory proteins. The nucleotide of interacting, regulatory proteins. The nucleotide victor containing NGR3 is useful for screening for RFLP associated with certain discorders, for genetic mapping, and for gene therapy. The vector containing NGR3 is useful for isolating and purifying animals. The NGR3 binding antibody is useful for isolating and purifying
                                                                                                                                                              Cerebroprotective, neuroprotective, cytostatic, Nogo receptor homologue, NGR2, MGR3, MGR3, Sacoal growth; central nervous system; CMS: cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; Marchiafava Biquami disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; canavan's disease; metachromatic leukodystrophy; Krabbe's disease; immune; bait protein; genetic mapping; gene therapy; transgenic animal; unrequlated cellular growth; cancer; tumour; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Nogo receptor homolog polypeptide, NGR2 or NGR3, useful for treating central nervous system disorder, cerebral injury, spinal cord
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                                                                                                                    Genomic sequence encoding a human NgR2 protein.
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injury, stroke, and demyelinating diseases
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Sequence 143899 BP; 36346 A; 35277 C; 35318 G; 35657 T; 1301 other;

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2000US-0246474.
2000US-0246475.
2000US-0246476.
2000US-0246477.
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2000US-0246532.
2000US-0246609.
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2000US-0234998.
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2000US-0237039.
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2000US-0231968.
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                                                                                                                                                                                                                                                                                                                                                                Human, immune; haematopoletic; immune/haematopoletic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                      0; Gaps
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             Length 143899;
                                                   Indels
                 DB 24;
           Score 27.2; DE pred. No. 25; 0; Mismatches
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20000S-0225757.
20000S-0225759.
2000US-0225759.
2000US-0226279.
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2000US-0190076.
2000US-0198123.
             Query Match 44.6%;
Best Local Similarity 67.9%;
Matches 38; Conservative (
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Human; connective tissue related disorder; cancer; gene therapy; cytostatic; gene; ds.
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2000US-0231242.
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2000US-0180628.
2000US-018664.
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2000US-0189374.
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23-AdG-2000;

30-AdG-2000;

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16-MAR-2000;

18-APR-2000;

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19-MAY-2000;

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                                                                                               Homo sapiens.
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              26-SEP-2000;
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The present invention relates to the isolation of novel human connective tissue related polypeptides (AAUB6435-AAUB6923) and the polynucleotide (CDNA and genomic) sequences encoding them. The sequences of the juvention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of Bhime-1 strain of Red sea bream iridoviris.
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65.5%; Pred. No. 50;
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                                                                                                                                                                                                                 Disclosure; SEQ ID No 1596; 673pp; English.
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(KURI/) KURITA J.
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                                     (HUMA-) HUMAN GENOME SCI INC.
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18-SEP-2000

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19-SEP-2000

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nucleotide sequence of the Ehime-1 strain of Red sea bream iridoviris
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                                                                                   DB 24; Length 112414;
                                                  Sequence 112414 BP; 26205 A; 29684 C; 30351 G; 26174 T; 0 other;
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Pred. No. 67;
0; Mismatches 12;
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2000US-0184664.
2000US-0184664.
2000US-0186360.
2000US-0198123.
2000US-0198123.
2000US-020515.
2000US-020467.
2000US-020467.
2000US-0206467.
2000US-0206467.
2000US-0216486.
2000US-0216486.
2000US-0216486.
2000US-0216486.
2000US-0216880.
2000US-0216880.
2000US-0216880.
2000US-0216880.
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2000US-022526.
2000US-022526.
2000US-022526.
2000US-0225270.
2000US-0225447.
2000US-0225757.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
                                                                               Query Match 42.3%;
Best Local Similarity 73.3%;
Matches 33; Conservative
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                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 - JAN - 2000; 24 - FEB - 2000; 22 - ARR - 2000; 22 - ARR - 2000; 23 - ARR - 2000; 24 - ARR - 2000; 26 - ARR - 2000; 26 - ARR - 2000; 26 - ARR - 2000; 26 - ARR - 2000; 26 - ARR - 2000; 26 - ARR - 2000; 26 - ARR - 2000; 26 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - ARR - 2000; 27 - A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2001;
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01-SEP-2000;
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                   (RSIV).
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                         Human cDNA clone (5'-primer) SEQ ID NO:5249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000; 2000EP-0116126.
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                                                                                                                                                                                          Homo sapiens.
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09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishii S,
amino acid sequences given in AMM2170 to AMM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and can be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK84942 to AAK84950 and AAM82169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 25277; 3071pp + Sequence Listing; English.
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0; Mismatches 19; Indels
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2000US-0250160.
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2001US-0259678
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                                                17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
10-DEC-2000;
10-DE
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Yamamoto J;

Saito K, Ya , Otsuki T;

Isogai T, Nishikawa T, Hayashi K, S Sugiyama T, Wakamatsu A, Nagai K,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence'3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13612 represent human cDNA sequences; AAB92446 to
                                                                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligo-dribe complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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Claim 1; SEQ ID 5249; 2537pp + CD ROM; English.
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AAC77940/c
ID AAC77940 standard; CDNA; 1030
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5618 GTGGGGGTGGGGCTGGTGTGAGACCCTGGGGGTGGGGCTGGGGGTG 5673

AAH08414 standard; cDNA; 686 BP.

AAH08414/c

RESULT

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AAH08414;

aminobutyric acid B receptor; GABA B receptor;

Human ATFx coding sequence with 5' extension.

transcription factor; ss

WO200116596-A2.

08-MAR-2001.

Homo sapiens.

gamma

30-MAY-2001 (first entry)

AAE77880;

AAF77880 standard; cDNA; 1105 BP.

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dermatological, neuroprotective, cardiant; thrombolytic; coagulant; nootropic, vasotropic; antipsociatic and antianglogenic. The nootropic, vasotropic; antipsociatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating to inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate haemostatic or thrombolytic activity, modulate bactoris, repection, modulate haemostatic or thrombolytic activity, modulate bactoris, repection, modulate haemostatic or thrombolytic activity, modulate and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44400 represent sequences used in the exemplification of
                                                                                                                                                          diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antinheumatic; antiarthritic; antiviral; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; almoure disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antibacterial; antibacterial; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer
                                                                                                            cancer associated gene; cancer antigen; detection; cancer;
Human cancer associated gene sequence SEQ ID NO:334.
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                                                                                                                     4 AGGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGCGGGGGCGGAGT
                                                                              ö
                                       DB 21; Length 1030;
                                                                              Indels
Sequence 1030 BP; 175 A; 362 C; 287 G; 195 T; 11 other;
                                                                            0; Mismatches
                                     Score 25.2; Pred. No. 72;
                                                                            36; Conservative
                                     Query Match
Best Local Similarity
                                                                            Matches
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RESULT 9 AAF77880/c

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The present invention relates to a method for identifying a modulator of gamma anihobityric acid. B (GABA_B) receptor-mediated activity, by monitoring the interaction between a CRED/ATF transcription factor capable of binding to GABA_B receptor. The present sequence is the coding sequence for human ATFX, which was used in the method of the present invention. ATFX is a member of the CRED/ATF family of transcription factors. ATFX contains a DZIP domain, by which it interacts with the coiled coil domain of GABA_B receptor. Modulators of GABA_B receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system disorders. The present sequence encodes an ATFx protein with a N-terminal extension (compared to AAB80892).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity are useful for treating central nervous system or peripheral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mediated activity by monitoring the interaction between GABAB recand the CREB/ATF transcription factors in the presence of a test
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66.7%; Pred. No. 72;
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Best Local Similarity
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14 AUG-2000; 2000US-0222568.
14 AUG-2000; 2000US-0222568.
14 AUG-2000; 2000US-022570.
14 AUG-2000; 2000US-0225751.
14 AUG-2000; 2000US-0225758.
14 AUG-2000; 2000US-0225758.
18 AUG-2000; 2000US-0225759.
22 AUG-2000; 2000US-0226681.
22 AUG-2000; 2000US-0226681.
23 AUG-2000; 2000US-0226681.
23 AUG-2000; 2000US-0227009.
30 AUG-2000; 2000US-0227009.
31 SEP-2000; 2000US-022709.
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14-AUG-2000; 2000US-0225266.
14-AUG-2000; 2000US-0225267.
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08-SEP-2000; 2000US-0231242.
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12-SEP-2000; 2000US-0231968.
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                                WO200155343-A1.
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01-SEP-2000; 2
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06-SEP-2000;
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19-MAY-2000;
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26-SEP-2000;
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26-JUL-2000;
   Homo sapiens
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                                                               02-AUG-2001
   The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 1'-end sequence complementary to a
coligonucleotide which comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
charlength cDNAs. The primers allow obstanting of the full-length
charlength cDNAs. The primers allow obstanting of the full-length
charlength cDNAs. The primers allow obstanting of the full-length
charlength cDNAs. The primers allow obstanting of the full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13632 represent human cDNA sequences; AAB9246 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
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66.7%; Pred. No. 73;
Live 0; Mismatches 18; Indels 0;
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                                                                                                         27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899
                                                           28-JUL-2000; 2000EP-0116126
                                                                                            99JP-0248036
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                                                                                                                                                                                                                                                                   WPI; 2001-318749/34.
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EP1074617-A2
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2000US-0229344. 2000US-0229345. 2000US-0229509.

2000US-0229513. 2000US-0230437.

2000US-0234998 20000S-0235484

2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0225213.

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2000US-0215135 2000US-0216880 2000US-0217487 2000US-0217496

2000US-0186350

2000US-0184664

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01-DEC-2000, 2000US-0250160.
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06-DEC-2000, 2000US-0251479.
06-DEC-2000, 2000US-0251479.
08-DEC-2000, 2000US-0251866.
08-DEC-2000, 2000US-0251869.
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2000US-0249207.
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27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-SEP-2000; 20-SE
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(HUMA-) HUMAN GENOME SCI INC

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tissue related polypeptides (AAU86435-AAU86923) and the polynocieotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                   The present invention relates to the isolation of novel human connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p53-dependent apoptosis-associated protein and its encoding gene p53AIPI, used for screening apoptosis mediated remedies for cancer and as controllers of apoptosis induction
                                                                             Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human p53-dependent apoptosis-associated protein, P53AIPI comprising fully defined 806, 777, 2659 nucleotide sequences (ABL54631-ABL54633 respectively) given in the specification
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66.7%; Pred. No. 82;
tive 0; Mismatches
                                                                                                                                               Disclosure; SEQ ID No 1153; 673pp; English.
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              Ruben SM;
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(ONCO-) ONCOTHERAPY SCI INC.
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hes 36; Conservative
              Barash SC,
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                                            WPI; 2001-565190/63.
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                                             86 and 108 amino
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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and the three respectively encoded human p53-dependent apoptosis-associated proteins having fully defined 124, 86 and 108 ami acid sequences (ABBO8837-ABBO8839 respectively) given in the specification. The protein and encoded gene have cytostatic activity, useful in screening for regulators of apoptosis for subsequent use as cancer treatments. The present sequence is that of the Human p53AIPI associated DNA, useful to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in
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66.7%; Pred. No. 85;
                                                                                                                                                                                                                                                                                          Sequence 9305 BP; 2133 A; 2438 C; 2570 G; 2164 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene #2926 used to diagnose liver cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN96428 standard; DNA; 275 BP
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related protein (PROAP). The polypeptides and polynucleotides can be used for the diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders Disorders associated with decreased expression or activity of include arteriosclerosis, cirrhosis, hepatitis, psoriasis, melanoma, lymphoma and cancers of the breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human proliferation and apoptosis related protein polypeptides used for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders -
                                                                                                                                                                                                                                                                                                                             Human; proliferation and apoptosis related protein; PROAP; psoriasis; cell proliferative disorder; immunological disorder; hepatitis; reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma; cancer; acquired immune defliciency syndrome; AIDS; allergy; anaemia; asthma; diabetes mellitus; osteoarthritis; endometriosis; uterine fibroid; menstrual cycle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "proliferation and apoptosis related protein"
                                          Gaps
                                                                                                                                                                                                                                                                                               cDNA encoding a human proliferation and apoptosis related protein.
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Score 25; DB 24; Length 275;
Pred. No. 75;
0; Mismatches 10; Indels
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Shih LL;
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                                                                                             148 GGACCTCATAGGGAGCCAGGGGGCAGGGGCCGGGGAGT
                                                                        17 GAATCTTATGGGCACCCAGAGGGGGGGGGGGGGGGGGAGT
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82..303
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n MR, Yang J,
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99US-0118559.
99US-0172229.
        41.0%;
75.6%;
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                                                                                                                                                                                                                                                              (first entry)
       Query Match 41.0
Best Local Similarity 75.6
Matches 31; Conservative
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11-FEB-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS; Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis; arthritis; psoriasis; digestive; endocrine; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polynucleotides. Specific uses are
                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; prevention; treatment; protein therapy;
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                                                           Score 25, DB 21; Length 303;
Pred. No. 75;
0; Mismatches 20; Indels
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Lafleur DW;
Shi Y, Sopp
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein cDNA fragment containing gene 15.
                  Sequence 303 BP; 67 A; 85 C; 110 G; 41 T; 0 other;
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C, Florence KA, Komatsoulis GA,
Olsen HS, Rosen CA, Ruben SM,
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                                                                                                                                                                                                                                                                                               AAX37383 standard; cDNA; 541 BP.
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9705-0095369
9705-0056389
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9705-0056555
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9705-0056629
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                                                           Match 41.0%;
Local Similarity 64.9%;
es 37; Conservative
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19-AUG-1997;
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Moore PA,
Young PE;
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                                                               Query Match
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described for each of the 70 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, asthma, sepsis, diabetes, Alzheimer's and cognitive disorders, schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine disorders, infections and AIDS. The human secreced proteins of the invention are represented in AAX37369-X3744.V77850 and the encoding nucleic
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BAM800472 AGENCOURT
AL514251 AL514251
BQ708179 AGENCOURT
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                                                                     June 13, 2003, 02:37:44; Search time 151.839 Seconds (without alignments) 6506.409 Million cell updates/sec
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AGENCOURT_6419113 NIH_MGC_71 Homo saplens cDNA clone LWAGE:5534991 BM800472
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MSIH MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Braal: cgapbs-remail.in.fh.gov
Tissue Procurement: AUCC
CDN Library Preparation: Life Technologies, Inc.
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution Information can be
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                                                         Length 1208;
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http://image.llnl.gov
Plate: LLAM1222 row: f column: 16
High quality sequence stop: 635.
Location/Qualiflers
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                                                      Score 30.4; I
Pred. No. 69;
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                                                                                                                                                                                                                                                                                                                    1208 bp mRNA linear EST 24-MAY-2002
AGENCOURT_7751176 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6062177
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NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-remail.nih.gov

Tissue Procurement: ArCOCTOCTO/DTP

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
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Pred. No. 19;
0; Mismatches 14; Indels 0;
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www-bio.llnl.gov/bbrp/image/image.html
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Location/Qualifiers
                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 74.1%;
Matches 40; Conservative
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/Clone=lib="LTI_NFL006_PL2"
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/note="Vector: powyspor 6; Site_l: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco Ry sites of the pcWyspor 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Library was constructed by
Life Technologies. Contact: Feng Library Library Library has constructed by
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGENCOURT_8292191 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280902 BQ708179
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1 (bases 1 to 1084)
NHH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2472 rown column: 07
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Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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1 (bases 1 to 688)
Li,W.B., Gruber.C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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http://fulllength.invitrogen.com"
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Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6280902"
                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_113"
//lab_host="DH/DB (phage=resistant)"
//lab_host="DH/DB (phage=resistant)"
//note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Mong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Organ: Drain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcWVSPORT 6 Vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, advision of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL530561 ALI_NFL001_NBC4 Homo sapiens CDNA clone CSODD007Y022 5
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
Genoscope - Centre Erryr cedex - France
BP 191 90006 ERRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                     y Match 47.2%; Score 28.8; DB 14; Length 1084; Local Similarity 69.6%; Pred. No. 1.96+02; hes 39; Conservative 0; Mismatches 17; Indels 0;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/lab_host="DH10B"
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189 c 337 g 38 t 11
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Best Local Similarity 55.2%; Pred. No. 2.4e+02;
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/db_xref="taxon:9606"
/clone="CSODD007Y022"
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57

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/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using AP-cDNA synthesis kit (Stratagene) and Superscript Library."
                                                                                                                                                                                                                           AGENCOURT_6640847 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5434071 BM999483
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S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

L Upublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: gapbbs-remail.nih.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation

CDNA Librar
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Prlmates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                         46.2%; Score 28.2; DB 14; Length 1729; 68.4%; Pred. No. 2.9e+02; Live 0; Mismatches 18; Indels 0;
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/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_99"
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BQ521472.1 GI:21380341
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/organism="Hordeum vulgare"
/db_xref="Laxon:4513"
/db_xref="Laxon:4513"
/clone=lib="Hordeum vulgare seedling shoot EST library
HVCDNA0003 (Exiclated and unstressed)"
/tissue_type="Seedling shoot"
/tissue_type="Seedling shoot"
/lab_host="Tuol21"
/note="Vector: lambdaZAP; Site_1: EcoRl; Site_2: Xhol;
Seeds were surface sterilized then genminated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedling shoots were
then harvested, total RNA was prepared, poly(A) RNA was
purified, one primary unamplified cDNA library was made,
and I million plu were in vivo excised to give pBluescript
SK(-) cDNA phagemids. These steps were performed in the TJ
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the Clemson University of California,
Riverside (Choi, Close, Fenton). Phagemids were performed and
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wilmy, Yu, Frisch, Henry, Simmons, Oates
Pambo, Main, The sequence has been trimmed to remove
                                                                                                                                                                                                                                                                                                                         Hordeum vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticeae; Hordeum.

1 (bases 1 to 735)

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library
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                                                                         EST 22-OCT-2001
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                                                HVSMEC0002B16f Hordeum vulgare seedling shoot EST library HVCDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEC0002B16f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 156 c 264 g 116 t 10 others
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On Feb 22, 2001 this sequence Version replaced gi:13109940.
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68.4%; Pred. No. 2.7e+02;
Live 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Fax: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 718.
Location/Qualifiers
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Total hq bases = 300
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Best Local Similarity 68.47
Matches 39; Conservative
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RESULT 7
BG309093
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1. .403

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| Corganism= Silurana tropicalis" |
| Ab_xref="taxon.8364" |
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| Aclone="inhAcE:33664" |
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| Ab_host="naibud" |
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CDNA Library Preparation:

CDNA Library Preparation:

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: Mational Institutes of Health Intramural

Sequencing Center (NISC)

Sequencing Center (NISC)

Close distribution: NGT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llnl.gov.w.A.G.E. column: 1

Plate: LLAMINGS rower primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pgnlc.pk0l0.k15 normalized chicken lymphoid cDNA lihear EST 01-MAY-2002 gallus cone pgnlc.pk0l0.k15 5' similar to no significant hits BQ038856
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopoinae; Silurana.

1 (bases 1 to 403)

NIH *XCG http://lange.lnl..gov/image/html/xenopuslib_info.shtml.

National Institute of Child Health and Human Development, National Cancer Institute, Xenopus Gene Collection
Unpublished (2002)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 530)

Morgan, R. W. and Burnside, J.

Chicken lymphoid ESTs
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On Mar 27, 2002 this sequence version replaced gi:19772396.
Contact: Joan Burnside
Molecular Endocrinology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 14; Length 403; Pred. No. 2.9e+02;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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/db_xref="taxon:9031"
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Best Local Similarity
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BQ038856
                                                                                    REFERENCE
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Matanabe, H. and Sakaki, Y.
Direct Submission Submission Submission Submitted (02-MuG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Faurumi-ku, Yockhama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:B1-45-503-9111, Fax:B1-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-132E07.R.
Pan troglodytes
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Pan Troglodytes DNA, clone: PTB-132E07.R, genomic survey sequence.
AG122806
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                            /tissue_type="thymus, bursa, spleen, PBL, bone marrow"
/lab_host="E.coli EMDH10B"
/clone="pgnlc.pk0l0.k15"
/clone_lib="normalized chicken lymphoid cDNA library"
/sex="Male and Female"
                                                                                                                                                                                                                                 Gaps
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BAC end sequences of Library PTB
Unpublished
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/clone_lib="PTB Chimpanzee Male BAC Library"
258 c 92 q 177 +
                                                                                                                                                                                  Query Match 45.9%; Score 28; DB 14; Length 530; Best Local Similarity 66.7%; Pred. No. 2.9e+02; Matches 40; Conservative 0; Mismatches 20; Indels
                                                                                                                            33 others
                                                                                                                                                                                                                             20; Indels
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                                                                                                  /note="Vector: pCMVSPORT 6"
149 c 142 g 126 t
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/db_xref="taxon:9598"
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R.Site 2 : Raci
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AG122806/c
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lissue Procurement: CGAP (Stanford)
                                                                                                                                              High quality sequence stop: 438.
Location/Qualifiers
1. .1434
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/clone="IMAGE:6270062"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 45.6%;
l Similarity 69.1%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library."
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02.40G-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RTKEN), Genomic Sciences (Center (63C); 1-7-22 Suehiro-chou, Tsurumi', Vökohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                           Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-089K05.R.
Pan troglodytes
                                    GSS 03-NOV-2001
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                                      90162 712 bp DNA linear GSS 03-NOV-200 troglodytes DNA, clone: PTB-089K05.R, genomic survey sequence.
                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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Fuliyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Tottoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                  Fujiyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="lymphoblast"
/cell_type="lymphoblast"
/clone_lib="prB Chimpanzee Male BAC Library"
/230 c 205 q 150 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Pan troglodytes"
/db_xref-"taxon:9598"
/clone="PTB-089K05.R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
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R.Site 1 : Saci
R.Site 2 : Saci.
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BH756447 452.05.n Arabidopsis thaliana TDNA insertion lines Arabidopsis clone SALK_053697.52.05.n, DNA Arabidopsis thaliana genomic clone SALK_053697.52.05.n, DNA
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/lab_host="hepatocellular carcinoma, cell line"
/not="lorgan liver; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACAGG(G). Size-selected >500pp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Limmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Arabidopsis thaliana
Enkaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
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CDNA Library Arrayed by: The I.M.4.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.4.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1/52
Fax: 858 558 6379
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Pred. No. 3.7e+02;
0; Mismatches 17;
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/note=Torgan: Drain; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: EccRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
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/db_xref="taxon:3702"
/clone="%ALK_038697.52.05.n"
/clone="%ALK_038697.52.05.n"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
a 160 c 112 g 106 t 12 others
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MIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLMM1479 row: k column: 08
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436 c 297 g 187 t
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/lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5191807"
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Location/Qualifiers
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BI489045.1 GI:15328273
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Matches 36; Conserva
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
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Db 754 TGGGCGGGAGTTTTATGGTTATCCTGCGGCGGGGGGCCGGATGCTTAC 705
Search completed: June 13, 2003, 05:58:15
Job time: 156.839 secs
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(without alignments) 4027.262 Million cell updates/sec
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61
1 gtgaggagtgggctgggaat......gggggcggagggggggggctct 61
                                                                                                                                    June 13, 2003, 02:39:09; Search time 4.64516 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                   441362 segs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                            - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Maximum DB :
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Sequence 3, Appli
Sequence 3, Appli
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Sequence 17, Appl
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Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 26, Appli
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Sequence 27, Appli
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Sequence 3, Appli
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Sequence 11, Appl
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Sequence 3, Appli
                        Sequence 3, Appli
         Description
                     US-08-459-568-3
US-08-394-11-3
US-08-516-859A-3
US-09-586-472-3
US-09-528-706-3
US-08-290-665A-139
US-08-290-665A-140
US-08-290-665A-140
US-08-836-075A-17
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US-09-336-536-1
US-09-346-310-30
US-09-346-310-30
US-09-346-310-30
US-09-346-310-30
US-09-346-536-1
Query
Match Length DB
                                                                                                       4403765
4411529
53526 3
53526 3
53577 3
24189 4
24189 4
1001 3
1001 3
1001 3
1338 4
1338 4
1347 4
1347 4
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5868
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Gaps ; 0

Score 24.8; DB 1; Length 5183; Pred. No. 12; 0; Mismatches 17; Indels 0

40.7%;

1..5158

; US-08-459-568-3

Query Match 40.7
Best Local Similarity 67.3
Matches 35; Conservative

Sequence 1, Appli Sequence 1, Appli Sequence 135, App Sequence 136, App Sequence 137, App Sequence 138, App Sequence 136, App Sequence 136, App Sequence 136, App Sequence 136, App Sequence 138, App Sequence 138, App Sequence 144, App Sequence 158, Appl Sequence 158, Appl		Interacting 700
US-08-336-408B-1 US-08-290-665A-135 US-08-290-665A-136 US-08-290-665A-137 US-08-290-665A-138 US-08-290-665A-144 PCT-US95-10398-135 PCT-US95-10398-136 PCT-US95-10398-137 PCT-US95-10398-144 US-08-17-235-3 US-08-17-235-3 US-08-17-235-3 US-08-17-235-3 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85 US-08-17-238-85	ALIGNMENTS	oma Protein - Proteins s Drive, Suite OS .0, Version #1 ,568
1866 5 1866 5 1866 5 573 2 573 2 573 2 573 2 573 2 573 5 873 5 803 1 86 1 86 2 86 2 86 3 86 3 86 4 86 2 86 3 86 3 86 3 86 3 86 3 86 3 86 3 86 3		shi shi seti: zinc s: 93 ss: 93 seti: zinc si zinc si zinc si zinc jolla jolla spy di compa id sepy di compa id sepy di compa id sepy di compa in DATA: seti seti seti seti seti seti seti seti
3.3.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4		1 10. 569-3/C 10. 63, Application UI 10. 511304 11. A. S. 511304 11. A. S. 511304 11. E. O. INVENTION: Re TLE OF INVENTION: Re TLE OF INVENTION: Re TLE OF INVENTION: Re MERE PONDENCE ADDRESS ADDRESSEE: Caulfornia GOUNTRY: USA ADDRESSEE: California COUNTRY: USA ADDRESSEE: California COUNTRY: USA MEDIUM TYPE: Floppy COMPUTRY: USA MEDIUM TYPE: Ploppy COMPUTRY: BEADABLE FORM MEDIUM TYPE: Ploppy COMPUTRY: DAY MEDIUM TYPE: Ploppy COMPUTRY: DAY MEDIUM DAY MEDIUM ADDRESSEE: APPLICATION DAY APPLICATION NUMBER: FILING DATE: OG-WAR TORNEY/AGENT INFORMA APPLICATION NUMBER: TORNEY/AGENT INFORMA NAME: CAMPDELL OF SETTING TORNEY/AGENT INFORMA NAME: CAMPDELL OF SETTING TORNEY/AGENT INFORMA NAME: CAMPDELL OF SETTING TORNEY/AGENT INFORMA NAME: LEDENAX: G019) 535- TELEPROME: (619) 535- TELEPROME: (619) 535- TELEPROME: (619) 535- TELEPROME: (619) 537- TENDING: AUTHORITAIN INFORMA TOPOLOGY: linear NAME/KEY: CDS
222222222222222222222222222222222		SULT 1  -08-459-568-3/C  Sequence 3, Application Patent No. 5811304  - APPLICANT: Huang, S  TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: CAMPESSEE: 4370 La J CITY: San Diego STARE: 4370 La J CITY: San Diego STARE: 12P: 92122  COMPUTER: BADBALE FC COMPUTER: END PC OPERATING SYSTEM: SOFTWARE: PATENTION APPLICATION NUMBER FILING DATE: 02-3  CLASSIFICATION INVENTION FOR SEQUENCE TAPPHONE: (619) TELECHONE: (619)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 US-08-459 Sequence Sequence Sequence APPL TITL TITL TITL NUMB CORR ST CORR APPL ST CORR APPL ST CORR APPL ST CORR APPL ST TITL TITL TITL TITL TITL TITL TITL
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NUMBER OF SEQUENCES: 106
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LENGTH: 5868 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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121..5278
   COMPUTER READABLE FORM:
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Best Local Similarity
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APPLICANT: Huang, Shi
TILLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
                                                                                                                                                                     APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBERF: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION WINBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08516859A Patent No. 6069231
                                                                                                                   Sequence 3, Application US/0839411 Patent No. 5831008 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                San Diego
California
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Best Local Similarity
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US-08-516-859A-3/c
                                                                                                   US-08-399-411-3/c
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US-08-399-411-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                    RESULT 2
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DB 3; Length 5868;
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Patent No. 6333335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
CORRESPONDENCE: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC_COMPATIBLE
COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAEDATIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
COMPUTER: IDM PC compatible
COMPUTER: IDM PC compatible
COMPUTER: IDM PC compatible
COMPUTER: IDM PC compatible
SOFTWARE: PETENTS.
SOFTWARE: PETENTS.
SOFTWARE: PETENTS.
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 13-AuG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR.1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AuG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REDISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELEFONDUMICATION INFORMATION:
TELEFONDUMICATION INFORMATION:
TELEFAN: (619) 535-8949
INFORMATION FOR SED ID NO: 3:
CONTEMNEY CANADAMENTED FOR TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-Jun-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 11-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.7%; Score 24.8; Diarity 67.3%; Pred. No. 13; Conservative 0; Mismatches
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ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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R.H.
NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                               DB 4; Length 5868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 573;
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                                                                                                                                 40.7%; Score 24.8; Di
ilarity 67.3%; Pred. No. 13;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/290,665A
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                                                                                                                                                                                                                                                                                                                                              ; Sequence 139, Application US/08290665A; Patent No. 5882852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET WINDER: 2026.
TELEPONNUNICATION INFORMATION:
TELEPONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEYX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHERD W. BORK
REGISTRATION NUMBER: 36,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: homosapiens
INDIVIDUAL ISOLATE: Z4
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCL
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQ
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS: 263
                                                           CDS
121..5278
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BUKH, J., APPLICANT: PURCELL, F
                                                                                                                               Query Match
Best Local Similarity
Matches 35; Conserve
                       linear
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     STRANDEDNESS:
TOPOLOGY: 11n
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                                                                                                                                                                                                                                                                                                                              US-08-290-665A-139/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                           ;
US-09-528-706-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: N. COUNTRY:
                                                           NAME/KEY:
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                                       FEATURE:
                                                                                                                                                                                                                                                                                                            RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09528706
Patent No. 6468985
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: 2 inc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,706
                                                   ATTORNEY ACENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPRA: (619) 535-9001
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24.8; DB; Pred. No. 13; 0; Mismatches
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
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APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-906-1994
ATTORNEY,AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            LOCATION: 121..5278
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             LENGTH: 5868 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.7%;
Best Local Similarity 67.3%;
Matches 35; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 43,0
CITX: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                          FEATURE
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLARES OF HEAPAITIES C VIRUS AND THE USE OF REAGENEYS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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NUCLEOTIDE AND DEDUCED
                                                                                                                                                                                                                          PRIOR DALE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 UNDE 1993
PRIOR APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 30,459
REFERENCE/DOCKET NUMBER: 30,699
TELLEPHONE: (212) 758-4800
TELLERAX: (212) 758-6849
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-10398-140/c

Sequence 140, Application PC/TUS9510398

GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TILLE OF INVENTION: MUCLEOTIDE AND DEDUCE
TITLE OF INVENTION: CORE GENES OF ISOLATE
TITLE OF INVENTION: AMINO ACID SEQUENCES;
TITLE OF INVENTION: AMINO ACID SEQUENCES;
TITLE OF INVENTION: SEQUENCES IN DIAGNOST;
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
                                                                                                                                  SYSTEM: PC-DOS/MS-DOS WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
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                                                                                       FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: homosapiens;
INDIVIDUAL ISOLATE: 24
PCT-US95-10398-139
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Best Local Similarity 70.2
Matches 33; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: NEW YORK STATE: NEW YORK
NEW YORK
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ORIGINAL SOURCE:
                                                                                                                                                       SOFTWARE:
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TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLARES OF HERATITES C VIEUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
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                                 Sequence 140, Application US/08290665A Patent No. 5882852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
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70.2%;
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                                                                                                                                                                                                                                                                                                                                  STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: homosapiens INDIVIDUAL ISOLATE: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Conservative
                                                                                                                                                   TITLE OF INVENTION: NUCLITIES OF INVENTION: ANINITIES OF INVENTION: AND TITLE OF INVENTION: AND NUMBER OF SEQUENCES: 263 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                    STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10154
                       US-08-290-665A-140/c
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INNS:004
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Batent No: 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09103840A Patent No. 6294328
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APPLICANT: FLEISCHMAN, Robert D.
REFERENCE/DOCKET NUMBER: IIINFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                            LENGTH: 957 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                Best Local Similarity 68.09
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 63.8
Matches 37; Conservative
                                                                                                                                linear
                                                                                                                                TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                            ; ANTI-SENSE: NO US-08-836-075A-17
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LENGTH: 4403765
                                                                                                                                                                      HYPOTHETICAL:
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APPLICANT: STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 GCCGGGGATCATTTGGCCCCCAAGACGGTCGAGAGCCGCGGGGGGAC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MACTOSOft Word 6.0 / ASCII text output
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION NUMBER: PCT/FP95/04155
FILING DATE: 23 Oct 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
40.3%; Score 24.6; D
Best Local Similarity 70.2%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches
                                                                                                                                                                      NAME: RICHARD W BORK
REGISTRATION NUMBER: 36,459
REPERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 94870166.9 FILING DATE: 21 Oct 1994 PRIOR APPLICATION DATA:
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                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-836-075A-17/c
; Sequence 17, Application US/08836075A
; Patent No. 6180768
                                                                                                                                                                                                                                                     TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: KAMMERER, PATRICIA A. REGISTRATION NUMBER: 29,775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NEW SET TITLE OF INVENTION: AND THE TITLE OF INVENTION: AGENTS NUMBER OF SEQUENCES: 207 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: Z8
PCT-US95-10398-140
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
CLASSIFICATION:
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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: WENEER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 243566-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOSTWARE: PALENTING DATE: 1998-06-24
SOSTWARE: PALENTING DATE: 2
SOSTWARE: PALENTING VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FILTED MAY, NOSILE D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VEWTER, John C.
TITLE OF INVENTION: TUBRECULOSIS
FILE REFERENCE: 2436-20007.00
CURRENT APPLICATION NUMBER: 05/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.0%; Score 24.4; DB 4; Length 4403765; 63.8%; Pred. No. 30;
Live 0; Mismatches 21; Indels 0;
                                                                                                                                          343 TGTGCCGGGGGTCGTTTGGGCCCCACGAGGGGCGAGAGCCCCGGGGGGGAC 294
                                                          ö
                                                                                                         40.0%; Score 24.4; DB 4; Length 957; 68.0%; Pred. No. 14; ive 0; Mismatches 16; Indels
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SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pair
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                            CITY: FRAMINGHAM
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                                                                                                                                                               GENERAL INFORMATION:
                                              16496 C 16496
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               61 C 61
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ZIP: 01701
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                                                                                                                                                            0; Gaps
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                                                                                            Score 24.4; DB 4; Length 4411529; Pred. No. 30;
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                                                                                                                               21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CUBRENT APPLICATION DATA:
APPLICATION UNBER: US/08/323,443B FILING DATE: 12-OCT-1994 CLASSIFICATION: 435
                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0372/0A462
            TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                        APPLICANT: KLINGER, KATHERINE W. APPLICANT: LANDES, GREGORY M. APPLICANT: BURN, TIMOTHY C. APPLICANT: CONNORS, TIMOTHY D. APPLICANT: DERMINO, GREGORY APPLICANT: GERMINO, GREGORY APPLICANT: GIAN, FENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                           Sequence 1, Application US/08323443B Patent No. 5654170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Lidwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372/
TELEPHONE: (212) 527-7700
TELEPRONE (212) 527-7700
TELEPRA: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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62.3%;
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Best Local Similarity 62.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
                                                                                                            Sest Local Similarity 63.8 Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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NY
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LENGTH: 4411529
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US-08-323-443B-1
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                                                             US-09-103-840A-1
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Sequence 2. Application US/0658136
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Sequence 3. Application US/0658138
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Sequence 3. Application US/0658138
Sequence 3. Application US/0658138
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Sequence 3. Application US/0658136
Sequence 3. Application US/0658136
Sequence 3. Application US/0658136
Sequence 3. Application US/0658136
Sequence 3. Application US/0858136
Sequence 3. Appl
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APPLICANT: CONNOES, TIMOTHY D
APPLICANT: DACKONSEL, WILLIAM
APPLICANT: DACKONSEL, WILLIAM
APPLICANT: GENEROL, GREGORY
APPLICANT: GENEROL, GREGORY
APPLICANT: GENEROL, GREGORY
APPLICANT: GLAW, ENG
CONTRESSEE: GENEROLES POLICYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
ADDRESSEE: GENEROLE PORM:
APPLICANT ON THE : PRANTHON: COMPATER READALE FORM:
APPLICANT ON STEM: PC-OMPATER ROAD
COUNTRY: UNA PC-OMPATER ROAD
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TYPE: DNA
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Sequence 1596, Ap
Sequence 1596, Ap
Sequence 314, App
Sequence 3153, Ap
Sequence 225, Appl
Sequence 25, Appl
Sequence 318, App
Sequence 318, App
Sequence 318, App
Sequence 318, App
Sequence 318, Appl
Sequence 318, Appl
Sequence 1539, A
Sequence 153, Appl
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                                                                June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds (without alignments) 4579.068 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                            cgn2_6/ptcdata/1/pubpa/USO7_PUBCOMB.seq:*

cgn2_6/ptcdata/1/pubpa/PCT_NEW_PUB.seq:*

cgn2_6/ptcdata/1/pubpa/PCT_NEW_PUB.seq:*

cgn2_6/ptcdata/1/pubpa/VSO6_PUBCOMB.seq:*

cgn2_6/ptcdata/1/pubpa/VSO7_NEW_PUB.seq:*

cgn2_6/ptcdata/1/pubpa/PCTUS_PUBCOMB.seq:*

cgn2_6/ptcdata/1/pubpa/NCTUS_PUBCOMB.seq:*

cgn2_6/ptcdata/1/pubpa/NCSO8_NEW_PUB.seq:*

cgn2_6/ptcdata/1/pubpa/VSO8_PUBCOMB.seq:*

                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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10 US-09-252-301-334
10 US-09-922-301-334
10 US-09-925-301-334
10 US-09-764-847-1153
10 US-09-860-107-2925
1 US-01-144-929-25
2 US-10-964-899-30
0 US-09-864-761-4800
0 US-09-864-761-4800
0 US-09-864-761-21539
US-10-024-4-60-3
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US-09-899-046-193
US-09-878-291-193
US-09-864-761-24263
US-09-864-761-7558
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                                                                                                                                                                          1029858 seqs, 724030393 residues
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                                                                                             US-09-826-581-3_COPY_612_672
                                                                                                                                                                                                                                                                                    Published_Applications_NA:*
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Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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GENERAL INFORMATION:
APPLICANT: Andersson, Leif
APPLICANT: Andersson, Leif
APPLICANT: Andersson, Leif
APPLICANT: Andersson, Leifman, L. Hollger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 E
FILE REPERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                  Sequence 1, Appli
Sequence 1, Appli
Sequence 10204, A
Sequence 10204, A
Sequence 1796, Ap
Sequence 1795, Ap
Sequence 1, Appli
Sequence 213, App
Sequence 213, App
Sequence 218, App
Sequence 1487, Ap
Sequence 1489, Ap
Sequence 1489, Ap
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 28, Appl
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Sequence 28, Appl
Sequence 218, Appl
Sequence 30, Appl
Sequence 30, Appl
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Sequence 1596. Application US/20030054375A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
9 US-10-223-085-33

9 US-10-223-084-33

9 US-10-223-090-33

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9 US-10-223-090-33

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9 US-10-077-14.1

9 US-00-144-191-5477

9 US-09-764-891-15024

9 US-09-784-891-15024

9 US-09-784-891-10204

10 US-09-784-86-1795

10 US-09-784-65-1795

10 US-09-784-65-1795

11 US-10-171-581-213

12 US-10-144-090-210

13 US-09-764-868-1489

14 US-09-764-868-1489

15 US-09-96-96-973-114

16 US-09-96-973-114

17 US-09-96-973-114

18 US-09-96-973-114

19 US-09-96-973-114

10 US-09-96-973-114

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Pred. No. 1.8e-12;
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100.0%; Score 61; DE
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 61; Conservative 0; Mismatches
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US-09-826-581-3
   672
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US-10-092-154-1596
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                                                                                                                                                                                                                                           Score 25.2; DB 10; Length 1030;
Pred. No. 5.3;
0; Mismatches 18; Indels 0;
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4.7;
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Patent No. US20020132767A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper, NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009c1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.3%; Score 25.2; DB 10;
66.7%; Pred. No. 4.7;
tive 0; Mismatches 18;
                                                                  NAME/KEY: misc_feature

| DCATION: (1006)

| DCATION: (1006)

| NAME/KEY: misc_feature

| LOCATION: (1023)

| OTHER INFORMATION: n equals a,t,g, or c

| USC-09-925-301-334
                         LOCATION: (989)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1153, Application US/10092154; Publication No. US20030054375A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                  41.3%;
66.7%;
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Best Local Similarity 66.7;
Matches 36; Conservative
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Matches 36; Conservative
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Best Local Similarity 66.7<sup>3</sup>
Matches 36; Conservative
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US-10-092-154-1153
         NAME/KEY: misc_feature
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US-10-092-154-1153/c
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US-09-764-847-1153/c
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                                                                                                                                                                                                                                                                42.6%; Score 26; DB 9; Length 17761; 65.5%; Pred. No. 2.3;
Live 0; Mismatches 20; Indels C
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPRESENCE: PA106
FURENT APPLICATION NUCLER: US/09/925,301
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR PPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1664
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 334
LENGTH: 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION NUMBER: US/09/764,847
CURRENT APPLICATION NUMBER: US/09/764,847
Prior application dare: 2001-07
Prior application dare: removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SEQ ID NO 1596
LENGTH: 17761
FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SCPTWARE: Patentin Ver. 2.0
SEQ ID NO 1596
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LOCATION: (59)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1596, Application US/09764847 Patent No. US20020132767A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 334, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                         Best Local Similarity 65.5
Matches 38; Conservative
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nes 38; Conservative
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US-09-764-847-1596
                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-092-154-1596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                      LENGTH: 17761
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APPLICANT: Olga Bandhan
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILLE REPERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
ESEQ ID NO 338
LENGTH: 1847
                                                                                                                                                                                                                         Sequence 30, Application US/09964899
Patent No. US2002174446a1
GENERAL INFORMATION:
I TITLE OF INVENTION: Identification of Genes Involved in
ITILE OF INVENTION: Alzhaimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-31512 A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 05/2964,899
PRIOR FILING DATE: 2000-09-29
PRIOR RILING DATE: 2000-06-29
PRIOR RILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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                        ;
0
                                                                      Query Match 41.0%; Score 25; DB 12; Length 1847; Best Local Similarity 64.9%; Pred. No. 6; Matches 37; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 41.0%; Score 25; DB 9; Length 1351; Best Local Similarity 64.9%; Pred. No. 6.2; Matches 37; Conservative 0; Mismatches 20; Indels
                          Indels
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; OTHER INFORMATION: Incyte ID No. US20020137081A1 344297.3
US-10-044-090-338
  Best Local Similarity 69.4%; Pred. No. 6.6;
Matches 34; Conservative 0; Mismatches
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; Patent No. US20020137081A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo Sapien
US-09-964-899-30
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US-09-864-761-4800
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US-09-964-899-30
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LENGTH: 1351
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1855 GAGGGGACAGAGCTAGGAGAAGGGAGGGAAGGGCAGGGGAGGGGTGCAGGGG 1802
                                                                                                                                          GENERAL INCORMATION:
GENERAL INFORMATION:
APPLICANT: Horne, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-WO:
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILLING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/231,379
PRIOR PLILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PREFERENT
SEQ ID NO 2925
LENGTH: 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Genbank Accession No. US20020142981A1 R62519

NAME/KEY: unsure

LOCATION: (1).(275)

; OTHER INFORMATION: n = a or c or g or t

US-09-880-107-2925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/10144929;
Publication No. US20030069405A1;
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 70 Human Secreted Proteins:
FILE REFERENCE: P2014P1;
CURRENT FILING DATE: 2002-05-15;
PRIOR APPLICATION NUMBER: US/10/144,929
CURRENT FILING DATE: 1999-02-17;
PRIOR APPLICATION NUMBER: US/09/251,329
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: PCT/US98/17044
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                                                                                                               ; Sequence 2925, Application US/09880107
; Patent No. US20020142981A1
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OTHER INFORMATION: n equals a,t,9,
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; OTHER INFORMATION: n equals a,t,g,
US-10-144-929-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 257
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-144-929-25/c
                                                                                    -09-880-107-2925
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LENGTH: 541
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Renk, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TILLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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N: EXPRESSED IN BT474, SIGNAL - 1.4
N: EXPRESSED IN BONE MARROW, SIGNAL - 1.1
N: EXPRESSED IN LUNG, SIGNAL - 2.6
N: EXPRESSED IN PLACEWIA, SIGNAL - 1.8
N: EXPRESSED IN PLACEWIA, SIGNAL - 0.98
N: NT HIT: 9111423021, EVALUE 0.00e+00
N: NT HIT: 951116, EVALUE 1.00e-09
N: EST_HUMAN HIT: BE885438.1, EVALUE 0.00e+00
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
LENGIH: 2837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24.8; DB 10;
Pred. No. 6.9;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-02-04
PRIOR PELICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04 2456.5
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR PRIOR DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/USO1/00662 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/USO1/00661 PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                      Sequence 21539, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAP TO AL031277.1
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67.3%;
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Best Local Similarity 67.33
Matches 35; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITTLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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OTHER INFORMATION: MAP TO AL031277.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BUNE, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.98
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                                                                                                                                                                                                                                                          FILE OF A TWARALDAY. GENE DATACASION ANALISIS CURRENT APPLICATION WEBER: US/09/864,761 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT APPLICATION NUMBER: US 60/180,312 PRIOR PRICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-27 PRIOR PRICATION NUMBER: US 60/236,359 PRIOR FILING DATE: 2000-09-27 PRIOR PRILING DATE: 2000-09-27 PRIOR PRILING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30 PRIOR PRILING DATE: 2001-01-30 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-20 PRIOR FILING DATE: 2
                                                            APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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                                                                                                                                                                             Chen, Wensheng
Patent No. US20020048763A1
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ORGANISM: Homo sapiens
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RESULT 12

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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: New sequences of hepatitis C virus
TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                          Gaps
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0
                                          Score 24.6; DB 9; Length 498;
Pred. No. 9.1;
0; Mismatches 14; Indels
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                                                                                                                                                                340 GCCGGGGATCATTTGGGCCCCAAGATGGCCGAGGAGCCGCGAGGAGAC 294
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SOFTWARE: Petentin Release #1.0, Version #1.25 (EPO)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/878,281
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
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                                                                                                                                                                                                                                                                   ; Sequence 193, Application US/09878281
; Publication No. US20030032005A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                        40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.3%;
70.2%;
                                        Query Match
Best Local Similarity 70.2%
Matches 33; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                           RESULT 15
US-09-878-281-193/c
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LOCATION:
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US-09-878-281-193
    US-09-899-046-193
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                                                                       RESULT 13
US-10-024-450-3/C
Sequence 3, Application US/10024450
; Sequence 3, Application US/2003032606A1
; GENERAL INFORMATION:
    APPLICANT: Huang, Shi
    APPLICANT: Chadwick, Robert B.
    TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ
    TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ
    TITLE OF INVENTION: MUSER: US/10/024,450
    CURRENT APPLICATION NUMBER: US 60/256,582
    PRIOR APPLICATION NUMBER: US 60/256,582
    PRIOR PILLING DATE: 2000-12-17
    PRIOR FILLING DATE: 2000-12-19
    NUMBER OF SEQ ID NOS: 15
    SOFTWARE: FastSEQ for Windows Version 4.0
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Score 24.8; DB 9; Length 5868;
Pred. No. 6.5;
0; Mismatches 17; Indels 0
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APPLICATION NUMBER: US/09/899,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: New sequences of TITLE OF INVENTION: genotypes for di NUMBER OF SEQUENCES: 270 COMPUTER READABLE FORM: MEDLUM TYPE: FLOSPY disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 193, Application US/09899046
Publication No. US20030008274A1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 40.7%;
Best Local Similarity 67.3%;
Matches 35; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; LOCATION: (121)...(5277)
US-10-024-450-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
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LENGTH: 5868
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is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AX281582 Sequence AJ249977 Homo sapi AX099802 Sequence AX09976 Sequence AX09976 Sequence AX398333 Sequence AX398335 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX398337 Sequence AX09974 Sequence AX09974 Sequence AX09974 Homo sapi BC000588 Homo sapi AX364914 Sequence AR040588 Homo sapi AX364914 Sequence AR040588 Homo sapi BC00038 Homo sapi AX364914 Sequence AR087875 Homo sapi AX364914 Sequence AR087875 Homo sapi AX364916 Homo sapi AX364916 Homo sapi AX364916 Homo sapi AX364916 Homo sapi		bp DNA linear PAT 02-NOV-2001 305. Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo. Marklund, S.
SUMMARIES ID	AX281582 HSA249977 AX09802 AX09802 AX098004 AX09804 AX398333 AX398331 AX398331 AX398331 AX398335 AX398335 AX398335 AX398335 AX398335 AX398335 AX398335 AX398335 AX398319 AX099774 RNAPKGAM RNAPKGAM AX398337 AX398319 AX19819 AX195580 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX139104 AX1391	AF094764 AF084138 AY084138 AY084138 AY084138 AY0871581 AC1241521 AC129703 AC129703 AC129703 AC127107 AC127107 AC128070	1647 ) WO01777 )  Ordata; imates; amp-act; 18-OCT;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                   protein
              Location/Qualifiers
                                                                                                     /note="unnamed
                                                                                                                       /codon_start=1
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SSER RGKRRAKALWATROKSVEGEPPOGGSCOPRAPATES
DPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELAFEPPATEAWECELEGILEERPALC
LSPQAPPEPKLGWDCLLFSDCTASAAGSSTDDVELAFEPATEAWECELEGILEERPALC
LSPQAPPEKLGWDCLFSTROKATYMERTEBETFOYDAMATSKLYTFDYMLEIKKAFFA
LVANGVRAAPLWDSKRGFWGMLTITDFILVLHRYRSPLVQTYTEIGHKIETWREIY
LQGCFKPLVSISPNDSLFRAVYTLIKNRI HRLPVLDPVSGWVLHTTHRRLLFFEHIF
GSLLEPREFCTKTLQDIGTGFRRLAVYTLIKNRI HRLPVLDPVSGWVLHTTHRRLFKFHIF
GSLLEPREFCTKTLQDIGTGFRRLAVYTLIKNRI HRLPVLDPVSGWVLHTTHRRLFKFHIF
GYNFRYADFTQHLLGVVSGALRKFTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVATVDFTQHLLGVVSLSVGALRKFTLCLEGVLSCQPHESLGEVIDRIARE
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                                                              Vertebrata; Buteleostomi;
i; Hominidae; Homo.
  3 subunit
                                                                                     1 (bases 1 100 2090)
Cheung, P.C., Sall, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding Biochem. J. 346 pt 3, 659-669 (2000)
20164049
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Carling,D.
Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress Gro
Clinical Sciences Centre, Hammersmith Hospital, DuCane
London, W12 ONN, UNITED KINGDOM
  3 gene; gamma
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Catarrhini;
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/evidence-experimental
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1111111 501 TCCTCAN 501 TCCTCAN 502 TCCTCAN 561 CTTCAN AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX099802 AX0998	da da	\$ 6	2 6 a	Q.	dg dg	₹ da	λό a	δ ₀ q ₀	λο α <u>α</u> 	λο q _α	& 8 ———	Q G	vo da	& 43 ————————————————————————————————————	Z G	ÅÖ qa	y g	A G	Qy.
		TCCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAATGAAGGGAACTGGAGAACTCAGC 156 [	CTICATCTTCCCCCACCCCCATTGCTGGTTCACTATGATTCAGGTAGGCTCTGCC 161	AX099802 2115 bp DNA linear PAT 02-APR-20	Sequence AX099802 AX099802.	numan. 1 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	I (Dases 1 to 2115) Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Tannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.	Variation of the gamma chain of ampk, and sequences encoding to same, and uses thereng 2 22-MAR-2001;  AL Patent: WO 01200003-A 29 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);	Andersson, Lell (SE) ; LOOIL, Christian (DE) ; Kaim, Ernst (D Location/Qualifiers rce 1. 115 /organism="Homo sapiens"		/pucern_xa- /db_xref=61:13538837* /translation="MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG PEPPGGGEORGRERGRYTPERTTPLASSGLEAPPEGARAGESAAG GENDAVET WITH TRANSFOLEMT PER TENDAVE OF COMMENTED FOR THE ACCOUNTY OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMANCE OF THE PERFORMA	SOLDAMATOSEKI, PETERMECEEĞÜLEBEREKENELDEKREKANDEKU, IRM RPMQEHTCYDAMATOSEKI, PITTIFITMELETEKREFELIYANGYRAAPLUMOSK KOSTOKULTI TDFT LUVLHRYYRSPI,VQ IYB I EQHK I ETWIKB I YLQGCFK PLVST SPNDSLFEAVYTLI KNRI BRIZVI LIDPYSCONVI, BI I, TÜRKELİK İ, BI YEĞELLINBESETI, YRT I DÖLGÜLGÜTERBIL ANTI BRIZVI TAPATOT EVIDBEKANDEKI, KOSTOKULTA A KORTOKULTA A KORTOKULTANDEK	OUNT 460 8	88.2%; Score 1453; DB 6; Length 2115; illarity 97.3%; Pred. No. 0; Conservative 0; Mismatches 35; Indels 7; Gaps	GAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 15	TCAGARAGATCCGGGGAAACGGGGGGCCAAAGCCTTGGGGGAGGGGGGGG	CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CONTRACTOR   CON	TCCACCGGGTGGAGGCCACATTCCCCAAGACCACACTTGGCTCAAGCTGATCCTGCC  TCCACCGGGGTGGAGGCCACATTCCCCAAGACCACACTTGGCTCAAGCTGATCCTGCC  TTTTTTTTTT	TCCACCGGGCTGGAGGCCACATTCCCCAAGACCACACCTTGGCTCAAGCTGATCCTGCC 24

Query Match Best Local Similarity 97.3%; Pred. No. 0; Matches 1501; Conservative 0; Mismatches 35; Indels 7; Gaps 2; Qy 95 ATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCATGACCAGCTGTGACCAGCTGTGACCAGC 154				QY 335 GGGGTGGCACTCCACCAACAGGGTGGGACTGCCTCTGTGTACAGGCTCAGCT 394	QY 395 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCCCAGCCACAGAGGCTGG 454	QY         455         GAGIGIGACTAQAAGGCCTGCTGGAAGAGAGCCTGCCCTGTGCCTGTCCCCGCAGGCC         514           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 515 CCATTTCCCAAGCTGGGCTGGGAACTGCGGAAACCCGGCGCCCAGATCTACATG 574	QY 575 CGCTTCATGCAGCACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTCATC 634	QY 635 TTGGACATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCGACGGTGGGG 694	QY 695 GCAGCCCTCTATGGGACAGCAAGAGAGAGAGTTTGTGGGGATGCTGACCATCACTGAC 754	QY 755 TTCATCCTGGTGCATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAA 814	Qy 815 CAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCGAGGCTGCTTCAAGCTCTGGTC 874	QY 875 TCCATCTCTCTATGATAGCTGTTTGAAGCTGTCTACACCCTCATCAAGACCGGATC 934	QY 935 CATCGCCTGCTTGTCTTGACCGGGTGTCAGGCAACGTACTCCACATCAAA 994	QY 995 GGCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTCCCGGCCCTCCTTCCT	QY 1055 CGCACTATCCAAGATTTGGGCATCGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACA 1114
1321 GGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCTGCTGGCATCGAT 1380  QY	OY 1535 CAATGAAGGAACTGGAGAACTCAGCTTCATCTTCCCCCACCCCATTGCTGGTTCAG 1594	Qy 1595 CTATGATTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGCCT 1637 	RESULT 4 AF214519 LOCUS AF214519 DEFINITION Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)	ACCESSION AF214519 VERSION AF214519.1 GI:8215681 KEYNORDS HOMO Sablens	ORGANISM Homo sapiens  DEMATYOLA: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.	TITLE A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle skeletal muscle Selece 288 (5469), 1248-1251 (2000) MEDIANE 20280150		enetics, Sw Uppsala 751	Sweden Location/Qualifiers source 12115 //rdanism="Homo sapiens"	/db_xref="taxon:9606" /chromosome="2". /map="2p" /tissue type="skeletal muscle"	gene 12115 /gene="PRKAG3" CDS 11395 //cons="PDFSAG3"	/ote="AMPKG3" /codon_start=1 /product="AMPC3" /product="AMPC3987.1"	/db_xref="d1:8215682" /translation="%SSWPSSWPSPAVTSSSERIRGKRAKALRWTRQKSVEEG EPPGGGEGPRSRPTAFLAGENSSWPSPATGPTPGWPTPTPGMCPPGWPGGEGGRGPRSFAGGEGFRFFTTPLAGGDPAGVGFPFGWPTSPCAGATVW SCMDDVRLATREPAFAWFAWFFKFITIFFPATGCFRFFT	REMOEHTCYDAMATSSKLYIFDTMLEIKKARFBALVANGYRAARLINGKKOSFOSHITI TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSKROSFOSHITI KNRIHRELVLDPVSOSNYLHILTHRELKRLHIFGSSLLERPSERLKRIDGDGGIGFRED. AVVI.FFAADITGAALTIFVRONGALDVANGACOONGG	GRALROFTICLEGYISCOPHESIGEVIDRIAREQYHRIVLYDETQHLIGYVSLSDILQ ALVISPAGIDALGA"  BASE COUNT 460 a 622 c 562 g 471 t ORIGIN

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ORIGIN  Query Match  Best Local Similarity 97.3%; Score 1447; DB 6; Length 2109;  Best Local Similarity 97.3%; Pred. No. 0;  Matches 1495; Conservative 0; Mismatches 35; Indels 7; Gaps 2;  Qy 101 TTCCTAGAGGAAAACAGCAGCTCATGGCCATCACCAGTGTGACCAGCAGCTCAGAA 160	61 AGANTCCTGGGAAACGCAGGGGAAGCCTTGACTCGACAGGCAGAAGTCGGTCG	Db	58 42 58 48	QY         581 ATGCAGGGCACGCTGCTACGATGCCATGCCAAGCTAGTCATCTTCGAC 640           1	Db   601   CTCTATGGGAAGAAGAAGCAGAGGGTTTGTGGGGATGCTGACCATCATGATTCTTC   600	### ##################################	Qy         941 CTGCCTGTTCTGACCCGGTGTCAGGCAACGTACTCCACACACA
09   1115   GCACCCATCCTGACTCCTTTTTTTGTGGACCGGGGTGTCTCTGCACTCCTGTG   1174   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   1111   11	Qy         1295 CTATGTCTGGAGGAGTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGGGAACTGATCGAC 1354           Db         1201 CTATGTCTGGAGGAGTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGGGAAGTGATCGAC 1260           Oy         1355 AGGATTGCTCGGGAGCTACACAGGCTGGTGCTAGTGGACGACACCAGCATCTCTTG 1414           Db         1261 AGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGACACCAGCATCTCTTG 1414           Db         1261 AGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGCACCCAGCATCTCTTG 1320	QY         1415 GGGGGGGGTCCTCCCTCCGACATCCTTCAGGCACTGGTGCTCAGCCTGCTGGGCATCGAT 1474           Db         1131 GGCGTGGTCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCTGGTGGATCGAT 1380           QY         1475 GCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACTGCACACTGGAAGC 1534           Db         1381 GCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCAACTGCACACTGGAAGC 1439           Ov         1535 CAATGAAGGGAACTGGAGAACTCAGCCTCCATCCACCTCCAACCCCCATTGCTGGTTCAG 1594	1440 1595 1494	AXO99776 AXO99776 2109 bp DNA linear PAT 02-APR-2001 LOCUS LOCUS Sequence 3 from Patent W00120003. AXO99776 ACCESSION AXO99776.1 GI:13538810 VERSION AXO997776.1 GI:13538810 VERSION AXO997776.1 GI:13538810 VERSION AXO997776.1 GI:13538810 VERSION AXO	e; e;	99	/note="unnamed protein product" /codon_start=1 /podon_start=1 /protein_id="CAC35799.1" /db_xref="G1:13538811" /db_xref="G1:13538811" /drasslation="MRFMQEHTCYDAMATSSKIVIFDFMLEIKKAFFALVANGVRAAP LWDSKKOSFVGMLTIPPILVLHRYRSPLVQIYIEIDQHKIETYLGGFKPLVS ISPNDSLFRAAVTLIKNIHTHLPVLDPVGSNVLHILTHKELLFEFLLFRESLLPREFEL YRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRYSALPVVNGCGQVVGLYSRFDVI HLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDE TQHLLGVVSLSDILQALVLSFAGIDALGA TQHLLGVVSLSDILQALVLSFAGIDALGA  458 a 621 c 560 g 470 t

QY 113 GAAAACAGCAGCTCATGGCCATCACGGCTG 	Qy 173 AAACGGAGGCCAAAGCCTTGAGATGGACAA	Qy 233 CCAGGTCAGGGGGAAGGTCCCCGGTCCAGGC	293 349	Qy 350 CCAACAGGGTGGGACTGCCCTCTGACT ¹ 	Qy 410 GATGATGTGGAGCCAGGGAGTTCCCAGG	9y 470 GGCCTGCTGGAAGAGAGGCCTGCCCTGTGCC 	Qy 530 GGCTGGGATGACGAACTGCGGAAACCGGGGG	Ay 590 CACACCTGCTAGGATGCCATGGCAACTAGCT		0y 710 GACAGCAAGAAGAGCTITGIGGGGAIGC 	Qy 770 CATGGTACTACAGGTCCCCCTGGTCCAGA	830	Oy 890 GATAGCCTGTTGAAGCTGTCTACACCCTCA 	П	1 1	Qy 1070 TTGGGCATCGGCACATTCCGAGACTTGGCTG'	Qy
1121 ATCCTGACTGCACTGGACATCTTTGTGGACGGCGTGTGTCTGCACTGCCTGTGGTCAAC 1180	GAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCCAG	1241 CAAACCTACAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGGACACTATGT 1300	1301 CTGGAGGAGTCCTTTCCTGCCAGCCCACGAGAGCTTGGGGGAAGTGATCGACGATT 1360	1361 GCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTCTTGGGCGTG 1420	1421 GTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGGTGGCATCGATGCCCTC 1480	1481 GGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCTGCACCCTGGAAGCCAATGA 1540 	1541 AGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCACCCCCATTGCTGGTTCAGCTATGA 1600 1440 AGGAATGAAA	TTCAGGTAGGCTCTGCCCTGGCCATGACACCAGCCT 1637		AX099804 N Sequence 31 AX099804		Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. I (bases I to 2022) Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,	<pre>royer'sdailard, c., tannucceill, N., Gellin, J., le Koy, P. and Chardon, P. Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof</pre>	Patent: INSTITUT Andersso		Query Match 71.2%; Score 1172.8; DB 6; Length 2022; Best Local Similarity 85.7%; Pred. No. 9.4e-260; Matches 1351; Conservative 0; Mismatches 217; Indels 8; Gaps 4;	GGATGAGCTTCCTAGAGCAA 11 
λο A	Oy Dp	ζζ O	çy Db	Qy	Qy Dp	QY	QY	Qy	RESULT 6	LOCUS DEFINITION ACCESSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL	SOUTCE BASE COUNT ORIGIN	Query Best Match	Qy Qq

CCCTCCTTCCTCTACCGCACTATCCAAGAT 1069 1129 1185 TCTGCACTGCCTGTGGTCAACGAATGTGGT 1189 649 ATCCTCACACACACGCCTGCTCAAGTTC 1009 1190 CAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCCAGCAACCTAC 1249 292 PGTGACCAGCAGCTCAGAAAGAATCCGTGGG 172 945 949 232 GCTGATCC -- TGCCGGGGTGGGCACTCCA 349 TGTACAGCCTCAGCTGCAGGCTCCAGCACA 409 525 529 585 589 645 GCCAACGGTGTGCGGGCAGCCCCTCTATGG 709 CTGACCATCACTGACTTCATCCTGGTGCTG 769 825 829 885 889 GCCACAGAGGCCTGGGAGTGTGAGCTAGAA 469 CTGTCCCCGCAGGCCCCATTTCCCAAGCTG TTCAAGCCTCTGGTCTCCATCTCTCCCAAT GTGGTGCTGGAAACGCCGCCCATCCTGACC AGGCAGAAGTCGGTGGAGGAAGGGGAGCCA CCAGCTGCTGAGTCCACCGGGCTGGAGGCC GCCCAGATCTACATGCGCTTCATGCAGGAG TCCAAGCTAGTCATCTTCGACACCATGCTG ATCAAGAACCGGATCCATCGCCTGCCTGTT GTGGTGCTGGAGACAGCACCCATCCTGACT TTCAAGCCTCTGGTCTCCATCTCTCTAAT ŏ

1346   CARGADACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTECTACONTEC	95 AIGAGCITCCTAGAGCAAGAAAACAGCAGCTCAIGGCCAICACCAGCAGC 154	TOGADAGATCCGTGGGAAACGGGGCCAAGCCTTGAGATGGACAGAGCGGACGTCG	ACCATGGGGACCAGGGACTAGAGGCTTTAGATGGAGAGGGAGG	121 GTAGAGGGGGCCTCCGGGCCCGAGGGAGGTCCCCAGTCCAGCCAG	181 TCCACCGGGCAGGAGGCCACATTCCCCAAGGCCACACCTTGGCCCAAGCCGCTCCCTTG 240	GCCGAGGTGGACAACCCCCCAACAGGGGGGACATCCTCCCCTCTGACTGTGACCCTCAACAGCGGGACATCCTCCCCTCTGACTGTGACGCGGGACATCCTCCCCTCTGACTGTGACGCGGGACACCTCTCCCTCTGACTGTGACGCGGACACCTCTCTCT	372 GUIGGAGGULLCAGUGAGAIGAIGAIGAGGUGGUGGUGAGAGAILLUCAGCUAGAGAGACA 33.	452 IGGGAGIGIGAGCIAGAAGGCCIGGAAGAGGCCIGCCCIGIGCCIGICCCCGCAG 511	512 GCCCATTTCCCAAGCTGGGCTGGGAATGACGAACTGCGGAAACCCGGCGCCCAGATCTAC 571	ATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTAG	632 APCTICGACACCARGCIGGAGATCAAGAAGGCCTICTITGCICTGGIGGCCAACGGTGIG 691 1	692 CGGCCAGCCCTCTATGGGACAGCAAGAAGCAGAGCTTGTGGGGATGCTGACCATCACT 751	752 GACTTCATCTGGTGCTGCATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATT 811	GAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCCTG	GICTCCATCTCCTAATAAAAAACTGTTTGAAGCTCTAACCCTCATCAAAAACCGGGTTCTAACAACCTCATCAAAAACCGGGTTCTCAACAACAACCTATCAACAAACTGTTCAAAAAACCGATCAACAAAAAAAA	932 ATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACAC 991	992 AAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCTGCTGCCCGGCCCTCCTTCCT	1052 TACCGCACTATCCAAGATTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGGGGG 1111	1112 ACAGCACCCTGACTGCACTGGACATCTTTGTGGACCGGGGTGTGTGT
246 CAGGTAGTGGGCCTCTACTCTGGTTGATGGGATCGCTGGGTGGCTGGC	60%	oy (	ga čo	da vo	qa "o	qa (	A 42	Qy	ζζ	oy oy	QV	QV Op	δ f	oy E	à VÕ	Qy Dp	QY	Qy	
그 그 그 그 그 그 그 그 그 그 그 그 그 그 그 그 그 그 그	CAGGTAGTGGGCCTCTACTCTCGCTTTGATGTGATCCACCTGGCTGCCCAACAACATACAAACAA	AACCACCTGGACATGAATGTGGGAGAAGCCTGAGGCAGCAGCGGACACTGTGTCTGGAAGGC	GTCCTTTCCTGCCAGCCCCACGACAGCTTGGGGGAAGTGATCGACAGATTGCTCGGGAGGGGGGAGTTTTTTTT	CAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTCTTGGGCGTGGTCTCCCTC	TCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGGTGGCATGCAT	GAAGATCTGAGTCCTCAAGCCACCTCCTGCAAGCCATGAGGGGAACTCTTGAGTCCCTCGAGGGAACTCTTGAGAGGCAATGAAGGGAACTCTTGAGAAGCCAATGAAGGGAACTCTTTTTTTT	GGGGAACTTGGGAACTTGCCCCCACCACACACACACTGGAAGCCAGGGAACCAGGAACCAGGAACTCAGGTATGAATTGCTGGTTCAGGTATGATTGAAGAACAGGAAACAGAAAAAAAA	GETGRACTCRACTCRACTCCCTCACTTGCTGTCTGGCTCTTGTTGTTGTGGGTAGGGTAGGGTAGGGGTAGGGGGGGG		AX398333 1873 bp DNA linear PAT 27-MAY Sequence 3 from Patent WO0220850.		í Sus scrota Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1	Rothschild, M.F., Clobanu, D.C., Malek, M. and Plastow, G. Novel prkag3 alleles and use of the same as genetic markers reproductive and mant quality traits.	Iowa State University Research Foundation, Inc. (U Location/Qualifiers 1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.1871   1.18				AVVLETABILYALDIEVDRKVSALEVVRETGQVGLYSRFT GEALEVRETCLEGVLSCQPHETLGEVIDRIVREQVHRILVLV ALVLSPAGIDAGA" OUNT 381 a 581 c 535 9 376 t	y Match 69.3%; Score 1142; DB 6; Length 1873; Local Similarity 85.8%; Pred. No. 1.2e-252; hes 1316; Conservative 0; Mismatches 210; Indels 8; Gaps

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HFWGEHTCYDAMATSSKIVIFDTMLETKRAFFALVANGVRAAPLWDSKKQSFVGMLTI
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GBALRQRFTCLEGVLEGCTBETLGEVIDRIVKREQVHRLVTLVDETQHLLGGVVSLSDIIQ
ALVLLSPAGIDALGA*
375 g 375 f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGAAAGAAGCCATGGGGAACCAGGGGAACAAGGCCTCTAGATGGACAAGGCAGGAGGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCCCAGCCACAGAGGCC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 GIGCIGITACCCAGGCIGGGCIGGGAIGAIGAGCIGCAGAAGCCGGGGCCCAGGICIAC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           572 ATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTC 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTICATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCCAGATCTATGAGATT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGAAAGAATCCGTGGGAAACGGAGGCCCAAAGCCTTGAGATGGACAAGGCAGAAGTCG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    632 ATCTICGACACCAIGCIGGAGAICAAGAAGGCCTICTITGCICIGGIGGCCAACGGIGIG 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGCAGCCCCTCTATGGGACAGCAAAGCAGAGCTTTGTGGGGGATGCTGACCATCACT 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAGCTTCCTAGAGGAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                          TCCACCGGGCTGGAGGCCACATTCCCCAAGACCACACCCTTGGCTCAAGCTGATCC---T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGGCCCTGCCCTGTGCCTGTCCCCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTICATCITGGIGCTGCACCGCTATTACAGGICCCCCTGGICCAGATCTACGAGAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGAGGAAGGGGAGCCAGGTCAGGGGGAAGGTCCCCGGTCCAGGCCAGCTGCTGAG
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                              Score 1140.4; DB 4; Length 1873;
Pred. No. 2.8e-252;
0; Mismatches 211; Indels 8;
                                                                                                                                                                                                                                                                                                                              69.2%;
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 85.7 Matches 1315; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1496
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skeletal muscle
Science 288 (5469), 1248-1251 (2000)
20280150
                                                                                                                                               1351
                                                                                                                                                                                                                                                                                          1471
GEGGECAACGAAFGEGGECAGGECGECTCTATTCCCGCTTTGATGTGATTCACCTG 1231
                                    GTGGTCAACGAAACTGGACAGGTAGTGGGCCTCTACTCTCGCTTTGATGTGATCCACCTG 1137
                                                                                          1352 GACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTC 1411
                                                                                                                                                                                                                                                                                                           1318 CIGGGCGTGGTGCCCTCTCTGACATCCTTCAGGCTCTGGGGCCTCAGCCCTGCTGGAATT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                       1531 AAGCCAATGAAGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCACCCCATTTGCTGGT 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia: Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 1873)
Milan, D. Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Lannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger.V., Robic,A.,
Milan,D., Jeon,J.T., Looft,C., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
                                                                                                                                                                   ACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGGCCCCCAGGAGGCTTGGGGGGAAGTGATC
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                                                                                                                                                                                                                                                                                          1412 TTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATC
                                                                          GCTGCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGGAGAAGCCCTGAGGCAGAGG
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/chromosome="15"
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DSNPDHLDGLGPGPREVABASGDELGLVEEKPAPCPSFEVLLPRLGWDDELQRFGAQVYM
HPWQEHTCYDAMFSSKLVIFDPMLEIKKAFPALVARGVRAAPLMOSKROSFVSHVII
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KNRA HRLEVLDBYGSRALHILTHRKLLKEHTGTILLBRSFLKTRI COLOGIGTREDL
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/db_xref="G1:13538835"

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Manmalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1873)
Andersson.L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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                                                                        ATCCATCGCCTGCTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAC
                                                                                                                              TACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAG
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JOURNAL Patent: WO 0220850-A 1 14-MAR-2002;  IOWA State University Research Foundation, Inc. (US)  Location/Qualifiers  11873  CDS   .1873  CDS   .1873  CDS   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD   .1874  COD	382	### 1140.4;  ###################################	QY         155 TCAGAAAGAATCCGTGGGAAAGGCCAAAGCCTTGAGATGGAAAGGCAAAGTCG         214	QY         275 TCCACCGGGCTGGAGGCCACATTCCCCAAGACCACACTTGGCTCAAGCTGATCCT 331           b	392 GCFGCAGGCTCCAGCACAGATGATGAGCCTGGCCACGGAGTTCCCAGCCACAGAGGCC 1	DD   418 GFGCTGTACCCAGGCTGGGGTGAGCTGCAGGGGGGGCCCAGGTCTAC 477
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reproductive and meat quality traits  JOURNAL Patent: WO 0220850-A 5 14-MAR-2002;  Iowa State University Research Foundation, Inc. (US)  Location/Qualifiers  10.1873  CDS 11.1875  CDS 10.1875  COS 11.1875  COS 11.1875  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.1876  COS 11.	/db_xref="61:2126/111" /db_xref=="61:2126/111" /translation="MgFLEQGESRSWPSRAVITSSERSHGDGGNRASRWTRQEDVEEG GPPGPRESPRSRYASSTGGRATPFRAPPLAGAAPLARDVDRPFTEDILFSEDCASAS DSWTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLIPRLGWDELGKPGAQVYM HPROBEPCYDAATSSKLVTEDWLEIKRAFFRAPLDRGKRGSFTGMLT TDFILLVLHRYRSEPLVOIYEIEEHKIETWREIYLGGGFRPLVSISPNDSLFEAVYALI KNRIHRLPVLDPVSGANLHLITHRRLLKFLHIGGTLEPPSFLYRTIQDIGIGTRDL AVVLETAPITALDIFVDRRYSALPVNNETGGVVGIYSRPDVIHLAAQQTYNHLDMNV GBALRQRTLCLEGGVLSCQPHETLGEVIDRIVSREPGVHLVUDETQHLLGVVSLSDILD ALVLSPAGIDALGA	SE COUNT 38 IGIN Juery Match Best Local Simi Matches 1314; 6 95 ATG		392 GCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGTTCCCAGCCAG	QY         512 GCCCATTCCCAACTGGGTGAGATGACGAACCGGGGCCCAGATCTAC         571           Db         418 GTCCTGTGCGTGGGATGATGAGCTGCAGGGCCCAGGCCCAGGTTAC         477           QY         572 ATGCCTTCATGCAGGAGCCCTACCTACGATGCCATGCCA	QY 692 CGGGCAGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGGATGCTGACCT 751
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TITLE Novel prkag3 alleles and use of the same as genetic markers for reproductive and meet quality traits  JOURNAL Patent: WO 0220850-A 7 14-MAR-2002;  IOWA State University Research Foundation, Inc. (US)  LOCATION/Qualifiers  SOURCE (ADARTES SCROFA"  (ADARTES TAXON: 9823"  1. 1395  (ADARTES TAXON: 9823"  1. 1395  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADARTES TAXON: 9823"  (ADA	COURTY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUETY MATCH  OUET	95 ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCGC	Db		572 572 478 632 538 692 692
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Rothschild, M.F., Ciobanu, D.C., Malek, M. and Novel prkag3 alleles and use of the same as reproductive and meat quality traits Patent: WO 1020950-A 9 14-MAR-2002; Iowa State University Research Foundation, I Location/Qualifiers
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HLAAQQTYNHLDNWGEALRQRTLCLERVLSCQPHETLGEVIDRIVREGVHRLVLVDE
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                                                                   GAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG
                                                                                                                           GTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGG
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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/db_xref-"SWISS-PROT:P80385"
/translation="MESTABERAPERPERBERSOFTPERNSYTTEMKSHRCYDLIPTS
SKLVVPDTSLQVRKAFRALVTHOVRAARLWESKRGSFVRTTJDFINILHRYKKSAR
VQIYELEBHKIETWREVYLQDSFKPLVCISPNASLFDAVSSLIRNKIHRLPVIDPESG
WTXITLHTHKRILKFRKFFTEFPREPRENSKSLEELQIGTYANIAWWFTTPVYVARLGIFVQHRYSALPVVDREKGRVPTTSKFFDYINLAARKTYNLDVSYTKALQHRSHYBGVL
KCYLHFILEALINRILVBARVHRLVVVDEHDVVKGIVSLDLLQALLVJTGGBKRXP"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                          Submitted (07-FEB-1996) D. Carling, MRC Clinical Sciences Centre, Department of Molecular Medicine, RPMS, Hammersmith Hospital, DuCane Road, London, W12 ONN, UK
                                                                                             gamma
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                                                                                                        in vitro
                                                            Davison, M.D., Scott, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 1328;
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/db_xref="G1:1185271"
/db vref="G1:1185271"
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                                                                                          protein kinase
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64.9%; Pred. No. 5.4e-85;
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                                                         Woods, A., Cheung, P.C., Smith, F.C.,
Beri, R.K. and Carling, D.
Characterization of AMP-activated p
                                                                                                                                                                                                                                                                                            /strain="Wistar"
/db_xref="taxon:10116"
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Carling, D.
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R.norvegicus mRNA for gamma subunit of AMP-activated protein
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X95578.1 GI:1185270
AMP-activated protein kinase; gamma
Rattus norvegicus.
Rattus norvegicus.
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481	992	541	1052	601	1112	199	1172	721	1232	781	1292	841	1352	901	1412	961	
qq	Qy	Db	Qy	qα	Qy	οp	QY	Db	Qy	Db	Qy	qq	QY	Db	Qy	qa	

Search completed: June 13, 2003, 04:39:40 Job time: 5204.55 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	PRKAG3 CDNA HOMO	Human AMPK damma s	Human AMPK damma s	Sus scrofa PRKAG3	Pig PRKAG3 polymor	Pig AMPK gamma sub	Pig wild-type PRKA	Pig PRKAG3 polymor	Pig PRKAG3 polymor
SUMMARIES			ID	AAH43685	AAD03320	AAD03296	AAD03321	AAD36457	AAD03319	AAD36456	AAD36458	AAD36459
			DB	22	22	22	22	24	22	24	24	24
			Length	1647	2115	2109	2022	1873	1873	1873	1873	1873
	æ	Query	Score Match Length DB II	100.0	88.2	87.9	71,2	69.3	69.3	69.2	69.1	69.1
			Score	1647	1453	1447	1172.8	1142	1140.4	1140.4	1138.8	1138.8
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	10	1138.8	1.69	1873	24	AAD36460	Pig PRKAG3 polymor
	1;	1134.4 448 B	68.50	1867	22	AAD03295	Pig AMPK gamma sub
	13	407.2	24.7	989	22	AAH4369	Human AMP-activate
	14	393.4	23.9	1578	24	ABK84324	CDNA dif
	12	393.4	23.9	1691	21	AAC98774	Human pancreatic c
	17	367.2	22.3	1774	24.	AAT85927 ABL39755	Mammalian AMPK-gam
	18	366.6	22.3	1435	20	AAX06882	Disease associated
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	2 5	278.2	7.81	1014	2 5	ABL18857 AAH43684	Drosophila melanog
O	22	252	15.3	3425	75	AAK72740	FREAGS INTROD 10 -
Ü	23	252	15.3	3425	22	AAK72741	
	77	222	13.5	1467	23	AAS84265	DNA encoding novel
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	22	168.2	10.2	1722	3 6	AAH43683	Human colon cancer
	28	159.8	9.7	2303	23	AAS84267	DNA encoding novel
	53	144.6	8.8	926	24	ABN74716	Bovine embryonic q
	30	137.6	4.1	765	77	ABL89686	Human polynucleoti
	37	127.2	7.7	39651	53	ABL18856	Drosophila melanog
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	37	106.2	6.4	615	23	ABV39323	prostate
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¥C	AAE	AAH43685;					
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preferably a carbohydrate metabolism disorder. Frimers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 a
                                                                                                                                                                                                                                                  Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; strKKA3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                            Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA
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/product= "Human complete Prkag3 protein"
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                                                                 GGCCATGACACCAGCCTCTTAGTCTTC 1647
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..1395
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heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                        335 GGGGIGGGCACTCCACCAACAGGGIGGGACTGCCTCCCCTCTGACTGTACAGCCTCAGCT
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                                                                                                  Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
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                                                                                                                                   Score 1453;
Pred. No. 0;
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Matches 1495; Conservative
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18-MAY-2000; 2000EP-0401388.
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                                                             1115 GCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTG 1174
                                                                                                                                      1235 GCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGGACA 1294
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                                                                                                                                                                                                                                                                                                  CGCACTATCCAAGATTTGGGCATCGGCACTTCCGAGACTTGGCTGTGGTGCTGGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK criticionally altered mutants are useful for the diagnostic artivity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to asequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transpenic animal and host cell transformed with PRKAG3 or a chetectriment AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity, Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
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Pred. No. 0;
0; Mismatches 35; Indels
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                                                                                                                                                                                                                           Looft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
(INRG ) INRA INST NAT RECH AGRONOMIOUE.
(ANDE) ANDERSSON L.
(LOOF/) LOOFT C.
(KALM/) KALM E.
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The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMFK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting
                 AGGGAACTGGAGAACTCAGCCTTCATCTTCCCCCACCCCCATTTGCTGGTTCAGCTATGA 1600
                                 Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; preprint adentification; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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/product= "Sus scrofa Prkag3 splice variant"
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                                                                               TTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGCCT 1637
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L.
                                                                                                                                                                                                                                                                                                      Sus scrofa PRKAG3 splice variant DNA
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1..1545
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(ANDE/) ANDERSSON I
(LOOF/) LOOFT C.
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from the expression of a functionally altered allele of PRKAG3.
Transpente animal and host cell transformed with PRKAG3 or a
beterotrineric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PKKAG3 is useful for detecting mutations in a PrKag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
of PKKAG3 and is useful in gene therapy.
                                                                                                                                                                                      GGCCTGCTGGAAGAGGCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTG
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0; Mismatches
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85.7%;
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                                                                                                                                                                                      polymorphic variant (PRKAG3-30)*
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/standard_name= "Single nucleotide polymorphism (SNP)"
                      GCACTEGACATCTTCGTGGACCGGCGTGTCTGCGCTGCCTGTGGTCGAAACTGGA
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                                                                                                                                                                                                                                                                            Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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Pred. No. 5.6e-288;
0; Mismatches 210;
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85.8%;
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Matches 1316; Conservative
                                                                                                                                                                                                                                 2002-393850/42
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMFK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 gene is located required to carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its function gate metabolism servaluation, genetic testing and prognosis of a metabolic disorder. preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Pransgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                            PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rogel-Gaillard C;
                                                                                                                                           complete PRKAG3 cDNA.
                                                                                                                                                                             subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                            /product= "Sus scrofa complete Prkag3 protein"
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J, Le Roy P, Chardon P;
                                                                                                                                             subunit muscle-specific isoform,
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ANDE// ANDERSSON L.
LOOF// LOOFT C.
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                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                 AAD03319 standard; cDNA; 1873 BP
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Iannuccelli N, Gellin
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Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

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                                                                   ATGAGCTTCCTAGAGCAAGAGAGCCGTTCATGGCCATCCCGAGCTGTAACCACCAGC
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                         Gaps
  Length 1873;
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6
                        Indels
 22;
Score 1140.4; DB 2;
Pred, No. 1.5e-287;
0; Mismatches 211;
69.2%;
85.7%;
                     Matches 1315; Conservative
            Similarity
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                                                                                           ACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCAGGAGAGCTTGGGGGGAAGTGATC 1351
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/standard_name= "Single nucleotide polymorphism (SNP)"
                                       GCTGCCCAGCAAACCTACAACCACCTGGACATGAGTGTGGGGAGAAGCCCTGAGGCAGAGG
                                                                                                                        GACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGGACCCAGCATCTC
                                                                                                                                                       TTGGGCGTGGTCTCCCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATC
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                              GTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGGCTTTGATGTGATTCACCTG
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                                                                                                                                                               AMP activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Pig PRKAG3 wild-type protein"
replace (89, C)
                                                                                                                                                                                                                                                 1591 TCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCC 1624
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                                                                                                                                                                                                                                                                                                                                                  Pig wild-type PRKAG3 gene.
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                                                                                                                                                                                                                                                                                                           Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig wild-type PRRAG3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1140.4; DB 24; Length 1873; pred. No. 1.5e-287; 0; Mismatches 211; Indels 8; 0
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                                                                                                                                                                                                 Malek M, Plastow
                                                                                                                                                (IOWA ) UNIV IOWA STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Fig 1; 109pp; English.
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                                             2000US-231045P.
2001US-260239P.
2001US-299111P.
                                                                                                                                                                                              Ciobanu DC,
10-SEP-2001; 2001WO-US28283
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Matches 1315; Conservative
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                                                                                                                                                                                            Rothschild MF,
                                             08-JAN-2001; 208-JAN-2001; 218-JUN-2001;
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274 180 331

us-09-826-581-5.rng

polymorphic variant (PRKAG3-52)"

"Pig PRKAG3

replace (154, A) /*tag= b

Location/Qualifiers 1..1395

ø /product-

/*tag=

(first entry)

/standard_name= "Single nucleotide polymorphism (SNP)"

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AMP activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP; gene; variant; ds.
                                      Pig PRKAG3 polymorphic variant DNA (PRKAG3-52)
                                                                                                                                                                                                                                                                                                   (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                             08-SEP-2000; 2000US-231045P.
                                                                                                                                                                                                                                                                      08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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P-PSDB; AAE22986.
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AAD36458;
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ATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTG
            CGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCATCACT
                                                 GTCTCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGG
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                                                                              GACTICATCCIGGIGCIGCATCGTACTACTACAGGICCCCCCTGGICCAGAICTAIGAGAIT
                                                                                                                     GAACAACATAAGATTGAAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG
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Malek M, Plastow

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                                                                                                                                                                                                                        The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-22).
Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                  Claim 34; Page 93-95; 109pp; English.
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AAD36458 standard; DNA; 1873 BP

AAD36458 RESULT

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1258 GACCGGATTGTCCGGGAACAGGTGCACCGCCTGGTGCTCGTGGATGAGACCCGGGCCTT 1317
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                                         GATGCCCTCGGGGCCTGAGAACCTTGGAACCTTTGCTCTCAGGCCACCTGGCACCTCGG
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                                                                                  GATGCCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGCCACCT-GCACACCTGG
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                          TIGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCCATC
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                                  958 TACCGCACCATCCAAGATTTGGGCATCGGCACTTCCGAGACTTGGCCGTGGTGCTGGAA
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for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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                                                                                              Gaps
                                                                       Length 1873;
                                                                    69.1%; Score 1138.8; DB 24; Lengt
85.7%; Pred. No. 3.8e-287;
ive 0; Mismatches 212; Indels
                                              Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
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                                                                                                                                                                                                               The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic meterial obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
                                                                                                                           Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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Pred. No. 3.8e-287;
Trantches 212; Indels
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                                                               Plastow G;
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                                                                                                                                                                                           Disclosure; Page 102-104; 109pp;
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18-JUN-2001;
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The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as that as myopathy and cardiovascular diseases, to modulate metabolism activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain compounds and is useful in gene therapy.
                         Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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I, Le Roy P, Chardon P;
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ANDE/) ANDERSSON L.
LOOF/) LOOFT C.
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                                                     GACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCA
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            1 TTCCTAGAGCAAGGAGAGCCGTTCATGGCCATCCCGAGCTGTAACCACCTCGAGAA
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68.9%; Score 1134.4; DB 22; Length 1867; 85.7%; Pred. No. 5.4e-286; Live 0; Mismatches 211; Indels 8; (

Best Local Similarity 85.7 Matches 1309; Conservative

Query Match

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1297
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                                                                                                                                                                                                                                                                                                                                                                                                           1078 AACGAAACTGGACAGGTAGTGGGCCCTCTACTCTCGCTTTGATGTGATCCACCTGGCTGCC 1137
                                                                               1358 ATTGCTCGGGAGCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTCTTGGGC 1417
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                                                                                                                           TGTCTGGAGGGAGTCCTTTCCTGCCCAGCCCCAGGAGCTTGGGGGGAAGTGATCGACAGG 1357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                1198 TGTCTGGAAGGCGTCCTTTCCTGCCACCCCACAGAGACTTGGGGGGAAGTCATTGACCGG
                                                                                                                                                                                                                                                           GTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATGCC
AACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCC
                                                                CAGCAAACCTACAACCCTGGACATGAGTGTGGGGAGAAGCCCTGAGGCAGAGGACTA
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27-APR-2000; 2000US-0560875.
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have arrious activities; including optoxine cell proliferation activities; including optoxine cell proliferation activities; including optoxine cell proliferation activities; activit cativity; issue growth activity; hamantopolesis required activities; hamantopolesis required activities; nemetor or inhibin-related activities; chemologica activities; activit activities; activit activities; preseptor or ligand activities; on may be involved in oncogenesis, cancer cell proliferation or metastasis.

CC immunomodulatory activity activit or second activities; on may be involved in oncogenesis, cancer cell proliferation or metastasis.

CC conditions, e.g., by protein or gene therapy. Such conditions include cancers, hematopoletic disorders (e.g., asthma or arthritis), conditions, e.g., by protein or gene therapy. Such conditions include cancers, hematopoletic disorders (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arthrial ischemania, bone disorders (e.g., asthma or arthritis), creptic (creptic or nucleic acids encoding them) may be used to promote wound inaunomodulatory activities may be used in the treatment of viral, barchials with growth. Por example, such polypeptides may be used to augment or replace cells demaged by illness, and in diagnosis of the above conditions, and in drugal indections and accidental damage. The co
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                                            oteins and DNA encoding sequences useful for preventing, or ameliorating a medical condition in a mammalian subject
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Pred. No. 3.5e-107;
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99.6%;
                                                                                                                                         Claim 1; Page 429; 1963pp;
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                                                                                        e.g. arthritis and cancer
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P-PSDB; ABB11241.
                                                 Human proteins
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TCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCC 977

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GCTTCAAGCCTCTGGTCTCCATCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCC 917

61

1038 GGCCCTCCTTCCTCACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGG 1097

241 ACATCTCACACACACACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCTGCCCC 300

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WO200228999-A2.
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                                             in intron 6.
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                         CTGTGGTGCTGGAGACACCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTG 1157
                                   301 GGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCAATTCCGAGACTTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                             Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of
                                                                                                                                                                                                      metabolic disease; diabetes; obesity; substitution; ds.
                                                                                                                                                                                                                                                                                                                                                                          /*tag= e
/number= "Intron 4"
/note= "5' portion of intron 4"
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                                                            TGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1189
                                                                      TGTCTGCACTGGCTGTGGTCAACGAATGTGGT 452
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/note= "3' portion of intron
22..177
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                                                                                                                                                                                                                                                                  "Intron 2"
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               "Intron 3"
                                                                                                                                                                                                                                                                                                   /number= "Exon 3"
178..541
                                                                                                                                                                                                                                                                                                                                                        "Exon 4"
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                                                                                                                       AAH43682 standard; DNA; 989 BP
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                                                                                                                                                                            PRKAG3 intron 2 - intron 4.
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                                                                                                                                                          21-JAN-2002
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a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                             540 AGGTCCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACACCCTTGGCTCAAGCTGATCCTGCCGGGGTGGGCACTCCACCAACAGGGTGGGACTG
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                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viral infection; parasitic infection; protozoal infection; fundal infection; sterile inflammatory disease; psoniasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA differentially expressed in granulocytic cells #895.
                                                                                                                                                                                                                                                             :686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    607 CATGGCAACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                          Score 407.2; DB 22; Length
Pred. No. 3.2e-96;
                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                     Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                       24.78;
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                                                                                                                                                                                                                                                                                    Similarity
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by Chi Achip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated CG, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent capable of modulating GCA or an inflammation (especially for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a chronic) in a tissue, an allergic response in a subject, exposure of a chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an inflammation of the issue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation, an inflammation of the issue of gene(s) from Gs in the tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue, M is useful for detecting at issue having GCA; M2 is useful for Getecting an inflammation in a tissue, M is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation expension of pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation exposures a subject to a pathogen or sterile inflammation exposure of a subject to a pathogen or sterile inflammation exposure of a subject to 
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                                                                                             Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is
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the printed specification, but was obtained in electronic
mat directly from WIPO at
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Vockley
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     Yamaga S,
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Pred. No. 1.5
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                                                                                                                                                                                                                         Claim 1; SEQ ID No 895; 114pp; English.
Weissman SM,
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65.1%;
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                                                 WPI; 2002-435328/46.
Beazer-Barclay Y,
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                 ACCEGATCCATCECCTECCTGTTCTTGACCCEGTGTCAGGCAACGTACTCCACATCCTCA
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                                                                                                                                                                                                                                                                                                                           GCACTACCACCCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC
CICTGGICTCCATCICCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA
                                                                                                                                                                              CCCACAAGCGCATTCTGAAGTTCCTCAAATTGTTTATCACTGAGTTCCCCAAGCCCAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; diagnosis; identification; cytostatic; neuroprofective; nordropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; ofromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscoular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreatic cancer antigen;
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Ruben SM;

Rosen CA,

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PPSDB; AAB54009.

PPSDB; AAB54009.

XX

New nucleic acid that is a pancreatic cancer antigen for preventing, proventing, or ameliorating a medical condition, particular pancreatic accept.

PT treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition.

SS claim 1; Page 498-499; 1379pp; English.

XX

AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to proteins, called pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, contraceptive, nootropic, immunomodulatory, relaxant, contraceptive, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, contraceptive, and antigent and antidition or in assays contraceptive, indian partners to the proteins and the activity of the proteins and the activity of the proteins and the activity of the proteins and the activity of the proteins can be used to design nucleic detect, treat or prevent pancreatic disorders, especially cancer.

Got diagnostic machage pathological conditions and the activity of for pancreatic cancer antigens can be used to design nucleic carcin probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to treat on provent neural, immune system, muscular, correctins can be used to treat or prevent neural, immune system, muscular, correctins can be used to treat or prevent neural, immune system, correction, and in vitro diagnostic and therapeutic methods. The proteins can be used to prevent neural, immune system, corrections and the present invention.

Corrections are seed in the exemplification of the present invention.

XX

Sequences used in the exemplification of the present invention.
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\$2 Sequence 1691 BP; 458 A; 382 C; 401 G; 449 T; 1 other;

Query Match
23.98; Score 393.4; DB 21; Length 1691;

Best Local Similarity 65.18; Pred. No. 1.6e-92;

Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0;

TCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGC 1106 987 CACACAAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCCTTCTT 1046 567 TCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGC 626 TAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACG 686 747 TCACTGACTTCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCCAGATCTATG 806 AGATTGAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGC 866 CTCTGGTCTCCCATCTCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCCTCATCAAGA 926 543 CCCACAAGCGCATTCTGAAGTTCCTCAAATTGTTTATCACTGAGTTCCCCAAGCCAGAGT 602 123 TGTATACTTCCTTCATGAAGTCTCATGGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 182 GTGTGCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGGGATGCTGACCA 746 ACCGGATCCATCGCCTGCTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA 986 1047 627 687 807 867 927 483 ò q δy qq δ g Ω g  $\Omega$ g δ g ã g δ g

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	1407 ATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCTCA 1457	1407	δγ
362	- ⊢	806	ΩĐ
1406	TGATCGACAGGATTGCTCGGGAGCAGGTACACAGGCTGGTGCTGGTGGACGAGGC 1406	1347	ΟY
905	- A:	843	Д
1346	1287 AGAGGACACTAIGTCIGGAGGGAGTCCTITCCIGCCAGCCCCACGAGAGCTIGGGGGAAG 1346	1287	δγ
842		783	qq
1286	1227 ACCTGGCTGCCCAGCAAACCTACAACCTGGACATGAGTGTGGGAAGCCCTGAGGC 1286	1227	δy
782		723	qq
1226		1167	ΟŸ
722	663 GCACTACCACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC 722	663	q
1166	TGGAG	1107	QY
662	603 TCATGTCCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC 662	603	đ

Search completed: June 13, 2003, 02:59:53 Job time: 601.355 secs

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RESULT 1
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AL533446 AL533446
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Copyright (c) 1993 - 2003 Compugen Ltd.
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9 AL533446
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Listing first 45 summaries
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344527	
CUS	B1344527 572 bp mRNA linear EST 30-JUL-2001
FINITION	373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
CESSION	BI344527
RSION	BI344527.1 GI:15037807
YWORDS	EST.
URCE	pig.
ORGANISM	Sus scrofa
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
FERENCE	1 (bases 1 to 572)
AUTHORS	Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
	Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
	and Keele,J.W.
TITLE	Design and use of two pooled tissue normalized CDNA libraries for
	EST discovery in swine
JOURNAL	Unpublished (2000)
MMENT	Contact: Smith TPL
	USDA, ARS, US Meat Animal Research Center
	PO Box 166, Clay Center, NE 68933-0166, USA
	Tel: 402 762 4366
	Fax: 402 762 4390
	Email: smith@email.marc.usda.gov
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	volveovotice, rector recent interests of those materials and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests and interests a
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                     /note-"Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 190 c 151 g 124 t lothers
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/clone_lib="MARC 2PIG"
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                                                                                                                        /tissue_type="pooled"
/lab_host="DH10B"
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GTTTTCCCAGTCACGACG
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/tissue_type="Adult brain"
//note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : haryland filangelifetech.com URL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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1 (bases 1 to 970)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 ENRY cedex - France

EMB11: segref@genoscope_cns.fr, Web : www.genoscope.cns.fr.
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230 c 217 g 268 t
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                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="csObN004YNN3"
/clone_lib="LTI_FI015_Brn1"
/sex="male"
                                                                                                                                                                                                                                                       Location/Qualifiers
1. .970
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973

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Arakawa, T. Carninci, North C. S. Furuno, M., Hanagaki, T., Hara, R., Harawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, R., Hiramoto, K., Hori, F., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayasahizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1274 GAAGCCCTGAGGCAGAGGACACTATGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCACGAG 1333
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                                                                                                                                                                                                                                                                                                                                                                            034 CCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGCCATCGGCACATTCCGAGAC 1093
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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URL:http://genome.gsc.riken.go.jp/
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AUTHORS
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TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCCGCTTTGATGTGATTC 1226
                                                                                     1227 ACCIGGCIGCCCAGCAAACCIACAACCAGGACAIGAGIGIGGGAGAAGCCCIGAGGC 1286
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Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.W.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
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                         870 TCATCAACAGGCTAGTGGAAGCAGAGTTCACCGACTTGTAGTGGTGGATGAAATGATG 929
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                614 ACTAGCICCAAGCTAGTCAICTICGACACCAIGCIGGAGAICAAGAAGGCCTICTITGCI
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Heinrich-Pette-Institute
Martinistr. 52, 2025I Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Pred. No. 2.9e-84;
0; Mismatches 230; Indels
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/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
238 c 186 g 166 t
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AJ396118 dkfz426 Gallus gallus c
AJ396118
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/clone_lib="dkfz426"
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Best Local Similarity 69.3%;
Matches 518; Conservative
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//Losse_Vptc_riscond
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCNVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Peng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliangfulietech.com URL:
http://fulllength.invitrogen.com"
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                                                                                     485 AGGCCTGCCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 GCTTCCAGATGGACGAGGAGGCCGTAGAGGAAGCAGAACCACCAGGTTTGGGAGAA 237
                                                     GGTCCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCAAGACC 307
                                                                                                                                                           308 ACACCCTIGGCTCAAGCTGAICC---TGCCGGGGTGGGCACTCCACCAACAGGGTGGGAC 364
                                                                                                                                                                                                            298 ACACCCTTGGCTCAAGCTGTTCCCTTGGCTGAAGCGGAGACCTCCCCCACAGGGTGGGAC 357
                                                                                                                                                                                                                                                            TGCCTCCCCTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGGTG 424
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: segref@genoscope.ons.fr, Web : www.genoscope.cns.fr.
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Li.M.B., Gruber.C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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/tissue_type="placenta"
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/db_xref="taxon:9606"
/clone="CS0D1042YD16"
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AL548987.1 GI:12884536
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RIKEN integrated sequence analysis (RISA) system--384-format
RIKEN integrated sequence with 384 multicapillary sequencer. Genome Res.
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno.H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                       yr. and Hayashizaki,y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinaqawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTV 3'], CDNA was
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="A030014A04" / Clone_lib="RIKEN full-length enriched, 6 days neonate
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0; Mismatches 134; Indels
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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                                                                                                                                                   /clone="CSOBKO07YE02"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 ACAAGATCCACAGGCTGCCAGTTATTGACCCAGAATCAGGCAATACTTTGTACATCCTCA 499
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 CDNA libraries and normalization
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Pred. No. 5.1e-80;
1; Mismatches 289;
                                                Sequencage
                         Contact: Genoscope
Genoscope - Centre National de Seque
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web
                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="CSDD1082YL23"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA librarles and normalization
Unpublished (2001)
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Pred. No. 1.8e-79;
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AL554278.1 GI:12894901
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AUTHORS
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BM548053 10-FEB-2002 1085 bp mRNA linear EST 20-FEB-2002 AGENCOURT_6531760 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732872
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AGATTGAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGC 866
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       633 GCACTACCACCCCGTCTATGTGGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               753 ATCTGGCAGCAGAAAAGACCTACAACAACCTAGATGTATCTGTGACTAAAGCCTTGCAAC
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DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.k column: 17
Plate: LLAM.12755 row: k column: 17
                                                                                                                                   CTCTGGTCTCCATCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA
                                                                                                                                                                                          393 CGCTTGTCTGCATTTCTCCTAATGCCAGCTTGTTTGATGCTGTCTTCTTTAATTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                 573 TCATGICCAAGICTCIGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCIATGGTTC
                                                                                                                                                                                                                                                               ACCEGATCCATCCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
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Context: Robert Strausberg, Ph.D.
Emall: cgapbs-rémail.nih.gov
Tissue Procurement: Invitrogen
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BM548053
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/clone_lib="NHH_MCC_18"
/clone_lib="NHH_MCC_18"
/tlssue_type="large cell carcinoma"
/tlssue_type="large cell carcinoma"
/tlsb_host="DHNB (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI: CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MCC Library."
                                                                                                                                                                                                                               EST 21-AUG-2002
                                                                                                                                                                                                                         BQ947745 937 bp mRNA linear EST 21-AUG-2003
AGENCOURT_8863556 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6423989
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     895 TCATCAACAGGCTAGNGGGAAGCAGAGTTCACCAACTTGTAATGGNTGGATGAAAAATGA 954
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nlh.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM2603 row: h column: 06
High quality sequence stop: 611.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                            955 TGGGGGCCAAGGGAATGTATCACTGTCTGACATCTTGCCAGCCCTGGTG 1003
                                                 GCATCTTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTG 1453
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ilarity 65.6%; Pred. No. 5.8e-78;
Conservative 0; Mismatches 277;
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
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                                                    Qγ
                                                                                                 /note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: Not1; RNA source male hippocampus, age 27. Library is oligo-dr primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 14 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                987 CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCCTCCT 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 655 GCACTACCACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 CCCACAAGCGCATTCTGAAGTTCCTCAAATTGTTTATCACTGAGTTCCCCAAGCCAGGGT 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AICGAICACATACTITIGAGGGTGTTCTCAAGTGCTACCTGCATGAGACTCTGGAGNACA 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747 TCACTGACTTCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGTCCAGATCTATG 806
                                                                                                                                                                                                                                            constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Length 1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                           4 others
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                                                                                                                                                                                                                                                                                                                                                                               Score 360.6; DB 13;
Pred. No. 2.5e-79;
0; Mismatches 323;
                                                                                                                                                                                                                                                                                                        286 t
/clone="IMAGE:5732872"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH108"
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BQ954908 944 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8826665 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6421343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 TCATGCTCGGCTGGGACGATGAGCTGCGGAAACCATGGGCTCAGGTCTACATGCACTTCA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 AGCT---CGGCCTGGTGGAAGAGAGGCCGGCCCATTGCCCGTCCCCGCAGGTGCCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               582 TGCAGGAGCACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTCATCTTCGACA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCC 701
                                                                                                                                                                                              /tissue_type="pooled"
/lab_nost="buflow"
/nab_nost="Vector: pcMv SPORT6; Site_1: NotI; Site_2: SalI;
Intrary made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 CCAGCACAGACGATCTGGATCAGGCCATATAGTTCTCAGCCCCAGCAGCGTGGGGGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 GCACCCCCACAACAAGAACGAGAACAGCCTCCCCTCTGACTGTACAGCCTCCGCTTCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTAGAAGGCCTGCTAGAAGAGGCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 CCGTGGGAAACGGAGGGCCAAAGCCTTGAG-ATGGACAAGGCAGAAGTCGGTGGAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CCTTGGGGAACAGAGGACCAAGGTCTCAAGTATGGAAAAGCCAGGAGGATGTAAAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                 21.5%; Score 354; DB 13; Length 81.5%; Pred. No. 7.8e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                             95;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                              adrenal, and endometrium.
173 c 163 g 93
                                                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG.
                                                                                         Location/Qualifiers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:22370386
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B<u>0</u>954908
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1189 TCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCCAGCAAACCTA 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACCACCTGGACATGTGGGAGAAGCCCTGAGGCAGAGGACACTATGTCTGGAGGG 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1309 AGTCCTTTCCTGCCAGCCCCACGAGAGCTTGGGGGAAGTGATCGACAGGATTGCTCGGGA 1368
                                                                                         1069 TITGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1128
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 IGITICTCAAGTGCTACCTGCATGAGA-CTCTGGAGACATCATNCACAGGCTAGTGGAAGC 719
                                                                                                                540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    720 AGAGGGTCACCGACTTGTAGTGGTGGATGAAAATGATGTGGTCAAGGGAANTGTATCACT 779
                                                                                                                                                                                                                                                                                                              421 GCTACAGATTGGCACCTATGCCAATATTGCTATGGTTCGCACTACCACCCCGTCTATGT 480
                                             241 TGCCAGCTTGTTTGATGCTGTCTCTTCATTAATTCGGAACAAGATCCACAGGCTGCCAGT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
      601 CAACAACCTAGATGTATCTGTGACTAAAGCCTTGCAACATCGATCACATTACTTTGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            b1//5360 548 bp mRNA linear
467815 WARC 2BOV Bos taurus cDNA 5', mRNA sequence.
B1775360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, UF
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1429 CTCCGACATCCTTCAGGCACTGGTGCTCA 1457
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MEDLINE
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AUTHORS
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                                                                                                  107 TGGAGACAGCACCCATCCTGACTGCACTGGACTGTTTGTGGACCGGCGTGTGTCTGCAC 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1346 GTGATCGACAGGATTGCTCGGGAGCAGGTACAGGCTGGTGCTAGTGGACGAGACCCAG 1405
                                                                                                                                                                                                                 IGCCTGTGGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGTTTC 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BJ504184 Tipear EST 08-AUG-2003 BJ504184 MF01FSA CDNA Oryzias latipes CDNA clone MF01FSA006A14 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524 AAGCTGGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCCTTCATG 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       680 TGCCAGIGGIGGAIGAGAAGGNGCGIGIGGACAICTACTCCAAGITIGAIGITAICA 739
                                                                                                                                                           GCACTACCACCCCCCTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC 679
                                                                                                                                                                                                                                                                                                                                                                                                     740 ATCTGGCAGCAGAAAAGACCTACAACAACCCTAGATGTATCTGTGACTAAAGCCTTGCAA 799
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
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Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
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National Institute of Genetics
1111 Yata, Wishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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/sex="mixture of female and male"
/tissue_type="whole embryo"
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/db_xref="taxon:8090"
/clone="MF01FSA006A14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 490; Conservative
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/clone="IMAGE:6421343"
/clone="IMAGE:6421343"
/clone="Lib="NHH_MC_18"
/tlssue_type="large cell carcinoma"
/lab_host="DHJBB (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
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/note="Organ: lung; Vector: poTB7; Site_1: XhoI; Site_2:
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/note="Organ: lung; Vector: poTB7; Site_1: XhoI; Site_2:
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2596 row: i column: 24
                                                                                                  NIH-WGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Pred. No. 1.9e-77;
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High quality sequence stop: 693.
Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                   620 TCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTG
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                                                                                                                                                                                                                                     Score 350.4; DB 14; Length Pred. No. 8.9e-77;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                CAGGAGCACACCIGCTACGATGCCATGCCAACTAGCTCCAAGCTAGTCATCTTCGACACC
                                  ATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed Dy: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAMI3323 row: n column: 18
High quality sequence stop: 636.
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/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="mammary adenocarcinoma, cell line"
/lab_host="mammary adenocarcinoma, cell line"
/lab_host="mammary adenocarcinoma;
/note="mammary action: pcMv-sPoNHT6; Site_l: Not!;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
full-length sis a NHH_MGC Library."
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12001 row: a column: 02
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/db_xref="taxon:9606"
/clone="IMAGE:5392777"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Location/Qualifiers
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BI858240.1 GI:15998987
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/tissue_lype="placenta"
/tissue_lype="placenta"
/tissue_lype="placenta"
/note="vector: pcMYSPORT 6; Site_l: Not!; lst strand cDNA
/was primed with a Not!-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMYSPORT 6
vector: Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 83/1
Email: filiang@lifetech.com URL:
http://fulllength.invitrogen.com"

39 a 222 c 199 g 247 t lothers
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781 AAATGATGTGGTCCAGGGAAATGGTATCACTGTCTGACATCCCTGCAGCCCTGGTGCTCC 840
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
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BI344527 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. BI344527 BI344527.1 GI:15037807	pig. Sus scrofa Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria, Cetartiodactyia; Suina; Suidae, Sus.	<pre>1 (bases 1 to 572) Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,T.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.</pre>	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine (Unpublished (2000))	Contact: Smith 'Pb. USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4356 Fax: 402 762 4390 Bmall: smith@mall.marc.usda.gov	Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e., Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.  PCR PRIMERS FORWARD: AGGAAACAGCTATGACCAT
RESULT 1 B1344527 LOCUS DEFINITION ACCESSION VERSION	SOURCE	REFERENCE AUTHORS	JOURNAL	COMMENT	

B1344527 373008 MA AL533446 AL533446 AJ396118 AJ396118 BB630381 BB630381 AL546987 AL555228 AL555228

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                /tissue_type="pooled"
/lab host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
190 c 151 g 124 t l others
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0; Mismatches 56;
                                                                                                                                                                                                                                       Score 456.4;
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Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1.572
BACKWARD: GTTTTCCCAGTCACGACG
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/tissue_type="Adult brain"
//tissue_type="Adult brain"
//note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oljago(dr) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact : Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax : (1) 301 610 8371 Email :
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
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http://fulllength.invitrogen.com"
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Pred. No. 3.3e-85;
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/clone_lib="LTI_FL015_Brn1"
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794 GTCCAGATCTATGAGATTGAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAA 853  [1	1094   TTGGCTGTGGTGCTGGAGCAGCCCATCTGACTGGACATCTTTGGGACCGG   153	Z	The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/
		RESULT 4 BB630381 LOCUS DEFINITION ACCESSION VERSION VERSION VERSION KEYWORDS SOURCE ORGANISN AUTHORS TITLE JOURNAL COMMENT	
1167 TGCCTGTGGTCAACGAATGTGGTCAGGTCCTGTTTCCCGCTTTGATGTGTTC   126	AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 CORGANISM BUTHORS AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 ACMANINA AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ396118 AJ3	36 9-9 37 a 1	

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/db_xref="texcologics"
/clone_lib="LTI_NFL006_PL2"
/clone_lib="LTI_NFL006_PL2"
/tissue_lype="placenta"
/note="Vector: pCMVSPORT 6; Site_l: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Peng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
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     178 GCTTCCAGATGGACGAGACAGGAGGCCGTAGAGGAAGCAGAACCACCAGGTTTGGGAGAA 237
                                                                                                                                                          308 ACACCCTTGGCTCAAGCTGATCC---TGCCGGGGTGGGCACTCCACCAACAGGGTGGGAC 364
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.4e-81;
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Liw,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDMA libraries and normalization
Unpublished (2001)
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http://fulllength.invitrogen.com"
217 c 206 q 255 t
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AL548987.1 GI:12884536
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                                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
waqi,K., Fullwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawal,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCAAGAGCTCTTTTTTTTTTTTTV 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="%Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GGGCTGGCCACATGGAGCCCGGGCTGGAGCACGCACTGCGCAGGACCCCTTCCTGGAGC 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched, 6 days neonate
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/lab_host="DH10B"
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

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                                                                               CTCTGGTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                         Length 940;
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Pred. No. 1.8e-79;
); Mismatches 290; Indels
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/db xref="Laxon:9606"
/clone="CSODI082YL23"
/clone=lib="LYI NFL006_PL2"
/tissue_type="placenta"
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64.8%;
                                                                                                                                                                                                                                                                                                                                               prime, mRNA sequence.
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ALSS4278
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/lab_host="DH10B" [phage resistant)"
//lab_host="DH10B" [phage resistant)"
//note="Organ: lung: Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NTH MCC Library."
                                                                                                                                                     AGENCOURT 8863556 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6423989
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 895 TCATCAACAGGCTAGNGGGAAGCAGAGTTCACCAACTTGTAATGGNTGGATGAAAAATGA 954
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
http://inage.llnl.gov
Plate: LLCMASGO3 row: h column: 06
High quality sequence stop: 611.
Location/Qualifiers
                                  1405 GCATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTG 1453
                                                        955 TGGGGGCCAAGGAATGTATCACTGTCTGACATCTTGCCAGCCCTGGTG 1003
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Pred. No. 5.8e-78;
3; Mismatches 277;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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/db_xref="taxon:9606"
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65.6%;
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                                                                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: Not1; RNA source male hippocampus, age 27. Library is oligo-dr primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012.
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0; Mismatches 323; Indels
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               /clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                        Score 360.6;
/clone-"IMAGE:5732872"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                        /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTTGGGGAACAGGACCAAGGTCTCAAGTATGGAAAAGCCAGGAGGATGTAAAGGAAA
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ilarity 81.5%; Pred. No. 7.8e-78;
Conservative 0; Mismatches 95;
                                                                                                                                                                                                                                                                                  93 t
                                                                                                                                                                                                                                                             adrenal, and endometrium.
                                                                                                                                           /clone_lib~"MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"

    .548
    /organism="Bos taurus"

                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                             /db_xref="taxon:9913
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NIH_MGC_18
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FORWARD: AGGAAACAGCTATGACCAT
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5', mRNA sequence.
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.B., White, J., Cho, J., Fahrenkrug, S.C., Bennett
'G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                    949 TCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCACACAAAACGCCTGCTCAAGTT 1008
                                                                                                                                               TTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGAC 1128
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                   GCCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCCTGCCAGTGGTGAGAGGG
                                                                                                                                                                                                                                                                                                                                                                         1189 TCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCCAGCAAACCTA
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TGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGCCTGT
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NO Box 165, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                        1107 TGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGGACCGGCGTGTGTCTGCAC 1166
                                                                                                                                                                 1167 TGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTC 1226
                                                                                                                                                                                                                                                            127 ACCTGGCTGCCCAGCAAACCTACAACCA-CCTGGACATGAGTGTGGGAGAAGCCCTGAGG 1285
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Oryzias latipes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Narita, T., Jindo, T. and Takeda, H.
                                                                                                                                                                                                                                                                                  620 GCACTACCACCCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kohara, T., Shin-ir, Kimura, T., Narita, T., Jin Medka EST Project in Takeda's lab Unpublished (2001)
Contact: Tadasu Shin-ir Center: Tadasu Shin-ir Center For Genetic Resource Information National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
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68.1%; Pred. No. 2e-77;
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/clone_lib="MF01FSA cDNA"
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ECORI: CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                            Dmail: cgapbs-rémail.nih.gov
rissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can
found through the I.M.A.G.B. Consortium/Linl.at:
                   Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 944)
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Pred. No. 1.9e-77;
0; Mismatches 312; Indels
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//lab_host="DH10B (phage-resistant)"
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Plate: LLCM2596 row: 1 column: 24
High quality sequence stop: 693.
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
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AGENCOURT_7571059 NIH_MGC_68 Homo sapiens cDNA clone LMAGE:6058577
BQ224866
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MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTCATCTTCGACACC
                                                                  ATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LINL at:
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/db_xrei='taxou.>v.v.
/dlone='ImAGE:6058577"
/clone=lib="NHLMGG:608"
/issue_type='large_cell carcinoma"
/iab_host="DH10B (phage-resistant)"
/note='Organ: lung: Vector: pCMV-SPORT6; Site_l: NotI:
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1160 TCTGCACTGCCTGTGGTCAACGAATGTGGGTCAGGTCGTGGGGCCTCTATTCCCGGTTTTGAT 1219
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Pred. No. 8.9e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 306;
                                                                                                                                                                                                                                                                                                             284 t
                                                     /organism="Homo sapiens"
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Location/Qualifiers
1. .1070
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Best Local Similarity
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987 CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCCCCCCCGCCCTCCT 1046
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                                                                                                                                                                                                                                                                                                                                                                                                         IGCCIGIGGICAACGAAIGIGGICAGGICGIGGCCCICIAIICCCGCITIGAIGIGATIC 1226
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431 CGCTTGTCTGCATTTCTCCTAATGCCAGCTTGTTTGATGCTGTCTCTTCATTAATTCGGA 490
                                                         927 ACCGGATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 TGCCAGTGGTGGATGAGAGGGCGTGTGGTGGACATCTACTCCAAGTTTGATGTTATCA 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 864)

NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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/db_xref⇔"taxon:9606"
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   781 AAATGATGTGGTCCAGGGAAATGGTATCACTGTCTGACATCCCTGCAGCCCTGGTGCTCC 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 1e-76;
1; Mismatches 266; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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/db_xref="taxon:9606"
                                                         1458 GCCTGCTGGCATGCCCTCG 1481
                                                                                                                  841 CCGGTGGAAGAAAAAAAACCCTTG 864
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AL552459
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65.6%;
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                     Gaps
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  Length 864;
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Query Match 21.1%; Score 346.8; DB 13; Best Local Similarity 65.3%; Pred. No. 6.3e-76; Matches 555; Conservative 0; Mismatches 292;
 DB 13;
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Search completed: June 13, 2003, 05:58:20 Job time: 4104.65 secs

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4027.262 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-232-463-14
US-09-056-105-18
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US-08-878-989-14
US-09-272-796-14
US-08-232-463-14
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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Length 1576; Indels

Score 390.2; DB 3; Pred. No. 2.1e-93; 0; Mismatches 313;

23.78; 64.98;

Query Match 23.7% Best Local Similarity 64.9° Matches 578; Conservative

REGISTRATION NUMBER: 32,257 REFERENCE/DOCKET NUMBER: DC-0050 TELECOMMUNICATION INFORMATION:

TELEPHONE: (856) 810-1515
TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 63.
SEQUENCE CHARACTERISTICS:

Single

STRANDEDNESS:

ANTI-SENSE:

US-09-101-146-63

TYPE: Nucleic acid

1576

LENGTH:

567 TCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGC 626

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Patent No. 6124125
GENERAL INFORMATION:
APPLICANT: Dartmouth College, St. Vincents Institute of APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION:
NO. 6124125el AMP Activated Protein Kinase CORRESPONDENCE: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
  US-08-967-727-13
US-08-017-230D-13
US-09-056-105-9
US-09-218-489-1
US-09-103-840A-2
US-09-103-840A-2
US-09-103-840A-1
US-09-249-585A-2
US-09-249-585A-2
US-09-239-081-2
US-09-130-114-1
US-09-130-114-1
US-09-620-925-1
US-09-620-925-1
US-07-884-811-15
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US-07-884-811-15
US-08-917-15
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US-08-144-088-15
US-08-144-088-15
                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,146
FILING DATE: UCCODER 7, 1998
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1996
ATTORNET, BROWNER: PN450
FILING DATE: 8 JAN 1996
ATTORNET, JAN 1996
ATTORNET, JAN MASSEY LIGATE
NAME: Jane MASSEY LIGATE
NAME: Jane MASSEY LIGATE
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Jane Massey Licata, Esq. STREET: 66 E. Main Street
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11495 4
1125 4
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   STATE:
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CACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCTGCCCGGCCCTCCT 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTGGTCTCCCATCTCTCCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA 926
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Pred. No. 3.3e-87;
0; Mismatches 334;
                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: RastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
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                              Incyte Pharmaceuticals,
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 I
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%;
62.9%;
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                                                                                                                                                        COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                            Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
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                                                            Palo Alto
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CLONE: 1452972

US-08-878-989-14
                                                                                             USA
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                                                                                                                                                                                                                                            FILING DATE:
                                                                                                            ZIP: 94304
                               ADDRESSEE:
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                                                            CITY: Pa.
STATE: CA.
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                                                                                                                                                                                                                         AGATTGAACAACATAAGATTGAGACCTGGAGGGGAGATCTACCTGCAAGGCTGCTTCAAGC 866
                                                                                                                                                                                                                                            CICTGGTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA 926
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                              TAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08878989 Patent No. 5885803 GENERAL INFORMATION:
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
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Length 1435;

us-09-826-581-5.rni

TELECOMMUNICATION INFORMATION:  TELEFAX: 415-855-0555  TELEFAX: 415-845-4166  TELEX: 18LEX:  INFORMATION FOR EQ ID NO: 14:  SEQUENCE CHARACTERISTICS:  LENGTH: 1435 base pairs  TYPE: nucleic acid  STRANDEDNESS: single  TOPOLOGY: linear  IMMEDIATE SOURCE:  LIBRART: PENITUT01  CLONE: 1452972	Query Match 22.3%; Score 366.6; DB 4; Length 1435; Best Local Similarity 62.9%; Pred. No. 3.3e-87; Matches 567; Conservative 0; Mismatches 334; Indels 0; Gaps 0; Qy 567 TCTACATGCAGGAGCACACCTGCTACGATGCCAATGCTCAAGCACAGC 626  Dh 183 TTTACATGCCATTCATACGAGAGAACAATGAACAAATGCAAAAGCAAAAAAAA	627 TASTCATCTTCGACCACGTGGGGGACACGAGGGCTTCTTTGCTGGTGGCCAACG 627 TASTCATCTTGGACACCATGCTGGAGATCAAGGGCCTTCTTTGCTTGGTGGCCAACG 628 TITLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 747 TCACTGACTTCATCCTGGTGCTACTACTACAGGTCCCCCTGGTCCAGATCTATG 806	QY         807 AGATTGAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGC 866	QY         927 ACCGGATCCATCGCTGTTCTTGACCCGGTGTCAGGCAACGTACTCCACATCCTCA 986	1047 TCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGC	DD 723 ALCCAGRCAACGAATCTGCCACCAGGGCCCCTCTATTCCGCCTTTGATCTGATC 782  QY 1167 TGCCTCTGGTCAACGAATCTGGTCAGGTCGTCGGCCTCTATTCCCGCTTTGATGTATTC 1226  DD 783 TGCCTGTTGTGGATGAGTCAGGAAAAGTTGTATTCCAAATTTGATGTAATTA 842	QY 1227 ACCTGCCCACCAACCTACAACCCTGGACATGAGTGTGGGAAAGCCCTGAGGC 1286	OY 1287 AGAGACACTATGTCTGGAGGAGTCCTTCCTGCCAGGAGAGCTTGGGGGAAG 1346
603 CCCACAAAAGAATCCTCCAGCTTTTTATGTCTGATATGCCAAAGCCTGCCT	QY         1227 ACCTGAGGAACACTAACAACGGAACATGGGAAGACCCTGAGGG         1286           Db         843 ATCTTGCTGCTGAGAAACATACAATAACCTAGATATCAGGTGACCCCAGGCCCTTCAGC         902           Qy         1287 AGAGGACACTATGTCTGAGGGGAGTCCTTTCCTGCAGCCCCAGGAGACTTGGGGAAG         1346           Qy         1287 AGAGGACACTATGTCTGAGGGAGTCCTTTCCTGCAGCACCCCAGGGGAGCTTGGGGAAG         1346           Db         903 ACCGTTCACAGTATTTTGAAGGTGTTGTGAAGTGCAATAAGCTGGAAATACTGGAACACCA         962	1347 963 1407 1023	OY 1467 G 1467 Db 1083 G 1083	4 Applicatí 07148 RMATION: Bandman Hillman	APPLICANT: COrley, Neil C.  APPLICANT: Guegler, Karl G.  APPLICANT: Lal, Preeti  APPLICANT: Bah, Purvi  TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  TITLE OF INVENTION: KINASES  NUMBER OF SEQUENCES: 21		COMPUTER KEADELE FORM:  MEDIUM TYPE: Diskette  COMPUTER: IBM Compatible  POPERATING SYSTEM: DOS  SOFTWARE: FastERO for Windows Version 2.0		

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1164 CACTGCCTGTGGTCAACGAATGTGGTCAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGA 1223
                                                                                        CCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGG 1103
                                                                                                                                                                                                                     1104 IGCTGGAGACAGCACCCATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCT 1163
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Patent No. 6287569
GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
APPLICANT: WIN YUNQI
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT PAPLICATION NUMBER: 09/09/056,105
CURRENT PILING DATE: 1998-04-06
RABLIER APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 09/043,467
NUMBER: OF SEQ ID NOS: 35
SOSTWARE: FASTESQ for Windows Version 3.0
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44.7%; Pred. No. 0.14;
ive 0; Mismatches 198;
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ORGANISM: Homo sapiens
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US-08-232-463-14/c
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                                                              1407 ATCTCTTGGGCGTGGTCTCCCTCTCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTG 1466
                                                                                               984 TCACACACAAACGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCCT 1043
963 TCGTGGACAGAATAGTAAGAGCTGAGGTCCATCGGCTGGTGGTGGTAAATGAAGCAGATA 1022
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2.6%; Pred. No. 0.0027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEB: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PEPLIANTON NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703)836-9300
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LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; IMMEDIATE SOURCE;
; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 10; Conserva
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ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                      G 1083
                                                                                                                                                                                       1467 G 1467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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TELEX: 89
                                                                                                                                                                                                                                                   1083
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Sequence 18, Application US/09056105
Patent No. 6287569
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STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                             44.48;
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 44.4
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                   GENERAL INFORMATION:
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US-08-299-849B-14
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                                                                                                                                                                                                                                                         SEQ ID NO 18
LENGTH: 1022
                                                                                                                                                                                                                                                                                                                            us-09-056-105-18
   JS-09-056-105-18
                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 GCCTTGAGATGGACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GGGGCTGGCCACATGGAGCCCGGGCTGGAGCACGCACTGCGCAGGACCCCTTCCTGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.4%; Score 40.2; DB 1; Best Local Similarity 4.5%; Pred. No. 0.55; Matches 12; Conservative 150; Mismatches 103;
                                                   APPLICANT: DORNER, F.
APPLICANN: SCHEIFLINDER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30472/114 IMMU FELECOMMUNICATION INFORMATION:
                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 GGTCCCCGGTCCAGGCCAGCTGCTG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP 91 114 300.
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US/07/935,313
FILLING DATE:
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703)683-4109
                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                           Cli..
STATE: VA
COUNTRY: USA
T. 22313-0299
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                                                                                                                                                                                       CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (7
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RESULT

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373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGA 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493 CCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 TCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 GAGAGTCATCAAAAATTACAAGGGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTC 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 GTTCCCAGCCACAGAGGCCTGGGAGTGTGAGCCTAGAAGGCCTGCTGGAAGAGGCCTGC 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                539 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACAC 598
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Determining Expression of A Tumor Antigen Precursor
: 48
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Patent No. 5612201
GENERAL INFORMATION:
BENERAL INFORMATION:
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre, De Smet, Charles; APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precedules OF SEQUENCES: 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1022;
APPLICANT: KIPPS, THOMAS J.
APPLICANT: WU, YUNQI
TITLE OF INVENTION: PACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT PILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 1977-04-10
NUMBER OF FLING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.4%; Score 39.6; DB 4; Length 1
14.4%; Pred. No. 0.38;
tve 0; Mismatches 199; Indels
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21P: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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978 TCATTITCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGA 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 CTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCAGATGATGTGGAGCTGGCCACGGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 GTTCCCAGCCACAGAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAGGGCCTGC 492
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44.4%; Pred. No. 0.54;
Live 0; Mismatches 199; Indels 0;
                                                                                                                                                                                                                                                                                                        Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPPEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUBBER:
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                               SEE: Felfe & Lynch : 805 Third Avenue New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Wordperfect
                                                                                                                 NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Ly
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                IBM
                                                                                                                                                                                                            CITI.
STATE: New
Tr. 10022
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1098 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACAC 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 CICTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGTGAGGTGGAGCTGGCCACGGA 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 199; Indels
                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hanson, No. 5612201man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5355
TELECOMMUNICATION: TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/299,849B FILING DATE: 1-SEPTEMBER-1994
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             APPLICATION NUMBER: 07/807,043 FILING DATE: 12-DECEMBER-1991 PRIOR APPLICATION DATE: 23-SEPTEMBER-1991 FILING DATE: 23-SEPTEMBER-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: genomic DNA
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MAGE-41 gene
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US-08-142-368A-14
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Sequence 14, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Brugen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                                  978 TCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGA 1037
                                                                                                                                                                                                                                                                                                                                                  1038 GAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTC 1097
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                                                                                                  433 GTICCCAGCCACAGAGGCCTGGGAGTGTGAGCCTAGAAGGCCTGCTGGAAGAGGCCTGC 492
                                                                                                                                                   918 CTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGC 977
                                                                                                                                                                                                 493 CCTGTGCCTGTCCCCGCAGGCCCCCATTCCCCAAGCTGGGCTGGGATGACGAACTGCGGAA 552
                                                                                                                                                                                                                                                                                                   553 ACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACCACGTGCTACGATGCCATGGC 612
                                                                                                                                                                                                                                                                                                                                                                                                   613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672
  373 CICTGACTGIACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGA 432
                                                 858 CACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGAGGGGGCCAAGCAC 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-MARCH-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26 MARCH-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: LUD 5353
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
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STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Ly
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STATE: Ne.
7. 10022
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US-08-037-230D-14
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Patent No. 6025474

GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672
                                                                                                                            673 TCTGGTGGCCAACGGTGTGCGGCCAGCCCCTCTATGGGACAGGAAGCAGAAGCTTT 730
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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44.4%; Pred. No. 0.54;
ive 0; Mismatches 199;
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FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 6025474man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DECEMBER-1991
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TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.4%;
Best Local Similarity 44.4%;
Matches 159; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Felfe & Lynch: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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954 ACCCGGTGTCAGGCAACGTACTCCACACACACACAAACGCCTGCTCAAGTTCCTGC 1013
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                                                                                                  553 ACCCGCCCCAGAICIACAIGCGCITCAIGCAGGAGCACACCIGCIACGAIGCCAIGGC 612
                                                                                                                                                                        613 AACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672
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                         493 CCTGTGCCTGTCCCCGCAGGCCCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGCGGAA 552
                                                                                                                                                                                                                                                                          126 NYNSYNYNSSYNYNSSYNYNSSYNYNSSYNYNSSYNYNSSYNYNYSYNYNYSY
                                                                                                                                                                                                                                                   673 TCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: SZOSTAK, JaCK W.
APPLICANT: ROBERTS, RICHARD W.
TAPLICANT: Liu, Rhibe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00766/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER PLILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
EARLIER PLILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 289;
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5.3%; Pred. No. 0.39;
tive 87; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 17, Application US/09007005B; Patent No. 6258558
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US-09-244-796-17/c
: Sequence 17, Application US/09244796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.4
Best Local Similarity 5.3%
Matches 10; Conservative
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US-09-007-005-17/c
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LENGTH: 289
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APPLICANT: KIPPS, THOMAS J.
APPLICANT: WI, YUND.
TITLE COF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FRALES FRALES FRALES FRALES FRALES FRALES FRALES FRALES FAMINGOWS Version 3.0
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Pred. No. 0.69;
0; Mismatches 199; Indels
                                                                                                                                                                                                            Score 39.6; DB 4; Length 2
Pred. No. 0.54;
0; Mismatches 199; Indels
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Patent No. 6287569
   14:
                                                                                                                                                                                                            Query Match 2.4%;
Best Local Similarity 44.4%;
Matches 159; Conservative
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Best Local Similarity 44.4%;
Matches 159; Conservative (
                                                                                                               MOLECULE TYPE: genomic DNA
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2531 base pairs
TYPE: nucleic acid
                                                                                                                                                   ; NAME/KEY: MAGE-41 gene US-08-037-230D-14
                                                                              single
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                                                                      STRANDEDNESS
TOPOLOGY: 1:
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954 ACCCGGTGTCAGGCAACGTACTCCACATCCTCACACACAAACGCCTGCTCAAGTTCCTGC 1013
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APPLICANT: Dietrich, Paul S.
APPLICANT: McGlvern, Joseph G.
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT FILIG DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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                                                       APPLICANT: Liu, Ribe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: POSIONS
TITLE OF INVENTION: POSIONS
TITLE OF INVENTION: POSIONS
CURRENT PAPLICATION NUMBER: US/09/244,796
CURRENT APPLICATION NUMBER: 06/035,963
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
SARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASLEEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.4%; Score 38.8; DB 4; Length 289; 5.3%; Pred. No. 0.39; tive 87; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Translation template
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COTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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GENERAL INFORMATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: Roberts, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.4%
Best Local Similarity 5.3%;
Matches 10; Conservative
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; LOCATION: (192)..(6716)
US-09-404-650-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 6816
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US-09-404-650-1
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                                                               631 CATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCGTGGTCGAACGGTGT 690
                                                                                                                                                                                          751 IGACTICATCCIGGTGCTGCATCGCTACTACAGGTCCCCCCGGTCCAGATCTATGAGAT 810
                                                                                                                                                                                                                                                           811 TGAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCT 870
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                                    0; Gaps
Score 38.8; DB 4; Length 6816;
Pred. No. 1.3;
0; Mismatches 127; Indels 0
 Query Match 2.4%;
Best Local Similarity 47.5%;
Matches 115; Conservative (
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Search completed: June 13, 2003, 06:00:59 Job time : 129.419 secs

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June 13, 2003, 04:39:50 ; Search time 520.839 Seconds (without alignments) 4579.068 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/NSO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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length: 2000000000
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1647
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Maximum DB :
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SUMMARIES

Query

Match Length DB ID

100.0 1647 10 US-09-826-581-2

23.9 1691 10 US-09-825-297-2

23.9 1691 10 US-09-825-297-2

23.9 1691 10 US-09-825-297-2

23.9 1691 10 US-09-825-297-2

23.9 1691 10 US-09-826-581-3

23.9 1691 10 US-09-826-581-3

24.7 1152 10 US-09-826-581-3

25.2 378 10 US-09-826-70

25.2 378 10 US-09-864-761-3373

26.4 57 10 US-09-864-761-3373

27.1 16.9 US-10-198-846-2282

28.2 11 U US-09-826-21108

28.2 821 10 US-09-826-581-1

28.3 90 9 US-10-198-846-282

28.4 520 9 US-10-188-846-282

28.4 520 9 US-09-826-581-1

29.8 520 9 US-09-826-581-1

20.8 520 9 US-09-826-581-1

20.8 520 9 US-09-864-761-693

20.8 520 9 US-09-884-332

20.8 520 9 US-01-184-544-332

20.8 520 9 US-01-184-543-332

20.8 521 0 US-09-984-332

20.8 52

1647 407.2 393.4 278.8 1168.2 1127.2 1127.2 123.6 63.2 53.2 52.2 52.2 52.4 46

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43.4 40.2 40.2 39.6

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1107   TCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC	Db 723 TGCCAGTGGTGGATGAGAGGGGCGTGTGGTGGACATCTACTCCAAGTTTGATGTTATCA 782  Qy 1227 ACCTGGCTGCCCAGCAACCTACAACCTGGACATCTGGAGAAGCCCTGAGGC 1286	RESULT 4  US-09-826-581-4  ; Sequence 4, Application US/09826581 ; Patent No. US20020122310A1 ; GENERAL INFORMATION: ; APPLICANT: Anderson, Leif ; APPLICANT: Authorn, L. Holger ; APPLICANT: Marklund, Stefan ; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SI ; FILLE REPERBNCE: 11145-007001 ; CURRENT APPLICATION NUMBER: US/09/826.581	CURRENT FILING DATE: 2001-04-05  PRIOR APPLICATION WINBER: US 60/195,665  NUMBER OF SEQ ID NOS: 14  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 4  LENGTH: 1014  TYPE: DNA  CREANTSW: HOME saniens	US-09-826-581-4  Query Match  Query Match  Best Local Similarity 97.6%; Pred. No. 1.1e-72;  Matches 283; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	п н	785 1478 845	QY         1538 TGAAGGGAACTGGACACTCACCTTCCCCCACCCCATTGCTGGTTCAGCTA 1597           DD         905 TGAAGGGACTGGAACTCAGCCTTCACCTCCCCCCCCTTTGCTGGTTCAGCTA 964           QY         1598 TGATTCAGGTAGCTCCCCTGGGCCATGACACCAGCCTTTGTTGCTGCTTCAGCTA 964           DD         965 TGATTCAGGTAGCTCTCCCCTGGGCCATGACACCAGCCTTTAGTCTTC 1647           DD         965 TGATTCAGGTAGGCCTTGGCCATGACACCAGCCTCTTAGTCTTC 1014
QY         547 GCGGAAACCCGGCGCCCAGATCTACATGCGCATCATGCAGAGCACACCTGCTACGATGC         606           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 3 US-09-925-297-2 Sequence 2, Application US/09925297 Sequence 2, Application US/09925297 Patent No. US20020081659A1 Patent No. US20020081659A1 TELENT NORMATION: Worleic Acids, Proteins and Antibodies FILE REFERENCE: PA105 CURRENT APPLICATION NUMBER: US/09/925,297 CURRENT FILING DATE: 2001-08-10 PRIOR FULING DATE: 2000-03-08 PRIOR FILING DATE: 12000-03-08 PRIOR FILING DATE: 1999-03-12 NUMBER OF ES ED ID NOS: 928 SOFTWARE: Patentin Ver. 2.0	SEQ 1D NO 2		QY         687 GTGTGGGGCAGCCCTCTATGGGACAGCAAGAACCAGAGCTTGTGGGGATGCTGACCA 746	303 TCACTGATTCATCAATATCCTGCACCGCTACTATAAATCAGCCTTGGTACAGATCTATG 807 AGATTGAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGC 11   111   111   111   1   1   1   1	867 CTCTGGTCTCCATCTTCTAATGATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGA   1	Db   483 ACAACATCCACAGGTGCCAGGTGTTGTTCAGGCAATACTTTGTACATCCTCA 542     Qy

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0096 ATTIGCATIGAATGAIGAIACIAACIAAATGGIATCCICIGCIAGGCGIGCIGCACAACC 10155
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                       9856 crececcaagriegriererereacacecagerierigiaaagaaggeerreraegeeer 9915
                                                                                                                                                                                          556 CGCCCCCAGATCTACATGCGCTTCATGCAGGAGCACCTGCTACGATGCCATGGCAAC 615
                                                                               616 TAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGCTCT 675
                                                                                                                                                                676 GGTGGCCAACGGTGTGCGGCAGCCCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGG 735
                                                                                                                                                                                                                                                736 GATGCTGACCATCACTGACTTCATCCTGGTGCTGCATCGCTACTACAGGTCCCCCCTGGT 795
                                                                                                                                                                                                                                                                                                                                                                                                             858 GCTTCAAGCCTCTGGTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCC 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              918 TCATCAAGAACCGGATCCATCGCCTGCCTGTTCTTGACCCGGTGTCAGGCAACGTACTCC 977
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ITILE OF INVENTION: POLYNUCLECTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  978 ACATCCTCACACACACACGCCTGCTCAAGTTCCTGCACATCT 1019
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CURRENT FILING DATE: 2001-03-29
PRIOR PRLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 559, Application US/09822846 Publication No. US20030027139A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agostino, Michael J.
Steininger II, Robert J.
Bowman, Michael R.
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LaVallie, Edward R.
Collins-Racie, Lisa A.
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Resnick, Richard J.
Gulukota, Kamalakar
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Wong, Gordon G.
Clark, Hilary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Ver. 2.0
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Treacy, Maurice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evans, Cheryl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-822-846-559
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SEQ ID NO 559
LENGTH: 1446
TYPE: DNA
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APPLICANT:
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APPLICANT:
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                                                                                            APPLICANT: Andersoo, Leif
APPLICANT: Andersoo, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: MARKING, Stefan
TITLE OF INVERTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SIGAM, Lynne
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANTON: WIGHER, Kim
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/108,605
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2001-01-16
PRIOR PLICATION NUMBER: US 69/761,142
PRIOR APPLICATION NUMBER: US 60/176,418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 168.2; DB 10; Length 1722;
Pred. No. 9.3e-40;
0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 70, Application US/10108605
Patent No. US20020160934A1
GENERAL INFORMATION:
APPLICANT: Broadus, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Drosophila melanogaster
                                  Sequence 3, Application US/09826581
Patent No. US20020142310A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.65
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3
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                 US-09-826-581-3
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Sequence 11096, Application US/09783590

Sequence 11096, Application US/09783590

Patent No. US20020110850A1

GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen M.
ITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REPERENCE: PO-16.20
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 1995-04-12
FRIOR PILING DATE: 1995-04-12
PRIOR PILING DATE: 1995-04-12
PRIOR PRILING DATE: 1994-11-21

PRIOR PRILING DATE: 1994-11-21
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HER INFORMATION: EXPRESED IN HELAT, SIGNAL - 4.1

HER INFORMATION: EXPRESED IN HELIO, SIGNAL - 3.9

HER INFORMATION: EXPRESED IN HELIOO, SIGNAL - 3.9

HER INFORMATION: EXPRESED IN BUILT LIVER, SIGNAL - 3.8

HER INFORMATION: EXPRESED IN BUT44, SIGNAL - 3.8

HER INFORMATION: EXPRESED IN PETAL LIVER, SIGNAL - 4.8

HER INFORMATION: EXPRESED IN BUDG, SIGNAL - 4.8

HER INFORMATION: EXPRESED IN BUDG, SIGNAL - 4.8

HER INFORMATION: EXPRESED IN BURG, SIGNAL - 4.8
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                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 3373
LENGTH: 378
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   PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
                                                                     PRIOR FILING DATE: 2001-01-30
PRIOR PEDIACATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2001-01-29
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LOCATION: (53)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 49117
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Best Local Similarity 94.6
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 427
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APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1370 CAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTTGGGCGTGGTCTCCCTC 1429
                                                                                                                                                                                                                                                1130 GCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1189
                                                                                                                                                                                                                                                                                                                                                                                           1190 CAGGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCCAGCAAACCTAC 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1250 AACCACCTGGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGGACACTATGTCTGGAGGGA 1309
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                                                                                                                                                                                                                                                                                                                                                                                                                                   245 GAGGTCCATCGGCTGGTGGTGGTAAATGAAGCAGATAGTATTGTGGGGTATTATTTCCCTG 304
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                               ;
                                                                                                             DB 9; Length 1446;
                                                                                                      Score 123.6; DB 9; Length
Pred. No. 1.6e-26;
0; Mismatches 134; Indels
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
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Patent No. US20020048763A1
                                                                                                      Query Match 7.5%;
Best Local Similarity 60.4%;
Matches 204; Conservative (
; ORGANISM: Homo sapiens US-09-822-846-559
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APPLICANT: Chen, Wenshang
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Accomica -x -1
CURRENT PILITING DATE: 2001-05-23
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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N: EXPRESSED IN HEART, SIGNAL = 4.1

N: EXPRESSED IN PLACENTA, SIGNAL = 4

N: EXPRESSED IN BALGAL SIGNAL = 3.9

N: EXPRESSED IN BULT LIVER, SIGNAL = 5.8

N: EXPRESSED IN BULT LIVER, SIGNAL = 5.3

N: EXPRESSED IN BULT LIVER, SIGNAL = 5.3

N: EXPRESSED IN BULT LIVER, SIGNAL = 4.8

N: EXPRESSED IN LUNG, SIGNAL = 4.2

N: EXPRESSED IN BRAIN, SIGNAL = 4.2

N: EXPRESSED IN BRAIN, SIGNAL = 4.3

N: EXPRESSED IN BRAIN, SIGNAL = 4.3

N: EXPRESSED IN BRAIN, SIGNAL = 4.3

N: EXPRESSED IN BRAIN, SIGNAL = 4.3

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PRIOR APPLICATION NUMER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00667
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-01-30
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                             Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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US-09-864-761-20146
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,9, or c NAME/KEY: misc feature LOCATION: (350)
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                                                                                                                                                                                                 OTHER INFORMATION: n equals a, t, g, or c
                                                                                                   OTHER INFORMATION: n equals a,t,g, or NAME/KET: misc feature
LOCATION: (132)
LOCATION: (73)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (259)
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (411)
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Matches 124; Conservative
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651 AGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTC 704

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Matches

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Sequence 20146, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:

us-09-826-581-5.rnpb

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SEQ ID NO 2472
LENGTH: 897
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LENGIH: 821
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 06/206,220
PRIOR RILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SEQ ID NO 2282
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
3.2%; Score 53.4; DB 9; Length 457; 53.6%; Pred. No. 7.8e-06; tive 0; Mismatches 96; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2472, Application US/10198846; Publication No. US20030099974A1; GENERAL INFORMATION:
                                                                                                                                            Sequence 2282, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION:
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LOCATION: 2, 3, 4, 5
OTHER INFORMATION: n = A,T,C or G
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Matches 111; Conservative
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
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US-10-198-846-2472/c
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APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INTENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 (
FILE REFERENCE: 11145-00701
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR PAPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111111111 | 1111 | 111 | 111 | 1111111 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.2%; Score 52.2; DB 9; Length 897; 56.8%; Pred. No. 2.2e-05; tive 0; Mismatches 73; Indels
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                                                                                                                    APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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Publication No. US20030073623A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 52; Conservative
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US-09-826-581-1
ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-918-995-16257
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US-10-198-846-2472
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1369 GCAGGTACACAGGCTGGTGCTAGTGGACGAGACCCAGCATCTCTTGGGCGTGGTCTCCCT 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 GCAGGTCCATCGGCTGGTGGTGGTAATGAAGCAGATAGTATTGTGGGTATTATTTCCCT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43.4; DB 10; Length 458;
Pred. No. 0.0073;
0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN PR474, SIGNAL = 7.6
OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 7.6
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN HBL3, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN HBL3, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
US-09-864-761-693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1429 CICCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCA 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 GTCGGACATTCTGCAAGCCCTGATCCTCACACCACCAGGTA 302
                                                                            FRIOR FILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2000-09-21

PRIOR PELING DATE: 2000-09-21

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers: 1.1

SEQ ID NO 633

LENGTH: 458
                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
     APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June 13, 2003, 09:00:38
Job time: 521.839 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.6%;
Best Local Similarity 64.4%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
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Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Renk, David R.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                                                                                                                                                                                418 GGAGCTGGCCACGGAGTTCCCAGGCACAGAGGCCTGGGAGTGTGAGCTAGAAGGCCTGCT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 GGAAGAGGCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       538 TGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 AGAAGAACCGCGAGGAGGAGGAAGAAGATCCGGCTGGTCAGCCACCCGGAGGAGCCCGT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACGATGCCATGGCAACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 GGCTGGTGCACACACACACACACGCCAAGCTCTTCATGGTGGCCGTGAAGCAGGAGTTGAG 295
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                             Query Match 2.8%; Score 46; DB 9; Length 396; Best Local Similarity 47.8%; Pred. No. 0.0012; Matches 133; Conservative 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    658 GAAGGCCTTCTTTGCTCTGGTGCCCAACGGTGTGCGGG 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 CCAAGCCAACTTTGCCACCTTCACCCAGGCCCTGCAGG 333
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-36
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-7
PRIOR PILING DATE: 2000-09-7
PRIOR PILING DATE: 2000-09-7
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16257
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CURRENT FILING DATE: 2001-05-23
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-16257
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Copyright (c) 1993 - 2003 Compugen Ltd.
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2115 bp mRNA linear PRI 03-JUN-2000 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3) AF214519
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RFWGWEHTCVDAMATGSKLVIFDPMLEIKKAFPALVANGVRAAPLABSKKOSFVORLTI
TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLGGCFKPLVSISPNDSLFRBAVYTLI
KNRIHELPULDPVSGNVHAHTTHFRIKLKFLHFEGSLLPRFSTRYRTIGDGGGFFRDL
AVVEETAPILTALDIFUDRRYSALPVNNECGOVGEYSREDYHHLDMSY
GEALRQPTLCLEGYLSCOPHESLGEVIDRIARRQVHRLVLVDFTQHHLGWVSLSDILQ
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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/db_xref="GI:13538837"
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LwdskkqsfvgaltitdpilvlhryrsPlvqiyeieqhkiffwreiklqgcfkplvs
Ispndslfravytiknrhrleyldpysgwhlhithkrlikfhikehhifgellprpsfy
Yrtigdslgffrdlavvletafpiltaldifvdrkvsalpvvnecgqvglysrfdyt
Hladqqtynhlidasvgellkogthchesqviscqphesigevidriareqvhrlvydb
TQHLLGvvslsdillqalvlspaqidalga"
621 c 560 g 470 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2109)
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Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (EE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Pred. No. 5.6e-08;
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/db_xref="G1:13538811"
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Sequence 3 from Patent WO0120003.
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/db_xref="taxon:9606"
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Arexis AB (SE)
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LVANCYRAAPLWDSKKOSFVGMLTTDPTLVLHRYYRSPLVQTYETBQHKTETWREIY
LQGCKRPLVSISPNDSLEBAYYLLIRNRIHRLPVLDPVSGNVLHILTHRRLLKFLHIP
GSLLPRPSELYRTIQDLGTGFRBLAVVLETAPILTALDIFVDRNSALPVVNBCGQV
VGLYSREDVIHLAAQQYYNHLDMSVGBALRKRTLCLEGVLSCQPHBSLGEVIDRIARR
QVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDPSGPEXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MEPGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTS
SSERIKGKRAKALWATPKQKVEDESPEGQERGENSRPASTGGLEBATFFKTTPLAQA
DPAGVGTPPTGWOCLPSOCTASARGSSTDDNELATEPATAMECELEGLLEERPALC
LSPQAPFPKLGWDDELRKPGAQIYMRFIEBHTCYDAMATSSKLVIPDTMLEIKKAFRAPA
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Arexis AB (SE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="AMP-activated protein kinase gamma 3 subunit"
/protein_id="CAB65117.1"
/db_xref="GI:6688201"
                                                                                                         Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
Blochem. J. 346 Pt 3, 659-669 (2000)
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                                                                                                                                                                                                                                         (bases 1 to 2290)
Carling, D.
Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress Group, M
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, M12 ONN, UNITED KINGDOM
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 61; Conservative 0; Mismatches 0;
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Sequence 2 from Patent WO0177305.
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SSTDDVELAFEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
RFWQEHTCYDAMATSSKIV1FDTMLEIKKAFFALVANGVRAAPLMDSKKQSFVGMLTI
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KNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSV
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                                                                                                                                                                                                                                                A mutation in PRKAG3 associated with excess glycogen content in pig
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AJ249977 AJ249977.1 GI:6688200
AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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0; Mismatches 0; Indels
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/db_xref="G1:8215682"
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/chromosome="2"
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Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152129)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                      Score 51; DB 6; Length 70.,; Pred. No. 5e-05;
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                                                                                                                                                                                                                                                        ch 83.6%; Score 51; DB 1 Similarity 100.0%; Pred. No. 5e-51; Conservative 0; Mismatches
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                                                                    /organism="Homo sapiens"
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arbitrary. Gaps between the contigs are represented as runs of M, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as its available and the accession number will be preserved.
                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
Consensus quality: 135376 bases at least Q40 Consensus quality: 14364 bases at least Q30 Consensus quality: 146503 bases at least Q20 Insert size: 161000; agarose-fp Insert size: 164029; sum-of-configs Quality coverage: 3.1 in Q20 bases; sum-of-configs Quality coverage: 3.3 in Q20 bases; sum-of-configs
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12556: contig of 2473 bp in length
12656: gap of 100 bp
15043: contig of 2387 bp in length
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38179: contig of 4111 bp in length
38279: gap of 100 bp
42366: contig of 4087 bp in length
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101193: contig of 7779 bp in length
101293: gap of 100 bp
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1928: contig of 2362 bp in length
128: gap of 100 bp.
24319: contig of 2291 bp in length
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51285: contig of 4820 bp in length
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60595: contig of 4624 bp in length
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contig of 5900 bp in length
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73218: contig of 6523 bp in length
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7115: contig of 3797 bp in length
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113091 113190: gap of 100 bp
113191 123496: contig of 10306 bp in length
123497 123596: gap of 100 bp
123597 133787: contig of 14241 bp in length
137938 152129: contig of 14192 bp in length.
Location/Qualifiers
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AC009974 206854 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
M (053108, USA
4 (bases 1 to 206854)
Waterston, R.H.
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Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
5 (bases 1 to 206854)
Waterston, R. H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Matazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
1 (bases 1 to 2068s4)
2 Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                        Gaps
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Center code: WUGSC
                                                                                                                          2925 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAAGCCACCACCAGGTCAGGGGGAAGGT 2875
                                                                                                1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51
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     Length 152129;
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
Unpublished (2001)
3 (bases 1 to 206854)
Waterston,R.H.
83.6%; Score 51; DB 2; Length 152
100.0%; Pred. No. 2e-05;
ive 0; Mismatches 0; Indels
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Contact: sapiens@watson.wustl.edu
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Query Match
Best Local Similarity 100.
Matches 51; Conservative
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281. .344
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/note="match to EST BF183086 (NID:g11061273)"
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                         'note="match to EST BE314060 (NID:99134719)"
                                                                                                                                                                                                                                                                      /note="similar to Homo sapiens EST BII14348 (NID:914565249)"
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599. .763
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(NID:914565249)"
967. .1085
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100.0%; Pred. No. 1.9e-05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                         The RPCI-11 human BAC library was made from the blood of one male donor, as described by Geogawa, K. Woon, P.Y., Zhad, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                         Mapping information for this clone was provided by Dr. John D. Mcherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/ssc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match to EST AW880850 (NID:g8042860)"
281. .344
/note="match to EST BE047599 (NID:g8364652) tz39c01.y1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match to EST BE047599 (NID:98364652) tz39c01.y1"
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  more than one subclone; and the assembly was confirmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"match to EST BF183086 (NID:g11061273)#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match to EST BF304755 (NID:g11251653)"
1. .37
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1. .37
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/note="match to EST AL567345 (NID:g12920610)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="match to EST AL567345 (NID:g12920610)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="match to EST BE908408 (NID:g10402954)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match to EST BE314060 (NID:99134719)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to Homo sapiens EST BI114348
(NID:g14565249)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match to EST C05773 (NID:g1502549)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                        (http://bacpac.med.buffalo.edu)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11"
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                                                                          "APPING INFORMATION:
                                                                                                                                                                                                                       SOURCE INFORMATION:
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Ouery Match 68.5%; Score 41.8; Best Local Similarity 80.3%; Pred. No. 0.0 Matches 49; Conservative 0; Mismatches
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AX099800
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1. 1873
/organism="Sus scrofa"
/db_xref="taxon:9823"
/chromosome="15"
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                                                                                                                                                                                                                                                                                                                               /gene="PRKAG3"
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                                    REFERENCE
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LWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVS
ISPNDSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRTIQDLGIGTFRDLAVUETAPILTALDIFVDRRVSALPYVNETGQVVGLYSNEDVI
HLAAQQTYNHLDMNVGEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVIDDE
TQHLLGVVSLSDILQALVLSPAGIDALGA"
1883 c 529 g 375 t
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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. and Andersson, L.
                                                                        PAT 02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 ACAAGGCAGGAGGATGTAGAGGAGGGGGGCCTCCGGGGCCCGAGGGAAGGTCCCCAGGTC 159
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                          Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
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                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product"
                                                                          DNA
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                                                                Sequence 1 from Patent W00120003.
AX099774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAC35798.1"
/db_xref="GI:13538809"
                                                                                                                                                                                                                                                                                                                                                                                                                          1. 1867
/organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                             AX099774.1 GI:13538808
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AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRPDVIHLAAQQTYNHLDMNV
GEALRORTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
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KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
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GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Roblo, A., Reinsch, N., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L. Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
1. 1873
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/db_xref="GI:8215684"
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Andersson, L., Doft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., 1e Roy, P. and
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0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="skeletal muscle"
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/translation-"MSFLEQGESRSWPSRAVTTSSERSHGDQGTKASRWTRQEDVEEG
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HFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLMDSKKQSFVGMLTI
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KNRTHRELPVLDPVSGAVLHILTHFRELKFLHFGTLLERSFELYRTIODLGIGFFRDL
AVVLETAPTLTALDIFVDRAVSALPVNHETGOVVGIXSREVYIHAAQOTYNHLDMN
GEALRORTLCLEGVISCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGWVSESDILQ
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothschild, M.F., Clobanu, D.C., Malek, M. and Plastow, G.
Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meet quality traits
Patent: WIO 202810-A 3 14-MAR-2002;
Iowa State University Research Poundation, Inc. (US)
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Pred. No. 0.021;
0; Mismatches 12;
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/note="unnamed protein product"
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AX398333
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/db_xref="taxon:9823"
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Local Similarity 80.3%;
les 49; Conservative (
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KEYWORDS
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KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
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KNRTHRLPVLDPYSGAVLHILTHKRLLKFLHIFGTLLPRESFLYRTIQDLGIGTFRDL
AVVLEFTRALITALDIFVDRRYSALPVVNETGQVVGLYSRFDVTHLAAQQTYHLIDMNV
GEALRQRYLCLEGOYLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA
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DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G. Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits Patent: WO 0220850-A 1 14-MAR-2002.

Iowa State University Research Foundation, Inc. (US)
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                                                                                                                                                                                                                                                                                                                                                                                       68.5%; Score 41.8; DB 6; Length 1873; 80.3%; Pred. No. 0.021;
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AX398331
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/db_xref="taxon:9823"
organism="Sus scrofa"
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DSNTTHILDEGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGNDDELQKPGAQVYM
HFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVQAAPLMDSKKQSFVGMLTI
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GEALRQRTLCLEGGVLSCQPHETLGEVIDRIVSEQVHRLVLVDETQHLLGVVSLSDILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOFILVLHRYTRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFBAYALI
KNRTHRLPLDPVSGAYHILTHREKELHFGTLLRPSETLYRDDDGJGGFPRDL
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GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
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HFWQEHTCYDAARTSSKLVIFOTMLEIKKAFPALVANGIRAAPLMDSKRQFFVGMLT
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Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 9 14 *MRR-2002;
Iowa State University Research Foundation, Inc. (US)
Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 7 14 MAR-2002,
Iowa State University Research Foundation, Inc. (US)
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/note="unnamed protein product"
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/db_xref="G1:21261115"
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/db_xref-"G1:21261113"
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/organism≃"Sus scrofa"
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                                             Score 41.8; DB 6; Length 1873;
Pred. No. 0.021;
0; Mismatches 12; Indels 0
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Human AMPK gamma s
PRKAG3 intron 2 -
Pig AMPK gamma sub
Pig AMPK gamma sub
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Pig PKRAG3 Polymor
Pig PKRAG3 Polymor
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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	10	41.8	68.5	1873	22	AAD36460 AAD03321	Pig PRKAG3 polymor
	12	40.2	62.9	1873	7	AAD36458	PRKAG3
	13	32.6	53.4	1095	24	AAD36461	PRKAG3
	14	31.4	43.5	808	4 6	AAD36462 AAS84523	PRKAG3 gene
	16	25.6	42.0	323	22	AAL21877	
	17	25.6	42.0	711	533	AAS84420	DNA encoding novel
ט ט	13	25.4	41.6	2238	7 7	AAD37390	Human IKca channel
	20	25.4	41.6	2261	25	AAX24825	Human calcium acti
	21	25.4	41.6	3632	20	AAT06978 AAY21373	T. thermophilus ga
	7.7	25.4	41.6	49999	0 0	AAZ23900	Human LOBO homolog
	24	25	41.0	260	24	ABK95404	Human retina speci
	25	25	41.0	1188	24	ABK95403	retina s
o c	25	2.5 5.5	41.0	1927	2 5	ABV23466 ABV29324	Human prostate exp
	28	25	41.0	4034	242	ABL68109	Ovary cancer relat
	29	25	41.0	4035	1	AAQ05872	Sequence encoding
	30	25	41.0	4035	11	AAQ06331	Human IL-2R beta c
	31	25	41.0	8670	20	AAZ32059	Human METH2 relate
	32	52	41.0	8670	7 6	AAC90316	X16619 CDNA clone.
	2,5	2. 4. c		2002	77	AAS45150	CONA encoding nove
	35	24.6	40.3	1068	23	ABL27039	Drosophila melanod
	36	24.6	40.3	2445	21	AAZ95746	Murine bone morpho
	37	24.6	40.3	2447	17	AAQ74084	Murine BMP-9 cDNA.
c	200	2. 4. 0. 4.	40.4	2448	14 C	AAQ35243 aau16987	Encodes murine bon
	40	24.6	40.3	2996	7 7	AAS62392	
υ	41	24.6	40.3	3140	23	ABL27038	phila
	42	24.6	40.3	3580	74	ABK13766	CD)
	43	24.6	40.3	5312	22	AAS40665 AAT06553	DNA encoding human Human reproductive
	45	24.6	40.3	5381	22	AAF30037	Apolipoprotein A-I
						ALIGNMENTS	
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                                                                                                                                                                                                                                                                                                                myopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC 60
                                                                                                                                                                New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obseity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution PTAA; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                       This sequence represents the full length cDNA encoding the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 61; DB 22; Length 1647; 100.0%; Pred. No. 6e-10; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
                                                                                                                Andersson L, Luthman H, Marklund S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                 Disclosure; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD03296 standard; DNA; 2109 BP.
                                             06-APR-2001; 2001WO-SE00765.
                                                                    07-APR-2000; 2000US-195665P.
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472..1389
/*tag= b
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Matches 61; Conservative
                                                                                                                                        WPI; 2001-657170/75.
                                                                                           (AREX-) AREXIS AB.
                                                                                                                                                  P-PSDB; QQB47679
WO200177305-A2
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                        18-OCT-2001.
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP) gamma subunit muscle-specific isoform, PRKAG3. Mutation in PrkAg3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders associated with muscle metabolism as diabetes, obesity, and disorders associated with muscle metabolism cuch as myopathy and cardiovascular diseases, to modulate AMPK cutivity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic amarker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a cheterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robic A, Rogel-Gaillard C;
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/product= "Human Prkag3 protein"
1390..2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersson L, Looft C, Kalm E, Milan D, Robic Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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                                                                                                                                                                                                                                                                                                  11-SEP-2000; 2000WO-EP09896.
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18-MAY-2000; 2000EP-0401388.
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hes 61; Conservative
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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
                                                                                                                                                                                                                                                                                                                                                     metabolic disease; diabetes; obesity; substitution; ds
                                                                                                                                                                   AAH43682 standard; DNA; 989 BP.
                                                                                                                                                                                                                                                                                            PRKAG3 intron 2 - intron 4.
                                                                                                                                                                                                                                                    21-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3 Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PKKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRRAG3 and is useful in gene therapy.
                                                                                                   PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                        Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ooft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a cDNA encoding human adenosine monophosphate
                                                                                  gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                        /product= "Human complete Prkag3 protein"
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ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
  (first entry)
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13-JUN-2001
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New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PKKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution of a Stor a C at nucleotide 550; and in exon 10 variation may be a substitution of a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a Substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                             intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "5' portion of intron 4"
                                                                                                                         /note= "3' portion of 22..177
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                                                                                          a "Intron 2"
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r= "Intron 3"
                                             Location/Qualifiers
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/*tag= d
/number= "Exon 4"
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Homo sapiens
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Gaps ; 0

Indels

Pred. No. 6.1e-10; 100.0%; Score 61; DB 22; 100.0%; Pred. No. 6.1e-10; 0; Mismatches

61; Conservative

Matches

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Best Local Similarity

Query Match

Length 2115;

9

1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC

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Looft C,
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P-PSDB; AAE00222.
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(ANDE/) ANDERSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 15; ss.
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                                                                                                                                                                                                                           PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                    gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                             1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGT 51
                                                 ö
                                                                                                                                                                                                 Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                             Length 989;
                                               0; Indels
                                                                                                                                                                                                                                                                                                                           /*tag= b
/product= "Sus scrofa PRKAG3 protein"
1390..1867
        Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
                            DB 22; I
                                               Mismatches
                            Score 51;
Pred. No.
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                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                            83.0%,
100.0%; Ple
                                                                                                                                     AAD03295 standard; cDNA; 1867 BP
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                                               51; Conservative
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                                      Similarity
                                                                                                                                                                                                                                                           chromosome 15; ss.
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Iannuccelli N,
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                                                                                                                                                                                                                                                                               Sus scrofa.
                           Query Match
Best Local S:
Matches 51;
                                                                                                                                                         AAD03295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myopathy
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5'UTR
                                                                                                                                                                                                                                                                                                                                                           3'UTR
                                                                                                                   RESULT 5
AAD03295
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SO
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                                                                   Qγ
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such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and lits functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transpenic animal and host cell transformed with PRKAG3 or a cheterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrKaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41.8; DB 22; Length 1867;
Pred. No. 0.00058;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Sus scrofa complete Prkag3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAT RECH AGRONOMIQUE.
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1..1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD03319 standard; cDNA; 1873 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.5%;
80.3%;
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18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 80.3°
Matches 49; Conservative
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1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
                                               /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein scharacterised by polymorphism(s) in the AMP activated protein is characterised by polymorphism(s) in the AMP activated protein finase requiatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig wild-type PRKAG3 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMF activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP; gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
                                                                                                                                                                                                                                                                                                                                               (IOWA ) UNIV IOWA STATE RES FOUND INC.
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     replace (599, A) /*tag= e
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20010S-260239P.
20010S-299111P.
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                                                                                                                                                                                               10-SEP-2001; 2001WO-US28283.
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nes 49; Conservative
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                                                                                                                                                                                                                                                                        08-JAN-2001;
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     variation
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Matches
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                                                                                                                                                         The present sequence is a cDNA encoding pig adenosine monophosphate

(AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

complete PRKAG3: Prkag3 gene is located in the RN locus of chromosome

15. Mutation in Prkag3 results in an altered regulation of carbohydrate

catabolism, particularly in skeletal muscle. PRKAG3 is useful as

therapeutic for treating carbohydrate metabolism disorders such as

catabolism, particularly in skeletal muscle metabolism

cubabetes, obesity, and disorders associated with muscle metabolism

cuch as myopathy and cardiovascular diseases, to modulate AMPK

activity, and for restoring a normal AMPK function. PRKAG3 sequence

and its functionally altered mutants are useful for the diagnostic

cativity, and for restoring and prognosis of a metabolic disorder.

cevaluation, genetic testing and prognosis of a metabolic disorder.

preferably a carbohydrate metabolism disorder. Primers that can detect

cevaluation marker linked to a sequence encoding PRKAG3, are

useful for detecting a dysfunction of carbohydrate metabolism resulting

from the expression of a functionally altered with PRKAG3 or a

grant programmal and host cell transformed with PRKAG3 or a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a sequence encoding the first cystathione beta synthase (CBS) domain
New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.8; DB 22; Length 1873;
Pred. No. 0.00058;
0; Mismatches 12; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRKAG3 and is useful in gene therapy
                                                                                                                      Claim 12; Page 62-64; 71pp; English.
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80.3%;
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Best Local Similarity
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us-09-826-581-5_copy_200_260.rng

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The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
                    /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                         Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.5%; Score 41.8; DB 24; Length 1873;
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                                                                                                                                                                                                                                                  Malek M, Plastow G;
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0; Mismatches 12
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Matches 49; Conservative
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P-PSDB; AAE22987.
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      variation
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                                                                                                                                                                                                                                                                                                                      Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PRKAG3-30)
                               /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein thase requiatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant DNA (PRRAG3-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41.8; DB 24; Length 1873;
Pred. No. 0.00058;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                               Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 89-91; 109pp; English.
                                                                                                                                                                                                                 (IOWA ) UNIV IOWA STATE RES FOUND INC.
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1..1395
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replace (89, C)
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.3%;
                                                                                                                                                    08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                        10-SEP-2001; 2001WO-US28283
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es 49; Conserv
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                                                            WO200220850-A2
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/product= "Sus scrofa Prkag3 splice variant"
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Best Local Similarity
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                                              22-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRŘAG3; diabetes; obesity; myopathý; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                        Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma subunit gene
                      /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subunit; adenosine monophosphate-activated kinase; AMPK;
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                                                                                                                                                                                    Malek M, Plastow G;
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                                                                                                                                                                                                                                                                                                     Disclosure; Page 102-104; 109pp; English.
                                                                                                                                                              (IOWA ) UNIV IOWA STATE RES FOUND INC.
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replace (599, A)
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                                                                                                               08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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                                                                                           10-SEP-2001; 2001WO-US28283.
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08-JAN-2001;
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Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism cativity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3. are useful for detecting a dysfunction of carbohydrate metabolism resulting crompounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 or a conding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or no a sequence encoding the first cystathione beta synthase (CBS) domain compounds and the strangatione beta synthase (CBS) domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTCC
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Pred. No. 0.00059;
0; Mismatches 12; Indels 0;
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                                                                                                                                                                                                (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDERSSON L.
(LLOGF/) LOOFT C.
(KALM/) KALM E.
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80.3%;
11-SEP-2000; 2000WO-EP09896.
                                                                            10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                  AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; polymorphism; short interspersed element; pig; SINE; ds.
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/note= "Direct repeat present between short
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                PRKAG3 gene 5' flanking region with SINE
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Best Local Similarity 74.5%;
Matches 38; Conservative 2
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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/number= 1
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/*tag= b
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826..979
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/standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                 "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
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                                                    AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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Pred. No. 0.0018;
0; Mismatches 13; Indels 0;
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                Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
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                                                                                                                                                            Location/Qualifiers
1..1395
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78.7%;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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es 48; Conservative
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08-JAN-2001;
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                               DNA encoding novel human diagnostic protein #20327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 20327; 103pp; English.
               AAS84523 standard; cDNA; 2541
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23-AUG-2000; 2000US-0649167.
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                                                                             13-FEB-2002 (first entry)
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                                                AAS84523;
AAS84523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 gene 5' flanking region including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                             AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; polymorphism; pig; ds.
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                                                                                                                                              Pig PRKAG3 gene 5' flanking region including exon and intron.
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Pred. No. 0.94;
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                                                AAD36462 standard; DNA; 808 BP.
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Local Similarity 74.5%;
les 38; Conservative 1
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18-JUN-2001; 2001US-299111P.
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               RESULT 14
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Tang YT;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the printed and to produce other types of data and products dependent on DNA and diagnostics coding sequences of the invention.

Sequence and to produce data for this patent did not appear in the printed to be a sequence data for this patent did not appear in the printed sequence that was obtained in electronic format directly from WIPO
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Best Local Similarity 67.3%;
Matches 37; Conservative (
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Eukaryota' Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Arakaryota; Lo 621)

Arakawa, T. Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A. Hiramcto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takahashi, F., Takeda, Y., Suzuki, H., Tagami, M., Tagami, M., Tagami, M., Tagami, M., Tagaki, S., Sasaki, S., Shinasawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
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Minimum DB : Maximum DB :

Database

H92825 AQ169119 BB823175

BM702805 BI085954 BQ642252

BI507914

ALIGNMENTS

BB630381 AW356079 38073 MAR AW427435 63185 MAR BF890374 291826 MA

BB630381 AW356079 AW427435 BF890374

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125459

Result No. BB629521

AW693375 NRC034101 BM466469 AGENCOURT BM466469 AGENCOURT BM466469 AGENCOURT BC244994 602358260 ALI73081 TETEAGACO BC44994 GC2558260 ALI73081 TETEAGACO BC46565 32.0088_B BC976192 AGENCOURT AW353555 33889 MAR BE33578 CMO-FN004 BW773644 283021 NA BH235980 452622 NA BH23599 ATZKD35TR BH23599 ATZKD35TR BH23599 ATZKD35TR BH23599 ATZKD35TR BH23599 ATZKD35TR BC33599 ATZKD35TR BC33599 ATZKD35TR BC33599 ATZKD35TR BC33599 ATZKD35TR BC33599 ATZKD35TR BC3360 BC32725 BC94119 BC33548 BC963198 GC2828235 BC963198 GC2828235 BC9783197 UI-R-CS0-BC301020 AGENCOURT BC301020 AGENCOURT BC301020 AGENCOURT BC301020 AGENCOURT BC31020 AGENCOURT

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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1711 (2000)

Konno, M., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishi, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-186 (2001

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dassa 1 to 655)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., M., Koya, S., Mustuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinadawa, A., Takahashi, F., Takeda, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninol.P., Shibata,Y., Bayatau,N., Sugahara,Y., Shibata,K., Itoh
M., Konno.H., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Normalization and Subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fuliwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
"S., Kawat,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [55
GAGAGAGAGAGACCATTITITITITIVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9226
             BB629521 RIKEN full-length enriched, adult male bone Mus musculus cDNA clone 9830138C07 5', mRNA sequence.
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/clone_lib="RIKEN full-length enriched, adult male bone"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
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/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                        sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3'j. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
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Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Rewal,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTCC 60
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Pred. No. 0.17;
0; Mismatches 14; Indels 0;
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/dev_stage="16 days neonate"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="9630039L22"
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Arakawar T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda
,M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
,D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Muramatsu, M., Tadawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y., et al. 2001)
Contact: Yoshihide Hayashizaki
DB630381 RIKEN full-length enriched, 6 days neonate skin Mus musculus cDNA clone A030014A04 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encyclopedia: real-time sequence clustering for construction of a norredundant CDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo.S., Shinagawa,A., Saito.T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carnincip.P. Shibata,Y., Hayatsu,W., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper_selected cDNAs to
prepare full-length cDNA libraries for rappid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsunra
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, "Suruwmi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1 (bases 1 to 399)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 0.17;
0; Mismatches 14; Indels 0;
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AWJO5079
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                                                                                                                                                                                                                                                           /tissue_type="skin"
/dev_stage="6 days neonate"
/lab_host="DH10B"
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                                                                                                                                                     /organism="Mus musculus"
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/clone="a030014A04"
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1 Similarity 77.0%;
47; Conservative (
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Keaton, M.P., Laegreid, W. W., Rohrer, G.A., Chitko McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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BF890374
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Email: smith@email.marc.usda.gov
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/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
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/tissue_type="pooled"
/lab_host="DH10B"
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  Plate: 32 row: F column: 22
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                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
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2 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E.W. Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
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PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
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/organism="Bos taurus"
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                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 17 row: P column: 9
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
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                                                                                                                                         and -minmatch 12 options.
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AW427435.1 GI:6955382
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/clone="lyaGE:1970001"
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NcI Mouse EST Project 1999

Unpublished (1999)

Other, ESTS: ukzbbo,xl

Contact: Marra M/WashU-NcI Mouse EST Project 1999
Washington University School of Medicine
4444 Porest Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science).
                                                                                                                                                                                                                 EST 10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                           AI664508 516 bp mRNA linear EST 10-M
uk25b05.yl Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1970001 5', mRNA sequence.
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139 c 171 a
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High quality sequence stop: 484.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL"
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 548)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertca, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
1 147 c 139 g 67 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
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                                                                                                                                                                                     Length 444;
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                                                                                                                                                                                                                                              Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                           13;
                                                                                                                                                                                     DB 12;
                                                                                                                                                           56.1%; Scc. 76.4%; Pred. No. 3, 76.4%; O; Mismatches
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173 c 163 q 93 t
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Plate: 90 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG.
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/clone_lib="MARC 2BOV"
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/lab_host="DH10B"
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72.1%;
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Best Local Similarity 72.1
Matches 44; Conservative
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Fax: 402 762 4390
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/tissue_type="whole embryo"
/dev_stage="stage 25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
Were oligo-dT primed and directionally cloned. Staging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleusiomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library
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BJ080431 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL075jl6 3', mRNA sequence.
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                                                  Medicago truncatula stem library
Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7568111.
Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cisue_______/dev__stem,
/dev_stagae"stem,
/dev_stagae"Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
a 107 c 137 g 200 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGG 44
                                                                                                                                                           The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USF Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 660 Std Error: 0.00
Pate: 063 row: H column: 10
Seq primer: TCACACAGGAAACAGCTATGAC.
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="NF063H10ST"
/clone_lib="Developing stem"
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                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .618
/organism="Medicago tr/db_xref="taxon:3880"
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Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
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/clone="madd7a1"
/clone="madd7a1"
/clone=lib="Aspergillus nidulans 24hr asexual
developmental and vegetative coNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBlueScript SK-; Site_1: EcoRI: Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript
a 118 c 96 9
         EST 31-JUL-1998
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Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
AA787203

365 bp mRNA linear EST 31-JUL-199 m8407a1.rl Aspergillus nidulans 24hr asexual developmental and vegetative CDNA lambda zap library Emericella nidulans CDNA clone
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ACAAGGCCCGTGTCGCGGGAAGAAGCCGACTCAGCAGGAGGAGGAAGAGGTAGCTGGTCC 3
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NF063H10ST1F1000 Developing stem Medicago truncatula cDNA clone
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Prade,R. and Roe,B.
                                                                                                                                                                                                                                                                                                                                                                                Contact: Bruce A. Roe, University of Oklahoma, broecou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oyal, Norman, OK 73019, USA
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Eurotiales; Trichocomaceae; Emericella.
1 (bases 1 to 365)
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Pred. No.
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                                                                     m8d07a1 5', mRNA sequence
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                                                                                                               AA787203.1 GI:2847434
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                                                                                                                                                           Emericella nidulans.
                                                                                                                                                                             Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: broe@ou.edu
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Fax: 405 325 7762
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1 243 c 241 g 161 t
                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute). " 128 c 196 g 150 t 1 others
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/tissue_type="spontaneous tumor, metastatic to mammary.
/tissue_lorigin."
/lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Cloud through the I.M.A.G.E. Consorthum/LLNL at:
http://image.llnl.gov
Plate: LLAMBS40 row: n column: 19
High quality sequence stop: 552.
Location/Qualifiers
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procutement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
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                                                                                                                    Length 669;
                                                                                                                                                       20; Indels
                                                                                                                Score 28; DB 13;
Pred. No. 2e+02;
0; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:3493458"
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                                                                                                                ch 45.9%;
l Similarity 66.7%;
40; Conservative
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/dev_stage="Breast,leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(ld,7d,14d post-hatch)" /lab_host="E. coli EMDH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Vector: pcwvSpORT6: Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
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AGENCOURT_6456404 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5579448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="pgm2n.pk010.p18"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves: Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 590)

Cogburn, A. and Monsonego-Ornan, E. BSTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate CDNA library, USDA/IPAFS Animal Genome
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
clone pgm2n.pk010.p18 5' similar to ref|NP_060575.1 (NM_018105)
hypothetical protein FLJ10477 [Homo sapiens] dbj|BAA91635.1|
(AK001339) unnamed protein product [Homo sapiens], mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27.4; DB 13;
Pred. No. 3e+02;
0; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .590
/organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strains 90 & 21"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Larry A. Cogburn
University of Delaware
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SW Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 151)

8 NIH-WGC http://Mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Ph.D.

Contact: Robert Strausberg, Ph.D.

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Contact: Robert Strausber
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="lib="NiH=MGC_67"
/clone=lib="NiH=MGC_67"
/tissue_type="retinoblastoma"
/lab_host="OH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: Not1:
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies:"
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Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAMI2336 row: c column: 01

High quality sequence stop: 681.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AAGGCACAAGTCGGTCGAGGAAGGCGAGCCACCAGGTCAGGGGGGAAGGT 51
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/clone_lib="WCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
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/db_xref="taxon:10090"
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providing samples: Gilbert Smith, NIH"

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4027.262 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-750-222h-1

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US-08-254-353h-1

US-08-254-353h-1

PCT-US95-0534h-1

PCT-US95-07084-1

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length: 2000000000
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Sequence 14, Appl
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; Patent No. TANGUCHI, TADATSUGU;HATAKEYAMA, MASANORI;MINAMOTO, SELIRO;KONO, TARESHI;DOI, TAKESHI;MIXASAKA, MASAYUKI;TSUDO, MITSURU;KANASUYAMA, HAJIME
                                                                                                                                                                                                                                                                                                                 APPLICATE: MO. TAKESHI, TADATSUGU; JATAKEYAMA, MASANORI;
MINAMOTO, SEJIRO; KONO, TAKESHI; DOI, TAKESHI; MIYASAKA, MASAYKI;
TSUDO, MITSURU; KARASUYMA, HAJIME
TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,059
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Length 4035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Indels
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us-09-139-7-787-214

us-09-182-145-13

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us-09-182-145-14

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us-09-298-568-1

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Pred. No. 16;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/88,592
FILING DATE: 9-UUL-1993
FRIDR APPLICATION DATE:
APPLICATION NUMBER: 865,155
FILING DATE: 08-APR-1992
APPLICATION NUMBER: 487,059
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.0%;
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Best Local Similarity 64.99
Matches 37; Conservative
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Best Local Similarity
  5198359-1/c
;Patent No. 5198359
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                                                                                                                                                                                               ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,132A
                                                                          GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFRENCE/DOCKET NUMBER: GI 5186A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-181
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDENNES: double
                                     Sequence 1, Application US/08050132A Patent No. 5661007
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STRAIN: C57846XCBA
TISSUE TYPE: liver
IMMEDIATE SOURCE:
LIBRARY: Mouse liver CDNA
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NAME/KEY: mat_peptide
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POSITION IN GENOME:
UNITS: bp
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                                                                                                                                                                                                                                                                           COUNTRY: US
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LOCATION:
FEATURE:
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US-08-050-132A-1
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RESULT 3
US-08-050-132A-1
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tive 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,222A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PROCR APPLICATION DATA:
APPLICATION NUMBER: 08/254,353
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
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                                    Sequence 1, Application US/08750222A
Patent No. 6034061
                                                                       GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
APPLICANT: Thies, Scott
IIILE OF INVENTION: BMP-9 COMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kapinos, Ellan J.
REGISTRATION NUMBER: 32,245
REFRENCE/CDCKET NUMBER: 61 51
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
STRAIN: C57B46xCBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 65.58
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: mat_peptide LOCATION: 1564..1893
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
610..1896
                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                     Sn
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ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , NAME/KEY:
; LOCATION:
US-08-750-222A-1
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RESULT 4
US-08-750-222A-1
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                                                           APPLICANT: ROSEN, VICKI A.
APPLICANT: ROSEN, VICKI A.
APPLICANT: ROSEN, John M.
APPLICANT: Geleste, Authony J.
APPLICANT: Song, Jeffrey
APPLICANT: Thies, Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
TOWBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
DOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Rapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-1170
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nuclet acid
STRANDENNESS: double
              ; Sequence 1, Application US/08254353A; Patent No. 6287816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Mus musculus
C57B46xCBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: mat_peptide LOCATION: 1564..1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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POSITION IN GENOME:
                                                      GENERAL INFORMATION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                ns
                                                                                                                                                                                                                                                              STATE: MA
COUNTRY: US
ZIP: 02140
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-254-353A-1
US-08-254-353A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                        ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
APPLICANT: Song, Jeffrey
APPLICANT: Thies, R. Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/815,652B
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                Sequence 1, Application US/08815652B Patent No. 6034062 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA tO mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
STRAIN: C57B46xCBA
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 65.55
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: mat_peptide
LOCATION: 1564..1893
                                                                                                                                                                                                                                                                                         ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
610..1896
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1..2447
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POSITION IN GENOME:
UNITS: bp
FEATURE:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                               nS
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LOCATION:
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; LOCATION:
US-08-815-652B-1
              US-08-815-652B-1
                                                                                                                                                                                                                                                                               COUNTRY:
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1 ACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCC 55
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tive 0; Mismatches 19; Indels 0;
                                 APPLICANT: Rosen, Vicki A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Releste, Anthony J.
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUMBER: PCT/US95/07084
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/CAGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
FREFERENCE/POCKET NUMBER: GI 5186C-PCT
TELECOMUNICATION INFORMATION:
TELECHONE: (617) 876-1210
TELEPAT: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
Sequence 1, Application PC/TUS9507084 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/09750580; Patent No. 6455280; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA to MRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
STRAIN: C57B46xCBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 65.55
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat_peptide
LOCATION: 1564.1893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE: liver
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POSITION IN GENOME:
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ORIGINAL SOURCE:
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NAME/KEY:
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FEATURE:
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PCT-US95-07084-1
                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US92/05374A
FILING DATE: 19920625
CLASSIFICATION:
                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                                              APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                           Sequence 1, Application PC/TUS9205374A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
STRAIN: C57846xCBA
TISSUE TYPE: liver
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide
LOCATION: 1564..1893
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610..1896
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1..2447
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PCT-US92-05374A-1
                                     RESULT 7
PCT-US92-05374A-1
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PCT-US95-07084-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 TCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGGTC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
ADDRESSEE: Totallectual Property
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-451-777A-7/c

Sequence 7, Application US/08451777A

Patent No. 578923

GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stanbollan, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
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40.3%; Score 24.6; Di
Best Local Similarity 70.2%; Pred. No. 22;
Matches 33; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: primer_bind
LOCATION: 320..338
OTHER INFORMATION: 17-42-319.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 3214..3232
OTHER INFORMATION: 17-41-250.mis complement
                                                                                       NAME/KET: primer_bind
LOCATION: 1632.12651
LOCATION: 1632.12651
COTHER INFORMATION: 17-40.rp complement
NAME/KET: primer_bind
LOCATION: 2964.13984
OTHER INFORMATION: 17-41.pu
NAME/KET: primer_bind
LOCATION: 3432..14454
OTHER INFORMATION: 17-41.rp complement
NAME/KET: primer_bind
LOCATION: 3432..14454
OTHER INFORMATION: 17-41.rp complement
NAME/KET: primer_bind
LOCATION: 300..318
OTHER INFORMATION: 17-42-319.mis
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CLASSIFICATION: 436
PRIOR APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
                      NAME/KEY: primer_bind
LOCATION: 1441.,12461
OTHER INFORMATION: 17-39.rp complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_binding
LOCATION: 307.331
OTHER INFORMATION: 17-42-319.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: 17-41-250.probe US-09-750-580-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: primer_bind
LOCATION: 3194.,3212
OTHER INFORMATION: 17-41-250.mis
OTHER INFORMATION: 17-40.pu
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LOCATION: 3201..3225
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                                                                                                         APPLICANT: Budgelert, Aymeric
APPLICANT: Bouguelert, Aymeric
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
APPLICANT: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REPRENCE: 89.08.2.C.P
CURRENT APPLICATION NUMBER: US 09/599,362
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR PLING DATE: 2000-06-21
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: US 60/113,686
PRIOR PLING DATE: US 60/113,086
PRIOR PLING DATE: US 60/114,032
PRIOR PLING DATE: US 60/141,032
PRIOR PLING DATE: US 60/141,032
PRIOR PLING DATE: US 60/141,032
PRIOR PLING DATE: DESERTED TOWN UMBER: US 60/141,032
PRIOR PLING DATE: DESERTED TOWN UMBER: US 60/141,032
PRIOR PLING DATE: DESERTED TOWN UMBER: US 60/141,032
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OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
OTHER INFORMATION: 1.1022
OTHER INFORMATION: 1.-12.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1241
OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: 17-42-319 : polymorphic base C or T NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 3213 OTHER INFORMATION: 17-41-250 : polymorphic base C or T
                                                                                       Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: primer_bind
LCCATION: 553..11575
ULCCATION: 553..11575
ULCCATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 899..11920
OTHER INFORMATION: 17-39.pu
NAME/KEY: primer_bind
LOCATION: 1246..12267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
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NAME/EEF. ins._feeture
LCCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
                      Denison, Blake
Bour, Barbara
Bihain, Bernard
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OTHER INFORMATION: exon 2
NAME/KEY: exon
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OTHER INFORMATION: exon 1
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1613..1724
OTHER INFORMATION: exon 3
  Yen, Frances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 2243..3940
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LOCATION: 319
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                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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5363 AAGGAACAACTCAGTGTGGGCAGCGGCCAGCCAGTCAAGAGCATGGGCCCTGG 5309
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APPLICATION NUMBER: US/08/998,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application PC/TUS9506743; GENERAL INFORMATION:
                                                                                                                              Sequence 7, Application US/08998208
Patent No. 5880105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-998-208-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.3%;
Best Local Similarity 65.5%;
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 7676 base pairs
                                                                                                                                                                                                                                                                                                                                                       CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-06743-7/C
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                                                                                                           JS-08-998-208-7/c
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                        RESULT 12
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Live 0; Mismatches 19; Indels 0.
                                                                                                                                                                                                                                                                                           40.3%; Score 24.6; DB 1; Length 7676; 65.5%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                    0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION VUNBER: US/08/451,778A
FILNG DATE: 26-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: 709 Swedeland Road/UW220 CITY: King of Prussla STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
ATTLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 37,126
REPERBNCK-POOKET NUMBER: P50268-1B
TELECOMUNICATION INFORMATION:
TELEPHONE: 610-270-5904
TELEPHONE: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-WAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7, Application US/08451778A ; Patent No. 5830649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Eagle, Alissa M. REGISTRATION NUMBER: 37,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 65.55
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                    36; Conservative
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TYPE: nucleic acid
                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19406-0939
COMPUTER READABLE FORM:
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                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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US-08-451-778A-7/C
                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                   ZIP: 19406-0339
COMPUTER READABLE FORM:
MEDIOM TYPE: FLOPPY disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICANT: Sergiam, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
TORRESPONDENCE: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkille Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/UW220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: 7109 Swedeland Road/UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
TILE OF INVENTION: Human Galactokinase Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24.6; DB; Pred. No. 23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 26-MAY-1995
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37,126
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LOCATION: 1239

CTHER INFORMATION: 20-828-311 : polymorphic base C or T

NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 20-841-149 : polymorphic base A or MAME/KEY: allele COCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : polymorphic base C or
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LOCATION: 1357...1377

OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer_bind
LOCATION: 12029...12050

OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581...12603

OTHER INFORMATION: 17-42.rp complement
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OTHER INFORMATION: 20-853.pu
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NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
                                                                                                                         OTHER INFORMATION: 5'regulatory region NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 15969.17969
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 20-853-415
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 20-841.rp
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STHER INFORMATION: 17-42-319
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LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
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LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
                                                                                                                                                                                                                                                           OTHER INFORMATION: exon 2
                                                                                                                                                                                            OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                                                               LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc_feature
LOCATION: 15969..17969
                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 13470..13526
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LOCATION: 14992..15012
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LOCATION: 42572..42591
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LOCATION: 45863..45883
                                                                                     NAME/KEY: misc_feature
                                                                                                           10946..12946
                                                                                                                                                                     LOCATION: 12947..12958
                                                                                                                                                                                                                                                                                                     13641..13752
                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: primer_bind
LOCATION: 1357..1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 77058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 15241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 42218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
                                                                                                                                                                                                                                                                            NAME/KEY: exon
LENGTH: 81001
                                                                                                         OCATION:
                                                                                                                                                                                                                                                                                                     COCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dumas Milne Lu....

APPLICANT: Duclert, Aymeric
APPLICANT: Bouqueleret, Lydie
APPLICANT: Bouqueleret, Lydie
APPLICANT: Bouqueleret, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Ebbets-Reed, Dana
TILE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-06-21
PRIOR PAPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR FILING DATE: 2000-06-21
PRIOR PLING DATE: 10899-12-20
PRIOR PILING DATE: 10899-12-20
PRIOR PILING DATE: 108 49/469/099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGGAAGGTCCCCGG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 40.3%; Score 24.6; DB 5; Length 7676; Best Local Similarity 65.5%; Pred. No. 23; Matches 36; Conservative 0; Mismatches 19; Indels 0;
                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yen, Frances
Denison, Blake
Bour, Barbara
Bihain, Bernard
Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-SEP-1944
ATTORNEY/AGENT INFORMATION:
NAMM: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REGISTRATION NUMBER: 950268-1
TELECOMMUNICATION INFORMATION:
TELEFRAX: 610-270-5024
TELEFAX: 610-270-5034
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/06743 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09750580 Patent No. 6455280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
Pennsylvania
                                      19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent.pm
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US-09-750-580-1
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APPLICANT:
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 40.3%; Score 24.6; DB 4; Length 81 Best Local Similarity 70.2%; Pred. No. 29; Matches 33; Conservative 0; Mismatches 14; Indels
                                                                                                       OCATION: 1220.1123
OTHER INCORATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240.1258
OTHER INCORATION: 20-828-311.mis complement
LOCATION: 12328.1246
OTHER INCORATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 1238-1256
OTHER INCORATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 1232-1256
OTHER INCORATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 1522.1250
OTHER INCORATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 1522.1250
OTHER INCORATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 42219.4237
OTHER INCORATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 4542: .4544
OTHER INCORATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 4542: .4546
OTHER INCORATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 4544: .4561
OTHER INCORATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INCORATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 77039..77077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 20-853-415.mis complement NAME/KEY: misc_binding LOCATION: 1227..1251
                                          OTHER INFORMATION: 20-853.rp complement NAME/KEY: primer_bind LOCATION: 1220..1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 17.41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20.841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20.842-115.probe
NAME/KEY: misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_binding
LOCATION: 12355..12359
OTHER INFORMATION: 17-42-319.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: 20-853-415.probe US-09-750-580-1
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US-09-103-840A-2/C
; Sequence 2, Application US/09103840A
; Patent No. 6284328
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_binding
LOCATION: 15229..15253
primer_bind
77166..77185
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## APPLICANN: FLEISCHAMM, Robert D.

## APPLICANN: FLEISCHAMM, Robert D.

## APPLICANN: FRASER, Claire M.

## APPLICANT: FRASER, Claire M.

## APPLICANT: TRANER, JOHN C.

## TITLE OF INVENTION: TUBERCULOSIS

## TITLE OF INVENTION: TUBERCULOSIS

## TITLE OF INVENTION: TUBERCULOSIS

## TITLE OF INVENTION: TUBERCULOSIS

## TITLE OF INVENTION: 1998-06-24

## CURRENT APPLICATION NUMBER: 1998-06-24

## NUMBER OF 58Q ID NOS: 2.1

## CURRENT FILMED DATE: 1998-06-24

## NUMBER OF 58Q ID NOS: 2.1

## NUMBER OF 58Q ID NOS: 2.1

## ORGANISM: Mycobacterium tuberculosis

## ORGANISM: Mycobacterium tuberculosis

## ORGANISM: Mycobacterium tuberculosis

## ORGANISM: Mycobacterium tuberculosis

## OTHER INFORMATION: "n" bases at various positions throughout the sequence

## OTHER INFORMATION: "n" bases at various positions throughout the sequence

## OTHER INFORMATION: "n" bases at various positions throughout the sequence

## OTHER INFORMATION: "n" bases at various positions throughout the sequence

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Sequence 16, Appli
Sequence 1640, Ap
Sequence 67, Appl
Sequence 32, Appl
Sequence 30, Appl
Sequence 301, Appl
Sequence 69, Appl
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Sequence 9241, App
Sequence 4, Appli
Sequence 2228, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5478, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 69, Appi
Sequence 2184, Ap
Sequence 179, App
                                                                                                       (without alignments)
4579.068 Million cell updates/sec
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                                                                                       June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
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2. /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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7. /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-826-581-2
0 US-09-960-352-1640
US-10-175-523-67
US-09-995-793A-30
US-09-995-793A-30
US-09-995-793A-30
US-09-977-768A-301
US-09-873-658-69
0 US-09-880-107-2184
US-10-091-572-817
US-09-764-891-9241
US-09-764-891-9241
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US-09-764-891-10205
                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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US-09-751-877-1
                                                                                                                                                                                                                                                     1029858 segs, 724030393 residues
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                                                                                                                                      US-09-826-581-5_COPY_200_260
61
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_NA:*
                                                           nucleic search, using sw model
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Match Length DB
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33795
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Maximum DB :
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Sequence 5, Application US/09826581
Fatent No. US20020142310A1
GENERAL INFORMATION:
APPLICANT: Andersson, Leif
APPLICANT: Authman, L. Holger
FILE REFERENCE: 11145-007001
CURRENT APPLICANTION NUMBER: US/09/826,581
CURRENT APPLICANTION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEG ID NOS: 14
SOUTWARE: PASLESC for Windows Version 4.0
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                                               sequence 5, Apply Sequence 1955, Ap Sequence 1962, Ap Sequence 1963, Ap Sequence 19192, A Sequence 19192, A Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 71, Appl Sequence 7617, Ap Sequence 263, Ap Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298, App Sequence 298,
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                                                          US-09-764-891-8575
US-10-199-550-1
US-10-199-864-761-19652
US-10-198-846-9038
US-10-198-846-12192
US-10-198-846-4363
US-10-198-846-4363
US-09-895-298-16
US-09-895-298-16
US-09-739-254-16
US-09-739-254-16
US-09-900-274-16
US-09-962-832-154
US-09-864-761-19511
US-09-294-093B-950
US-09-864-761-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 100.0%; Score 61; DB 10; Similarity 100.0%; Pred. No. 3.1e-11; 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             US-09-960-352-9061
US-09-822-849A-49
US-09-815-242-7677
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US-09-764-891-5637
US-09-764-891-5639
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US-09-826-581-2
; Sequence 2, Application US/09826581
; Patent No. US20020142310A1
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US-09-826-581-5
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Best Local Similarity
Matches 61; Conserva
                              260 A 260
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TYPE: DNA
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Sequence 32, Application US/09995793A
Publication No. US20030054446A1
Publication No. US20030054446A1
APPLICANT: Weber, Bernard H.F.
APPLICANT: Stoehr, Heidi
TITLE OF INVENTION: No. US20030054446Alel retina-specific human proteins C7orf9,
FILE REPRENCE: 033488-001
CURRENT APPLICATION NUMBER: US/09/995,793A
CURRENT FILING DATE: 2001-11-29
PRIOR EPILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
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0
                         TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS) FILE REPERENCE: 3235/1795-083
CURRENT APPLICATION NUMBER: 02/10/175,523
CURRENT FILING DATE: 2002-06-18
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tive 0; Mismatches 20; Indels
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; OTHER INFORMATION: genomic DNA, Exon from 101 to 460
US-09-995-793A-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.3%; Score 27; DB 9;
85.7%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                           PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FLING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-10-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PRECEITING VERSION 3.1
                                                                                                             PRIOR APPLICATION NUMBER: US 60/299,151
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Sequence 30, Application US/0995793A

Publication No. US20030054446A1

GENERAL INFORMATION:

APPLICANT: Weber, Bernard H.F.
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SOFWARE: Patentin version 3.1
SEQ ID NO 32
EBNOTH: 560
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Best Local Similarity 64.9%
These 37; Conservative
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Matches 30; Conservative
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; ORGANISM: Mus musculus
US-10-175-523-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 74868
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US-09-995-793A-32
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                APPLICANT: Anderssoo, Leif
APPLICANT: Anthera, L. Holger
APPLICANT: Anthera, L. Holger
APPLICANT: Marklund, L. Holger
APPLICANT: Marklund S. L. Holger
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
CURRENT PAPLICANTON NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
IIILE OF INVENTION: WICLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
IIILE OF INVENTION: WOSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1640
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 989;
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 08-Lib188-005-Q1-E1-B7
                                                                                                                                                                                                                                                                                                                                                                                                        83.6%; Score 51; DB 10; I
100.0%; Pred. No. 5.8e-08;
Live 0; Mismatches 0;
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Publication No. US20030096264A1
GENERAL INFORMATION:
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, David
APPLICANT: Hook, Derek
APPLICANT: Hook, Perek
APPLICANT: Laeng, Pascal
APPLICANT: Palfreyman, Michael
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Best Local Similarity 100.0
Watches 51; Conservative
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CORGANISM: Homo sapiens
US-09-826-581-2
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GENERAL INFORMATION:
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US-10-175-523-67/c
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5 GGCAGAAGTCGGTGGAGGGAAGCGGAGCCACCAGGTCAGGGGGGAAGGTCCCCGGTCCA 61
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  TITLE OF INVENTION: Methl and Meth2 Polynucleotides and Polypeptides CURRENT APPLICATION NUMBER: US/09/373,658
CURRENT APPLICATION NUMBER: US/09/373,658
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 125
SEQ ID NO 69
LENGTH: 8670
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Fatent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REPRENEUR: 44921-2508 WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
SPRIOR PLICATION NUMBER: US 200-10-02
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                                                                                                                                                                                                                                                                                                                          Score 25; DB 9; Length 8670;
Pred. No. 12;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Unknown Organism:Unknown US-09-373-658-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24.8; DB 10;
Pred. No. 12;
0; Mismatches 17;
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Patent No. US20020142952A1
GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc.
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Resnick, Richard J.
Gulukota, Kamalakar
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Local Similarity 64.9%;
hes 37; Conservative C
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Best Local Similarity 67.3%;
Matches 35; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wong, Gordon G.
Clark, Hilary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                         TYPE: DNA ORGANISM: Unknown
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Matches
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APPLICANT: Stoehr, Heidi
TITLE OF INVENTION: No. US20030054446Alel retina-specific human proteins C7orf9, C12d
FILE REFERENCE: 033488-001
CURRENT APPLICATION NUMBER: US/09/995,793A
CURRENT FILING DATE: 2001-11-29
PRIOR PEDICATION NUMBER: 60/253,751
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 301, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION;
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Gene Determination and Therapeutic Screening Using Signatu; TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
; OTHER INFORMATION: artificial sequence, Translation start at 347, stop at 604
US-09-995-793A-30
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Pred. No. 15;
0; Mismatches 20; Indels
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CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR PLILNG DATE: 2000-09-28
PRIOR PLILNG DATE: 2000-09-28
PRIOR PLILNG DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
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Publication No. US20030092900A1
GENERAL INFORMATION:
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Ruben, Steven M.
Jonak, Zdenka L.
Trulli, Stephen H.
Fronwald, James A.
Terrett, Jonathan A.
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64.98;
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64.9%;
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Best Local Similarity 64.9%
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Best Local Similarity 64.9
Matches 37; Conservative
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                          SEQ ID NO 30
                                                                                                                                                                                                                                                         TYPE: DNA
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R FILING DATE: 2000-08-14

R APPLICATION NUMBER: 60/236,369

R FILING DATE: 2000-09-29

R APPLICATION NUMBER: 60/224,519

R APPLICATION NUMBER: 60/220,964

R APPLICATION NUMBER: 60/220,964

R APPLICATION NUMBER: 60/220,964

R APPLICATION NUMBER: 60/220,964

R APPLICATION NUMBER: 60/241,809
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R APPLICATION NUMBER: 60(229,343)
R FILING DATE: 2000-09-01
R PILING DATE: 2000-09-01
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R APPLICATION NUMBER: 60(229,28)
R APPLICATION NUMBER: 60(229,28)
R PILING DATE: 2000-09-01
R PELING DATE: 2000-09-01
R PELING DATE: 2000-09-05
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R FILING DATE: 2000-09-29
R PLILING DATE: 2000-10-29
R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/237,038
R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/237,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/251,868
FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/229,344
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FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/237,037
FILING DATE: 2000-10-02
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FILING DATE: 2000-111-17
APPLICATION NUMBER: 60/236,327
FILING DATE: 2000-09-29
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APPLICATION NUMBER: 60/244,617
FILING DATE: 2000-11-01
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FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/236,368
FILING DATE: 2000-09-29
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FILING DATE: 2000-12-08
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FILING DATE: 2000-09-08
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FILING DATE: 2000-09-05
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APPLICATION NUMBER: 60/249,210
                                                          APPLICATION NUMBER: 60/224,518
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/241,785
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS CHER REPERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 179
                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA118C1
CURRENT APPLICATION NUMBER: US/10/091,572
CURRENT FILING DATE: 2002-03-07
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PRICOR PELICATION NUMBER: 60/179, 065
PRICOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR PLICATION NUMBER: 60/180, 628
PRIOR PLICATION NUMBER: 60/214, 886
PRIOR PLICATION NUMBER: 60/217, 487
PRIOR PLILING DATE: 2000-06-28
PRIOR PLILING DATE: 2000-06-28
PRIOR PLICATION NUMBER: 60/217, 487
PRIOR FILING DATE: 2000-07-11
PRIOR PLILING DATE: 2000-07-11
PRIOR PLILING DATE: 2000-07-14
PRIOR PLILING DATE: 2000-07-16
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PRIOR PLILING DATE: 2000-07-17
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Publication No. US20030054373A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60,225,759
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PRIOR FILING DARF: 2000-08-14
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PRIOR FILING DARF: 2000-09-27
PRIOR PELLOR FILING DARF: 2000-09-17
PRIOR PELLOR FILING DARF: 2000-09-17
PRIOR PELLOR FILING DARF: 2000-09-17
PRIOR PELLOR FILING DARF: 2000-11-17
PRIOR APPLICATION NUMBER: 60,249,218
PRIOR PELLOR FILING DARF: 2000-11-17
PRIOR PAPLICATION NUMBER: 60,249,218
PRIOR PELLOR FILING DARF: 2000-11-17
PRIOR PAPLICATION NUMBER: 60,249,213
PRIOR PELLOR FILING DARF: 2000-11-17
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PRIOR PELLOR FILING DARF: 2000-11-17
PRIOR PAPLICATION NUMBER: 60,249,214
PRIOR FILING DARF: 2000-11-17
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PRIOR FILING DARF: 2000-11-17
PRIOR PAPLICATION NUMBER: 60,249,214
PRIOR FILING DARF: 2000-11-17
PRIOR PAPLICATION NUMBER: 60,249,214
PRIOR FILING DARF: 2000-11-17
PRIOR PAPLICATION NUMBER: 60,249,214
PRIOR FILING DARF: 2000-11-17
PRIOR PAPLICATION NUMBER: 60,233,401
PRIOR PELLOR PAPLICATION NUMBER: 60,233,401
PRIOR PELLOR PAPLICATION NUMBER: 60,233,401
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PRIOR PAPLICATION NUMBE
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APPLICANT: DULLEL, APPLICANT:
APPLICANT: DULLEL, APPLICANT:
TITLE OF INVENTION: APOLIPOPROTEIN A-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNUCLEOTI
TITLE OF INVENTION: SEQUENCES AND BIALLELIC MARKERS THEREOF.
TITLE BOT INVENTION: SEQUENCES AND BIALLELIC MARKERS THEREOF.
TILE BOT STATE SOCPEC
CURRENT APPLICATION NUMBER: US/09/842,364
CURRENT APPLICATION NUMBER: US 09/599,362
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR APPLICATION NUMBER: US 60/114,032
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR PILING DATE: 1999-06-25
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: 9C006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT APPLICATION DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: 9tentin Ver. 2.0
SEQ ID NO 9241
LENGTH: 5312
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                                                                                                                                                             *Match 40.3%; Score 24.6; D. Local Similarity 65.5%; Pred. No. 18; les 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 9241, Application US/09764891; Publication No. US20030077808A1; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
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Publication No. US20030032783A1
GENERAL INFORMATION:
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Best Local Similarity 65.39,
Best Local Similarity 65.39,
Best Local Similarity 65.39,
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Bour, Barbara
Bihain, Bernard
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SOFTWARE: Patent.pm
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ORGANISM: Homo sapiens
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Best Local $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 17-42-319.mis complement
NAME/KET: primer_bind
LOCATION: 3194..3212
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
.OCATION: 3214..3232
OCHAIL INFORMATION: 17-41-250.mis complement
NAME/KEY: misc_bindding
LOCATION: 307..331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 17-40.pu
NAME/KEY: primer_bind
LOCATION: 1441.1246i
OTHER INFORMATION: 12-39.rp complement.
NAME/KEY: primer_bind
LOCATION: 1632.12651
LOCATION: 1632.12651
LOCATION: 2964.13984
OTHER INFORMATION: 17-41.pu
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LOCATION: 553..11575
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 899..11920
OTHER INFORMATION: 17-39.pu
                                                                                               NAME/KEY: misc_feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
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OTHER INFORMATION: exon 4
NAME: misc_feature
LOCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
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LOCATION: 3432..14454
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 300..318
OTHER INFORMATION: 17-42-319.mis
                                                                                                                                                      NAME/KEY: exon
LOCATION: 919.,930
OTHER INFORMATION: exon 1
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THER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                    LOCATION: 1613..1724
OTHER INFORMATION: exon 3
                                                         ORGANISM: Homo sapiens
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SEQ ID NO 4
LENGTH: 5381
                                          TYPE: DNA
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APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Denison, Blake
APPLICANT: Denison, Blake
APPLICANT: Denison, Blake
APPLICANT: Blabin, Bernard
APPLICANT: Blabin, Bernard
APPLICANT: Bouquelert, Aymeric
APPLICANT: Bouquelert, Lydie
APPLICANT: Salter-cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.US3.REG
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SEQ ID NO 4
LENGTH: 5381
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                                                                                                                                                                                               Gaps
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                                                                                                                                              DB 9; Length 5381;
                                                                                                                                                                                                                                                                13 TCGGTGGAGGAAGGGGAGCCACCACGTCAGGGGGAAGGTCCCCGGTC 59
                                                                                                                                       Query Match 40.3%; Score 24.6; DB 9; Length 5: Best Local Similarity 70.2%; Pred. No. 18; Matches 33; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1241
OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707 NAME/KEY: primer bind LOCATION: 1..11022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 17-42-319 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: 17-41-250 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KET: misc_feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 2243..3940
OTHER INFORMATION: exon 4
NAME. T. misc_feature
LOCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
; OTHER INFORMATION: 17-42-319.probe
; NAME/KEY: misc_binding
; LCCATION: 3201..325
; OTHER INFORMATION: 17-41-250.probe
US-09-842-364-4
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09751877
Patent No. US20020142949A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1.11022
OTHER INFORMATION: 17-42.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 919..930
OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 1442..1498
OTHER INFORMATION: exon 2
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: exon 3 NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1613..1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: conflict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                           US-09-751-877-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
CURRENT FILING DATE: 2001-06-14;
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
SOFTWARE: PATENTION UNBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
SOFTWARE: PATENTION OF 2000-10-02
SOFTWARE: PATENTION OF 2011
SEQ ID NO 2228
LENGTH: 8095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 5381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.3%; Score 24.6; DB 10; Length Best Local Similarity 70.2%; Pred. No. 18; Matches 33; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                     CUTHER INCORMATION: 17-40. PU
NAME/KEY: PTIMET_bind
LOCATION: 1441.1244.
CUTHER INCORMATION: 17-40. PU
CUTHER INCORMATION: 17-39.rp complement
NAME/KEY: PITIMET_bind
LOCATION: 1622..12651
CUTHER INCORMATION: 17-40.rp complement
NAME/KEY: PITIMET_bind
LOCATION: 2644..13984
CUTHER INCORMATION: 17-41.pu
NAME/KEY: PITIMET_bind
LOCATION: 3432..14454
UCHER INCORMATION: 17-41.rp complement
NAME/KEY: PITIMET_bind
LOCATION: 300..318
CUTHER INCORMATION: 17-42-319.mis
NAME/KEY: PITIMET_bind
LOCATION: 320..338
CUCHER INFORMATION: 17-42-319.mis complement
NAME/KEY: PITIMET_Bind
CUCHER INFORMATION: 17-42-319.mis complement
NAME/KEY: PITIMET_Bind
CUCHER INFORMATION: 17-42-319.mis complement
NAME/KEY: PITIMET_Bind
CUCHER INFORMATION: 17-42-319.mis complement
NAME/KEY: PITIMET_Bind
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NAME/KEY: PITIMET_Bind
CUCHER INFORMATION: 17-42-319.mis complement
NAME/KEY: PITIMET_Bind
CUCHER INFORMATION: 17-42-319.mis
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NAME/KEY: primer_bind
LOCATION: 553.11575
LOCATION: 553.11575
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 899..11920
OTHER INFORMATION: 17-39.pu
NAME/KEY: primer_bind
LOCATION: 1246..12267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_binding
LOCATION: 307..331
OTHER INFORMATION: 17-42-319.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 3201..3225
; OTHER INFORMATION: 17-41-250.probe
US-09-751-877-4
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ORGANISM: Homo sapiens
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LOCATION: 3214..3232
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GenCore version 5.1.6

No. is the number of results predicted by chance to have a Pred.

Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 2 18-OCT-2001;

REFERENCE AUTHORS TITLE JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

02-NOV-2001

PAT

linear

DNA

AX281579 989 bp Sequence 2 from Patent W00177305

AX281579 AX281579.1 GI:16608830

AX281579 LOCUS DEFINITION ACCESSION VERSION VERSION SOURCE ORGANISM

RESULT 1

Homo sapiens

human.

ALIGNMENTS

AC124396_.

AC099721 AC007873 AC131311 AC106429

AF214519 Homo sapi AC027416 Homo sapi AC027416 Homo sapi AC027416 Homo sapi AC02741 Homo sapi AX099774 Homo sapi AF214520 Sus scrof AX398331 Sequence AX398331 Sequence AX398335 Sequence AX398335 Sequence AX398337 Sequence AX398339 Sequence AX398339 Sequence AX398339 Sequence AX398339 Sequence AX398339 Sequence AX398339 Sequence AX398339 Sequence AX398339 Sequence AF214521 Sus scrof AF214521 Sus scrof AF214530 Rattus no AC122703 Rattus no AC12707 Rattus no AC127037 Rattus no AC127037 Rattus no AC127037 Rattus no AC127037 Rattus no AC127037 Rattus no AC127037 Rattus no AC127037 Rattus no AC127037 Rus muscu AF112855 Mus muscu AF112855 Mus muscu AC122075 Mus muscu AC122075 Mus muscu AC122075 Mus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122075 Hus muscu AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AC122078 Rattus no AX281579 Sequence AX281582 Sequence AX099776 Sequence AX099802 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES AF112855 AE007063 AC125735_( AE009112 AF214520 AX099800 AX398331 AX099776 AX099802 AX398333 AX398335 AX281579 AX398337 AE009874 а 10 DB 1000.0 1647 1000.0 1647 1000.0 12115 1000.0 2068129 1000.0 2068129 1000.0 2068129 1000.0 2068129 1000.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1873 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 1974 79.0 19 Length % Query Match Score 7.5 4444444444 7.888888444444 7.6688888888 7.66888888888 Result õ ပပပ υυ 00

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AX099776 2109 bp
Sequence 3 from Patent WO0120003.
                                                                                         Homo sapiens
                                                                                                                                                                              Chardon, P
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                          AX099776
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 COCUS
                                                                                       ORGANISM
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                            ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                           JOURNAL
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                                                                                                                                   REFERENCE
                                                                                                                                                   AUTHORS
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AX099802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQGCFKPLVSISPNDSLFBAVYTLIKNRIHRLPVLDPVSGNYLHILTHKRLLKFLHIF
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQV
VGLYSRFDVJHLAAQQTVNHLDMSVGBALRQRTLCLEGVLSCQPHESLGEVIDRIARB
QVHRLVLVDETQHLLGVYSLSDILQALVLSPAGIDALGA"
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Arexis AB (SE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                            1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
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                                                                                                                    Length 989;
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                                                                                                                 ch 100.0%; Score 61; DB 6; I Similarity 100.0%; Pred. No. 3.3e-10; 61; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
306 c 286 q 168
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Sequence 5 from Patent W00177305.
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              Location/Qualifiers
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Arexis AB (SE)
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VERSION
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AX281582
            FEATURES
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lwdskkospvcaltiddellvlhryrsplvojyeteohtkethreitscheptsus
lspndsleavytlknthripklpvldpvsgnvlhilthkrlikflhischeptspsfl
yrttodlegtprijavvleptapithriblipvdrkvysleogyvnscogyvcixsprdy
Hlaacotynhildwsvgealroptclecviscophesicevidriaredoyhruvudb
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   PAT 02-APR-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0120003-A 29 22-MAR-2001,
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   Variants of the gamma chain of ampk, dna sequences encoding the
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Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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   linear
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621 c 560 g 470 t
DNA
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Arganism-"Homo sapiens"
/db_xref='taxon:9606' 472. .1389
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Sequence 29 from Patent WO0120003.
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/db_xref="GI:13538811"
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/db_xref="taxon:9606"
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AX099802.1 GI:13538836
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/product="AMP-activated protein kinase gamma subunit"
/protein_id="AMF73887.1"
/db_xref="G1:8215682"
/db_xref="G1:8215682"
/translation="MSFLEGENSSMPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG
EPPGGGGGPRSRPTAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAG
                                                                                                                                                    SSTDDVELATEFPATEAWECELEGILEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
FRWQEHTCYDAMATSSKLVIEDWILEIKKAFFALVANOVRAADLWDSKQSFVGMITI
TDFILVLHRYTRSPLVQIYEIDGHKIETWREIYLQGERFUPSISPNDSIFERAYTLI
KNRIHRLPVLDPVGGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGFRPDL
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GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
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Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152129)
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO SAPIENS.
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KEYWORDS
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Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
                                                                                                                                                                                                                                                                            TOF ILVLHRYRSPLVQIYEIBQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYLLI
KNRTHRIPLYLDPVSGVVHJLTHRKILKFLHFGSLLERPSETLKRTIDGLGIGFFRDL
AVVLETAPILTALDIFVDRRVSALPVVNECGQVVGIXSREDVIHLAAQOTYNHLDMSV
GEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
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bepeggeberrprakstollarfyrTrTpLagabakdyrprgwpclapcypsbcTasbad
SSTDDVELAFERPATEAMECELEGILEERPALCISPQAPFPKLGWDDELRRPGAQIYM
RFWQEHTCYDAMATSSKIVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLII
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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M.,
Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Rome, H.,
Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
and Andersson, L.
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Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Ralm, E., Le Roy, P., Chardon, P. and Andersson, L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 494
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100.0%; Pred. No. 3.4e-10;
Live 0; Mismatches 0; Indels
                                  /note="unnamed protein product"
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/db_xref="taxon:9606"
                                                                                        /protein_id="CAC35801.1"
/db_xref="G1:13538837"
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/note="AMPKG3"
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AF214519.1 GI:8215681
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7319 77115; contig of 3797 bp in length 77215 gap of 100 bp 77216 85022; contig of 7707 bp in length 85023 85122; gap of 100 bp 85123 93314; contig of 8192 bp in length 93315 9344; gap of 100 bp 93415 101193; contig of 7779 bp in length 101194 101293; gap of 100 bp 113090; contig of 1779 bp in length 101294 113199; gap of 100 bp 113191 123496; contig of 10306 bp in length 11391 123496; contig of 10306 bp in length 123497 123596; gap of 100 bp 137497 123597; contig of 14241 bp in length 177938 137937; gap of 100 bp 137938 152129; contig of 1492 bp in length.
           73218: contig of 6523 bp in length
18: gap of 100 bp
77115: contig of 3797 bp in length
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/note="assembly_fragment"
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15144. .17123
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24420. .27059
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/note="assembly_fragment"
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66695; gap of
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     Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                            Contact: Sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project information
Center project name: 17458
Center clone name: 504_G_11

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 145503 bases at least Q20
Insert size: 161000, aqarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
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of 1286 bp in length
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contig of 2336 bp in length
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contig of 4820 bp in length
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Genome Center
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46365; cont
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46466 51285; cont
51286 51385; gap of
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34069 38179: cont
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6161: co
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66595; cc
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1106 2402;
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FEATURES
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Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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Direct Submission
Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 206854)
Waterston, R.H.
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Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Harris, A. and Cotton, M.
The sequence of Homo sapiens BAC clone RP11-459I19
Uppublication 2001)
3 (bases 1 to 206854)
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                                                                                                                                                                                                                           100.0%; Score 61; DB 2; 100.0%; Pred. No. 4.1e-10; ive 0; Mismatches 0;
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                       /3319. .77115
/note="assembly_fragment"
                                                       77216. .85022
/note="assembly_fragment"
                                                                                        85123. .93314 /note="assembly_fragment"
                                                                                                                                93415. .101193**
/note="assembly_fragment"
101294. .113090
/note="assembly_fragment"
/note="assembly_fragment"
73319. .77115
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Sulston, J.E. and Waterston, R.
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Center: Washington University Genome Sequencing Center

Center code: WUGSC

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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at the Roswall Park Cancer Institute (http://www.resgen.com) or Pieter de Jong (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                              all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Amunresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.
                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
                                                                                                                                                                                                                                               clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE047599 (NID:98364652) tz39c01.y1*
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/note="match to EST AL567345 (NID:g12920610)"
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    .37
    /note="similar to Homo sapiens EST BI114348
(NID:g14565249)"

Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
..... Summary Statistics
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                                                                                                         Center project name: H_NH0459119
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/db_xref="taxon:9606"
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LIVANGYRAARAMSKROSTGWLTTIPDFILVLAHRYRSPRVOYIPETBOHKLETRREIY
LOGCERPLYSISPHOSLFEAVYTLIKRRIHRLPVLDPSGNYLHILTHKRLLKFLHIP
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFYDRNSALEYVUNEGGY
VGLYSRFDVTHLAAQOTYNHLDMSVGRALRKRTLCLEGYLGCOPHESLGEVIDRIARB
QVHRLVLVDFTQHLLGVYSLSDILGALVLSPAGIDPSGPEKI"
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SSERIRGKRRAKALRWTRQKSVEEGEPPGGGEGPRSRPAAESTGLEATFPKTTPLAQA
DPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2290)
                          967. .1091
/note="match to EST AA043371 (NID:g1521226) zk53el0.rl"
967. .1090
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AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
  962. .1084
/note="match to EST AI656812 (NID:g4740791) tt54b06.x1"
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                                                                                                                                                                                                                                                                                               1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA
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Carling, D.
Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 ONN, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                            Length 206854;
                                                                                                             /note="similar to Homo sapiens EST BI114348 (NID:g14565249)"
967. .1085
                                                                                                                                                                                                       Query Match 100.0%; Score 61; DB 9; I Best Local Similarity 100.0%; Pred. No. 4.1e-10; Matches 61; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="match to EST A1670836 (NID:94850567) wa04g10.x1"
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                                                                  'note="match to EST A1670836 (NID:94850567) wa04g10.x1"
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                                                                                                                                                     /note="match to EST BG470047 (NID:g13402322)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match to EST BF183086 (NID:g11061273)"
281. .344
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281. .344
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594. .763
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281. .344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="match to EST BF304755 (NID:911251653)"
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                       to EST BE908408 (NID:g10402954)"
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                                                                                                                                                                                                                                                                            /note="match to EST AW880850 (NID:98042860)"
281. .344
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/note="similar to Homo sapiens EST BIll4348
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281, .344
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/note="match to EST AA043371
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3. .37
/note="match
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Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia: Eutheria, Cetartiodactyla; Suina: Suidae; Sus.

1 (bases 1 to 1873)
Milan, D., Jeon, J. T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. and Andersson, L.

A mutation in PRRAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSFLEQGESRSWPSRAVTISSERSHGDGGNKASRWTRQEDVEEG
GPPGFREGPGSRPVAESTGGEATFRATFLAAAPLAEVDRPFTERDILPSDCASASA
DSNTDHIDGIEFSASASGDELGIVEEKPAPCPSFEVILPRIGWDDELGKRGAQVYM
HRMQEHTCVDAMATGSKIVIEDTMIEIKRAFFALVANGVRAAPLMDSKGGSFOGHTI
TDFILVLHRYKRSFLVQIYEIEEHKIETWREIYLQGGFKFLVSISPNDSLEBAVYALI
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AVVLETAPILITALDIFVDRNSALPVVNETGQVVGLYSRFDVIHLAAQQTVNHIDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
                                                                                                                                                                                                                                                Z (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Ralm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="AMP-activated protein kinase gamma subunit"
/protein_id="AAF73988.1"
/db_xref="GI:8215684"
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Pred. No. 7.2e-06;
0; Mismatches 8; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="skeletal muscle"
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Science 288 (5469), 1248-1251 (2000)
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/db_xref="taxon:9823"
/chromosome="15"
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  Sus scrofa.
Sus scrofa
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mRNA, complete cds.
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ISPNDSLEEAVYALIKNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLRRPSFL
YRITODLGIGTRRLAVYLETAPILTALDIRVDRRYSALPVNEGGQYGLTSRRDVI
HLAAQQIYNHLDMNVGEALRQFYLCLEGVLSCQPHFTLGEVIDRIVREQVHRLVLVDF
TQHLLGVVSLSDILAALULAALULAALULAALULAALULAAVA
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                                                                                                                1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCCTTCATGCAGGA 60
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variants of the gamma chain of ampk, dna sequences encoding the
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                                                          <u>;</u>
                Score 57.8; DB 9; Length 2290;
Pred. No. 4.1e-09;
0; Mismatches 2; Indels 0;
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/db_xref="G1:13538809"
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/db_xref="taxon:9823"
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                                    96.78;
                Query Match
Best Local Similarity 96.7
Matches 59; Conservative
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/tb_xref="d1:21261107"
/translation="MSFLEGGESRSWPSRAVTTSSERSHGDGGNKASRWTRQEDVEEG
GPFGGPREGFREGFREATPFRATPLAQAAFLAEVDNPFTERDILFSDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCFSPEVLLPFLGWDDELGKPGAQVYM
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/db_xref="G1:13538835"
/translation="MSFLEGGESSKMPSRAVTTSSERSHGDGGNKASRWTRQEDVEEG
/proferedpgrepgerpvesyqgeatfpratplaqaaplaevDNppTerDILpsDcaasas
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HFMQEHTCYDAMATSSKLVIFDTMLEIRKAFFALVANGVRAAPLMDSKKQSFVGMLTI
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KNRTHRELPVLDPVSGAVHALITHREKEKHHFGTLLDRSPELKRTIQDLGIGFRFDL
AVVLETAPILTALDIFUDRRVSALPVVNETQOVGIXSREDVIHLAAQOTYNHLDMNV
GEALRQRTLCLEGVISCQPHETLGEVIDRIVREQVHRLVLVDBTQHLLGVVSESDILQ
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220855-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
                                                                             Chardon, P.
Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof Patent: Wo 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE) Location/Qualifiers
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                1 (bases 1 to 1873)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 7.2e-06;
); Mismatches 8; Indels 0
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/db_xref="taxon:9823"
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Best Local Similarity 86.9%;
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/translation="MSFLEGGESRSWPSRAVTUSSERSHGDOGTKASRWTRQEDVEEG
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                                                     AVVLETAPILTALDIFVDRRVSALPVNNETGQVVGLYSRPDVIHLAAĞQTVNHIDMNV
GEALRQRFLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
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TOFILVLHRYYRSPLVQIYEIEEHKIETWREIYLOGGFKPLVSISPNDSLFBAVALI
KNRIHRLPVLDPVSGAVLHILTHKRLIKFLHIFGTLLPRPSFLYRTIODLGIGTFRDL
                TDFILVLHRYYRSPLVQIYEIEBHKIETWREIYLQGCEKPLVSISPUDSLFBAYALJ
KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
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Novel prkag3 alleles and use of the same as genetic markers reproductive and meat quality traits
Patent: WO 0120880-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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Pred. No. 7.2e-06;
0; Mismatches 8; Indels 0
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/protein_id="CAD32626.1"
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/note="unnamed protein product"

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNR HRLPVLDPVSGAVLHILFHRRLIKFLHIFGTLLPRPSFLYRTIQDLGIGTERDL
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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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                                       PAT 27-MAY-2002
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                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                       Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: NO 0220850-A 5 14 *MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location, Qualifiers
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 7 14 *MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location, Qualifiers
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AX398335
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GEALRQRTLCLEGVLSCQPHETLGBVIDRIVREQVHRLVLVDBTQHLGGVVSHSDILQ
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Pred. No. 7.2e-06;
0; Mismatches 8
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Best Local Similarity 86.9%;
Matches 53; Conservative
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(without alignments)
6198.732 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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61
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			Description	PRKAG3 intron 2 -	PRKAG3 CDNA. HOMO	Human AMPK gamma s	Human AMPK damma s	Piq AMPK qamma sub	Pig AMPK gamma sub	Pig wild-type PRKA	Pig PRKAG3 polymor	Pig PRKAG3 polymor
SUMMARIES			ID	AAH43682	AAH43685	AAD03296	AAD03320	AAD03295	AAD03319	AAD36456	AAD36457	AAD36458
			DB	22	22	22	22	22	22	24	24	24
		Query	Length	686	1647	2109	2115	1867	1873	1873	1873	1873
	æ	Query	Match	100.0	100.0	100.0	100.0	79.0	79.0	79.0	79.0	79.0
			Score	61	61	61	61	48.2	48.2	48.2	48.2	48.2
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/note= "Causes P71A"

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13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCCAGATCTACATGCGTTCATGCAGGA 60
                                                                                                                                                          New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                       encoding the human AMP-activated protein kinase gamma 3 subunit (FRKAG3) DMA. Or a variant, is useful in determining the presence of the PRKAG3 DMA. Or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a glor a C at nucleotide 320, resulting in the amino acid substitution P71A, in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                               The sequences given in AAH43681-84 represents genomic fragments
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                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 61; DB 22; Length 989; 100.0%; Pred. No. 1.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                           Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
/note= "5' portion of intron 4"
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                     Marklund S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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230
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                                                                                                                                                                                                            Example 1; Fig 2; 25pp; English.
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/label= "C230G"
                                                          06-APR-2001; 2001WO-SE00765.
                                                                             07-APR-2000; 2000US-195665P.
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                                                                                                                     Andersson L, Luthman H,
                                                                                                                                                                                                                                                                                                                                                                                                 61; Conservative
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                                                                                                                                        WPI; 2001-657170/75.
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                                                                                                 (AREX-) AREXIS AB.
                    W0200177305-A2
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                                       18-OCT-2001
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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, cresulting in the amino acid substitution PPIA; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, cresulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on constitution 1 of the open reading frame.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gamma subunit, adenosine monophosphate-activated kinase; AMPK;
PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
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100.0%; Pred. No. 1.7e-12;
tive 0; Mismatches 0;
                                      /note= "Silent variation"
1037
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/label= "C1037T"
/note= "Causes R340W"
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/*tag= c
/label= "T559C"
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Best Local Similarity 100.

Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-657170/75.
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Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;

cystathione beta synthase; CBS; cardiant; gene therapy; ss.

Homo sapiens.

/product= "Human complete Prkag3 protein"

Location/Qualifiers 1..1395

Key

Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA,

(first entry)

13-JUN-2001

AAD03320;

AAD03320 standard; cDNA; 2115 BP.

RESULT 4

G 489

489

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The present sequence is a cDNA encoding human adenosine monophosphate (AMPP) gamma subunit muscle-specific isoform, PRKAG3. Mutation in PrkKag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders susceptions as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3. are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transpenic animal and host cell transformed with PRKAG3 or a chetcotriment AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain compounds and is useful in gene therapy.
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genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
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/product= "Human Prkag3 protein"
1390..2109
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                         Location/Qualifiers
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18-MAY-2000; 2000EP-0401388.
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                                                                                                                   Homo sapiens
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5'UTR
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AMPP-activated Kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a
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1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCCAGATCTACATGCGCTTCATGCAGGA

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Gaps

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Indels

100.0%; Score 61; DB 22; Length 2109; 100.0%; Pred. No. 1.8e-12;

pred. No. 1.8e-12;
0; Mismatches 0;

61; Conservative

Similarity

Query Match

Best Local

Matches

Kalm E, Milan D, Robic A, Rogel-Gaillard C; J, Le Roy P, Chardon P;

Andersson L, Looft C, Kal Iannuccelli N, Gellin J,

KALM E.

(KALM/)

(INRG ) INRA INST NAT RECH AGRONOMIQUE (ANDE/) ANDERSSON L.

18-MAY-2000; 2000EP-0401388.

99EP-0402236

10-SEP-1999;

11-SEP-2000; 2000WO-EP09896.

WO200120003-A2.

22-MAR-2001.

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79.0%;
86.9%;
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                                            Gaps
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                                                                                                                                                                                                                              gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                           0;
                          Length 2115;
                                                                                                                                                                                                                Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                           Indels
        Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                 scrofa PRKAG3 protein"
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Chardon P;
                        Score 61; DB 22;
Pred. No. 1.8e-12;
; Mismatches 0;
                                          0; Mismatches
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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J, Le Roy F
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/product= "Sus s
1390..1867
/*tag= c
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100.0%;
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18-MAY-2000; 2000EP-0401388.
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472..1389
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                                           61; Conservative
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                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    chromosome 15; ss.
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                                                                                                               495
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5'UTR
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Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as the case, obesity, and disorders associated with muscle metabolism cartivity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting cuseful for detecting a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
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Pred. No. 7.6e-08;
0; Mismatches 8; Indels 0;
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(ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                  "Single nucleotide polymorphism (SNP)"
"Single nucleotide polymorphism (SNP)"
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                                                                                                                                 /standard_name= "Single nucleotide polymorphism (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype staracterised by polymorphism(s) in the AMP activated protein Kinase regulatory gamma subunit (FRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters.
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Pred. No. 7.6e-08;
0; Mismatches 8
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                                                                                         replace (599, A)
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86.9%;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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Best Local Similarity 86.9
Matches 53; Conservative
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                                                                                            variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                         The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome is. Mutation in Prkag3 results in an altered regulation of carbohydrate encabolism. particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as the constitution of an analysis of diabetes, obesity, and disorders associated with muscle metabolism cutivity, and for restoring a normal AMPK function. PRKAG3 sequence activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic referably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3 or a resecution compounds able to modulate AMPK activity. Nucleic activity are useful for screening pRKAG3 is useful for detecting mutations in a PrkAG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                   Claim 12; Page 62-64; 71pp; English.
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                            WPI: 2001-244810/25
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Best Local Similarity
                                                 P-PSDB; AAE00222
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                                                                                                                                                           myopathy
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Gaps

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DB 24; Length 1873; 8; Indels 9

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1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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                                                                                 /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                 "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
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    Location/Qualifiers
                                                                replace (154, A)
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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                                                                  variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                               Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                           /product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)" replace (89, C)
                                                                                            /standard_name= "Single nucleotide polymorphism (SNP)"
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86.9%; Pred. No. 7.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 89-91; 109pp; English.
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Location/Qualifiers
1..1395
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08-JAN-2001, 2001US-260239P.
18-JUN-2001, 2001US-299111P.
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Best Local Similarity 86.39,
Best Local Si Conservative
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/product= '
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                                                               variation
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AAD36458
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The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (RRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                    "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
                                                                                                                                                                                                                                                                                                                                                                                                              Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                     /*tag= b
/standard_name= "Single nucleotide polymorphism (SNP)"
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Pred. No. 7.6e-08;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                 Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 102-104; 109pp; English.
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   Location/Qualifiers
1..1395
                                                                  replace (599, A)
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86.9%;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
                                  /*tag= a /*tag= a /*tag= prkAG3 polymorphic variant (PRKAG3-199)" /product= "Pig PRKAG3-199)" /*tag= b /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                              Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                  /standard_name= "Single nucleotide polymorphism (SNP)"
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Pred. No. 7.6e-08;
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Location/Qualifiers
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86.9%;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-393850/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAE22987
                                                                                                                                 WO200220850-A2
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                                                                  variation
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8; Indels

us-09-826-581-5_copy_529_589.rng

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Nucleic acids encoding a Ste20-related protein kinase designated SMAK, useful for the prevention, diagnosis and treatment of neoplasia development, lymphoproliferative conditions, inflammation, ischemia or
                                                                                                                                   Mouse; Ste20-related protein kinase; SWAK; caspase-3-cleavage; caspase activated protein kinase; apoptosis; neoplasia development; actin stress fiber dissolution; lymphoproliferative condition; inflammation; ischemia; stroke; autoimmune disease; ss.
                                                                                              cDNA sequence encoding a Ste20-related protein kinase called SMAK.
                                                                                                                                                                                                                                                                                                /*tag- a
/transl_except= (pos: 4..5, aa: Ser)
/transl_except= (pos: 1373..1376, aa: Xaa)
/product= "SMAK"
                                                                                                                                                                                                                                                                                                                                                                                             /note= "Xaa is the termination codon"
                                                                                                                                                                                                                                                                         Location/Qualifiers
56..3674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strokes and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0120784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-2000; 2000WO-CA00165.
                                                         20-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rudnicki MA, Sabourin LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYMC-) UNIV MCMASTER.
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les 36; Conserv
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                AAA64328;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                             Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in PRAG3 replication an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     evaluation, genetic testing and prognosis of a metabolic disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48.2; DB 22; Length 2022;
Pred. No. 7.7e-08;
0; Mismatches 8; Indels 0;
                                                                        "Sus scrofa Prkag3 splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                           Looft C, Kalm E, Milan D, Robic A, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                          (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                Location/Qualifiers
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18-MAY-2000; 2000EP-0401388.
                                                                          /product=
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Matches 53; Conservative
                                     1..1545
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Iannuccelli N,
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                                                                                                                 WO200120003-A2
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                                                                             The present sequence encodes a murine Ste20-related protein kinase designated SMAK. SMAR is a caspase activated protein kinase. SMAR activates 2 signalling pathways that are involved in mediating apoptosis. It also mediates actin stress fiber dissolution through caspase-3-cleavage and functions to activate the stress activated protein kinases (cjun-amino terminal kinase (JMK) signalling pathway). SWAK proteins and polynucleotides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate SMAK expression. The SMAK polypeptides may be used as antigens in the production of antibodies, and in assays to identify modulators (agonists and antagonists) of SMAK expression and activity. The SMAK protein is associated with apoptosis and may play a role in preventing neoplasia development, lymphoproliferative conditions, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 ATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.3%; Score 25.8; DB 21; Length 5259; 67.9%; Pred. No. 11;
tive 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5259 BP; 1744 A; 980 C; 1250 G; 1285 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ischemia or strokes and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA199683/c
ID AA199683 standard; DNA; 4403765 BP.
Claim 4; Fig 1; 78pp; English.
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AAA64328 standard; cDNA; 5259 BP.

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2322190 GGCGGCGAAGACCCCCAGCGCACCGCGGCCCCACCCATACCCGGGCTATCCTGGG 2322131
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les 39; Conservative
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                                                                                                            24-JUN-1998;
                                                      US6294328-B1
                                                                                                                                      24-JUN-1998;
                                                                                 25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monitoring.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AN199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCGTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                       Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC
                                                                                           Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemic monitoring; ds.
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Pred. No. 33;
0; Mismatches 22; Indels 0; G
                                                                 Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
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                                                                                                                                                                                                                                                                                                   Venter JC;
                                                                                                                                                                                                                                                                                                   Fraser CM,
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                                                                                                                                   Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                  Fleischmann RD, White OR,
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                                        (first entry)
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Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                1551 and H37Rv differ
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                                      15-JAN-2002
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            AA199683;
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Gaps

Indels

22; DB 22;

0; Mismatches Score 25.8; Pred. No. 33;

42.38;

Length 4411529;

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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen. Mycobacterium by determining the mucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 151 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID-6294328B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37RV differ -
variation; epidemiology; patient treatment; epidemic monitoring; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC;
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                                                                                            Mycobacterium tuberculosis.
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RPC193-EC BB711478

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.

1 (base; Bovinae; Bos.

1 (bases 1 to 444)

Smith, T.P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, J.G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4396
Bmail: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized I
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
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BF890374
BF890374.1 GI:12281760
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                                                                                  AA519383
CNS03ER5
BM468546
W68459
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BQ508350
BM088002
BG599496
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BE809466
BE755789
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BJ060200
BF135856
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AV753229
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BE394076
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BE198231
BG918873
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BF033403
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Contact: Smith TPL
                                                                                                               cow.
Bos taurus
21180013
DEFINITION
ACCESSION
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BB630381 BB630381
AL212510 Tetraodon
AL233007 Tetraodon
BG394974 602457369
                                                  June 13, 2003, 02:37:44 ; Search time 151.839 Seconds (without alignments) 6506.409 Million cell updates/sec
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                                                                                                1 gggctgggatgacgaactgc......acatgcgcttcatgcaggag
                                                                                                                                                    32308132
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                    16154066 seqs, 8097743376 residues
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61
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Maximum Match 100%
Listing first 45 summaries
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                                    nucleic search, using sw model
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em_gss_pro:*
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EST 25-APR-2001

bovine cDNA

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Score

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Minimum DB seq Maximum DB seq

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Sequence evaluation of four pooled-tissue normalized bovine CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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                                                                                                                                                                                                /db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tlosue_type="pooled"
/lab_host="bild"
/note="Vector: pcMv SPORT6; Site_l: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissiams muscle."
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                           74.8%; Score 45.6; DB 12; Length 444; 85.0%; Pred. No. 3.2e-05; tive 0; Mismatches 9; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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467815 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BI775360
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No Box 16c, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4390
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                                                           FORWARD: AGGAAACAGCTATGACCAT
BACKMARD: GTTTTCCCAGTCACGACG
Plate: 57 row: H column: 11
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                 /organism="Bos taurus"
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/clone_lib="MARC 2BOV"
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PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
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                                        PCR PRimers
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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BB630381 RIKEN full-length enriched, 6 days neonate skin Mus
musculus cDNA clone A030014A04 5', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
WRL:http://genome.gsc.riken.go.jp,
WR.:http://genome.gsc.riken.go.jp,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Wataliki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fel: 81-45-503-9226
Fax: 81-45-503-9216
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/note-"Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, thymus, semitendonous muscle, longissimus muscle, pancreas, adrenal and ondometrium land ondometrium
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Computer-based methods for the mouse full-length cDNA
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases 1 to 1010)
                                                                                                                                                                                                                                                                                                                              1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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/clone_lib="G"
/note="Genoscope sequence ID : COAG163AD09LP1~end : T?"
/ 263 c 305 g 160 t 3 others
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genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
/clone="005N22"
                                                                               /organism~"Tetraodon nigroviridis'
/db_xref="taxon:99883"
/clone="163G17"
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Pred. No. 49;
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/note="Genoscope so
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Submitted (12-APR-2000)
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AL233007.1 GI:7892142
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis
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1 (bases 1 to 910)

Roest-Crollins, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fisames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using retraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                      Anote="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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Roset-Crollius, B., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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                                                         /clone="A030014A04"
/clone_lib="RIKEN full-length enriched, 6 days neonate
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                                                                                                                       /tissue_type="skin"
/dev_stage="6 days neonate"
/lab_host="DH108"
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                   /organism="Mus musculus"
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                                      /db_xref="taxon:10090"
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GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93 Library for gene discovery and sequence-ready map construction Unpublished (1999)
Other GSSs: RPCI93-ECORI-4113.TV
Contact: Najib M. El-Sayed
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                                                                                                                          Actinopterygil, Neopterygil, Teleostel; Buteleostel, Neoteleostel, Acanthomorpha; Acanthopterygil; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyldae; Oryzinae;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUCA1446
RPCI93-ECORI-4I13.TJ RPCI93-ECORI Trypanosoma brucei genomic clone RPCI93-ECORI-4I13, DNA sequence.
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Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences search
page: http://www.tigr.org/tdb/mdb/tbdb/.
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Tadasus Ahin.i
Contact: Tadasus Ahin.i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fat: 81-559-81-6856
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235 c 119 q 91 + ^
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/clone_lib="WR01SSA_cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryzias latipes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"taxon:8090"
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AQ641446.1 GI:5118156
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Trypanosoma brucei
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Fax: 301 838 0208
                                                                       Oryzias latipes
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Class: BAC ends
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                                                                                                                          /note="Organ: eye; Vector: poTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into Ecorn/XhoI sites using the following 5' adaptor: GCCACGAGGG. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                          1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 717.
Location/Qualifiers
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Wath MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 58;
0; Mismatches 18; Indels
                                  21; Indels
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/lab_host="DH10B (phage-resistant)"
   65.6%; Pred. No. 50;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:4579696"
/clone_lib="NIH_MGC_16"
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Best Local Similarity 67.9%;
...hos 38; Conservative
Best Local Similarity 65.6
Matches 40; Conservative
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person, B., Kohli,S., Stin,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Ritter Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GCTGGGATGACGAACTGCGGAAACCCGGCGCCCCAGATCTACATGCGCTTCATGCAGGA 60
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This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, 2 cells egg'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                       Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="egg"
/dev_stage="2 cells"
/lab_host="DH10B"
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1. .248
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Best Local Similarity 65.5
Matches 38; Conservative
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                                                                                                                                                                                                                           Bohui Zhao in Pieter de Jong's laboratory (Roswell Brix
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
Drucei TREU927/4 GYPat 10.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPCT93-EcoRI segment) or Dpn II (RPCT93-DpnII
segment). High molecular weight fragments were ligated in
pBACe3: 6 vector digested with Eco RI or Bam HI,
respectively. The average insert size is 141 Kb. Total
coverage (both segments): > 90 X the haploid
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Iloh, K., Kawal, J., Kojima, Y., Konno, H., Konda, M., Matsuyama, T., Sakauta, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Taqawa, A., Takahashi, F., Takaku, Akahira, S., Tanaru, A., Toya, T., Watchiki, A., Yasunishi, A., Wuramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 bp mRNA linear BST 11-OCT-2001 clone B020024106 3', mRNA sequence.
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17-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
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URt.http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Haystsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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waqi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahit,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                 /clone="RPC193-EcoR1-4113"
/clone="RPC193-EcoR1-4113"
/clone="Wector: pBAC63.6; Site_1: Eco RI; Site_2: Eco RI;
Constructed for The Institute for Genomic Research by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Indels
                                   /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
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                                                                                          /db_xref="taxon:5691"
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Best Local Similarity
Matches 39; Conserva
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RESULT 13
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1 (bases 1 to 580)

Tomkins, J. P., Main, D., Golcoechea, J. L., Frisch, D. A. and Wing, R. A. A. Dep-Coverage BAC Library for Maize
Unpublished (2001)
                                                                                                                                                                                                                                             /noce-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI: Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                         /clone="IMAGE:1049954"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.6%; Score 26; DB 9; Length 349 65.5%; Pred. No. 1.2e+02; ative 0; Mismatches 20; Indels
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100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                 data is from the 3' end
High quality sequence stop: 326.
Location/Qualifiers
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High quality sequence stop: 510.
Location/Qualifiers
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/clone_lib="Maize B73"
                                                                                                                                                            /db_xref="taxon:10090"
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                                                                                                                                                                                                                                /lab_host="DH10B"
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                                                                                                                                           /strain="C3H"
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Fax: 864 656 4293
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ZMMBBb0002L18f Maize B73 Zea mays genomic clone ZMMBBb0002L18f, DNA
/tissue_type="Young leaves"
/lab_host="E. coli"
/note="Vector: PUGGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation, ordering clones and sequence analysis see
                                                                                                              http://www.genome.clemson.edu/projects/stc/maize/ZMMBBb " 221 c 138 g 146 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 593)
Tonkins,Jr., Main,D., Golcoechea,J.L., Frisch,D.A. and Wing,R.A.
A Deep-Coverage BAC Library for Maize
Unpublished (2001)
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                                                                                                                                                                                                        Length 580;
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Pred. No. 1.3e+02;
0; Mismatches 20;
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Pred. No. 1.3e+02;
0; Mismatches 20
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/lab_host="E. coli"
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
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/clone="2MMBBb0002L18f"
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Location/Qualifiers
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/strain="B73"
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                                                                                                                                                                                                   Query Match 42.6%;
Best Local Similarity 65.5%;
Matches 38; Conservative
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Best Local Similarity 65.5%;
Matches 38; Conservative
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Zea mays
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BH140663/c
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Unpublished (1997)
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TITLE
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CDNA Library Preparation: M Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CEAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
WWW-bio.llnl.gov/bbrp/image/image.html
Insert Length: 878 Std Error: 0.00
Seq primer: -400UP from Gibco
High quality sequence stop: 394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE198231 680 bp mRNA linear EST 26-JUN-2000 ug76b11.yl Soares_mammary_gland_NMLMG Mus musculus CDNA clone IMAGE:1548285 5' similar to TR:054988 054988 SERINE/THREONINE
AW024446 LOGAP_Kid3 Homo sapiens cDNA clone IMAGE:2525969 3' similar to TR:043176 043176 PEPTIDASE HOMOLOG;; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammala; Butheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 64)

NGT-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 680)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:2525969"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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/db_xref="taxon:9606"
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                                                                                         AW024446.1 GI:5877976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gland tissue from a lactating female, and was then primed with a Not I - Oligo(df) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pf773 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 738)
Contact: Robert Strausherg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pT/T3D-pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary
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Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
the cloud through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10899 row: p column: 20
High quality sequence stop: 715.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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/clone_lib="NGI_CASP_Mam6"
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/tissue_type="infiltrating ductal carcinoma"
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                                                                                                                                                                                                                                                                                                                                                               Query Match 42.3%; Score 25.8; DB 10;
Best Local Similarity 67.9%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 17;
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                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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                                                                                                                                                                                       High quality sequence stop: 472.
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/clone="IMAGE:1548285"
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                                                                                                                           MGI:953633
Seq primer: -40RP from Gibco
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Sequence Sequence Patent No.

5, Appli 4, Appli 4, Appli 3, Appli 4, Appli 34, Appli 13, Appli 14, Appli 14, Appli 34, Appli 34, Appli 34, Appli 34, Appli

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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN ANALYSIS IN MYCOBACTERIUM
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US-08-469-411-1
5166058-3
5166058-3
US-09-027-337-9
US-09-644-600-9
US-09-395-6748-5
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US-08-373-5
US-08-373-5
US-08-374-0258-3
US-09-244-093-3
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US-09-244-093-3
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09103840A

Sequence 2, Application US/09103840A

Patent No. 629428

SERERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A

NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
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OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
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Best Local Similarity 63.9%;
Matches 39; Conservative
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US-09-103-840A-2/c
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US-09-103-840A-2
LENGTH:
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4027.262 Million cell updates/sec
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Sequence 1, 2
Sequence 1, 2
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Sequence 1
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Sequence 1
Sequence 3
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-518-914-1

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US-08-993-358A-1

US-08-903-358A-1

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US-08-903-358A-1

US-08-903-358A-1

US-08-903-358A-1

US-08-903-358A-1

US-08-903-358A-1

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US-08-377-292-2
US-07-679-451-1
US-07-989-847-1
US-07-721-847A-3
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Match
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Pred. No. 5.2;
0; Mismatches 11; Indels
         Best Local Similarity 73.8%; Pred. No. 5.2;
Matches 31; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                        APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                  822 ACCAGCTGCGAGATCTGGGCGCCCCAGTTCTACGAGCGCTACA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        822 ACCAGCIGCGAGAICIGGGCGCCCAGIICIACGAGCGCIACA 863
                                                                        12 ACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA 53
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
OCMPOTTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
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join(374..420, 469..1819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey COUNTRY: United States of America ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                 E: Hoffmann-La Roche Inc.
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-518-914-1
; Sequence 1, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhlani, Parul P.
; APPLICANT: Adham, Nika
                                                                                                                                                                                                      US-08-744-231-1; Sequence 1, Application US/08744231; Patent No. 6358722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 73.8%;
Matches 31; Conservative (
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; LOCATION: ;
US-08-744-231-1
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
CORRESPONDENCE: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELEPHONE: (201) 235-4205
TELEPHONE: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(374..420, 469..1819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Hoffmann-La Roche Inc. STREET: 340 Kingsland Street
                                                                                                                                                                             ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/744,231
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08868435 Patent No. 6291221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2322130 G 2322130
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                                                                                                                                    LENGTH: 4411529
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                                                                                                                                                                                                                                                                                                                                                                                                                                            61 G 61
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US-08-868-435-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-868-435-1
                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACA 44
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APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 23.2; DB
; Pred. No. 26;
0; Mismatches
                                    COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/804,227C FILING DATE: FEBRUARY 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMFUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.0%;
70.5%;
                                                                                                                                                                                                                                                                                                                                     LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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36155..41830
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Best Local Similarity 70.59
Matches 31; Conservative
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31329..36071
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350..14002
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    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                           CLASSIFICATION: 435
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ZIP: 46285
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LOCATION:
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; LOCATION:
US-08-804-227C-7
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GENERAL INFORMATION:
APPLICANT: Borowsky, Beth E.
APPLICANT: OGOZIACH, Kristine L.
APPLICANT: OGOZIACH, Kristine L.
APPLICANT: Adhan, Nika
TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
FILE REFERENCE: 59138-AJPW
CURRENT APPLICATION NUMBER: US/09/518,914
CURRENT APPLICATION NUMBER: US 09/303,593
EARLIER APPLICATION NUMBER: US 09/303,593
EARLIER FILING DATE: 1999-05-03
NUMBER FOR SEQ ID NOS: 44
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                              38.4%; Score 23.4; DB 4; Length 1508; 67.3%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.4%; Score 23.4; DB 4; Length 1541; 67.3%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTTCATGCAGG
                                                                                                                                                                                                                                                                                                                                                         11 GACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                   0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DeHOOF, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Storen, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                CURRENT APPLICATION NUMBER: US/09/518,914
CURRENT FILING DATE: 2000-03-03
EARLIER FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 44
SOUTHARE: Patentin Ver. 2.1
LENGTH: 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08804227C Patent No. 5876991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-518-914-3
; Sequence 3, Application US/09518914
; Patent No. 6413731
                      FILE REFERENCE: 59138-A/JPW
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Best Local Similarity 67.35
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                   33; Conservative
                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-518-914-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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ZIP: 46285
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Gaps ö

13; Indels

DB 2; Length 44377;

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ADDRESSEE: No. 60602980 No. 6060298disk of No. 6060298th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                             37.4%; Score 22.8; DB 3; Length 1320; 66.0%; Pred. No. 18; tive 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDHA Compartible
OMPUTER: IDHA Compartible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,358A
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1481/96
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: 0522/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fuglsang, Claus
APPLICANT: Ohmann, Anders
APPLICANT: Ohmann, Anders
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                       35,127
ER: 5101.200-US
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                                       FILING DATE: 07-MAY-1997,
APPLICATION NUBBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08989358A Patent No. 6060298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-MAY-1997,
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
12-DEC-1997
UMBER: 0529/97
                                                                                                                                                            REFERENCE/DOCKET NUMBER: 51
TELECOMOUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 51(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1320 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.4.
Best Local Similarity 66.03
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lassen, Soren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bech, Lisbeth
                                                                                                                         NAME: Gregg, Valeta A
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gregg, Valeta A REGISTRATION NUMBER:
FILING DATE: 12-DEC APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
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APPLICANT: Lassen
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COUNTRY:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACA 44
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SOFTWARES FRACISED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LASSen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Puglsang, Claus
APPLICANT: Offnann, Anders
APPLICANT: Ostergaard, Peter
ITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/804,198
                  PLLING
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
; TYPE: nucleic acid
"TYPE: nucleic acid
"TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09221654
Patent No. 6054306
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                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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14046..20036
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36155..41830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.55
Matches 31; Conservative
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31329..36071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
20110..31284
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 350..14002
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NY COUNTRY: U.S.A. ZIP: 10174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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FEATURE:
NAME/KEY:
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; LOCATION:
US-08-804-198-1
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Sequence 27, Application US/08362670B Patent No. 5658882 GENERAL INFORMATION:
                                                                Celeste, Anthony J.
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 64.2<sup>3</sup>
Matches 34; Conservative
                                                                                                                                                                                                                                                                                              CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..1233
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US-08-333-576C-27/c
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LOCATION:
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; LOCATION:
US-08-362-670B-27
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                                                                                                                                                                                                                                                                                                                        4 CTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 1593;
                                                                                                                                                                                                                                Score 22.8; DB 3; Length 1320;
Pred. No. 18;
0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22.8; DB 3; Length 1:
Pred. No. 18;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ostergaard, Peter R.
TITLE OF INVENTION: Phytase Polypeptides
FILE REPERENCE: 5382.500-02.
FILE REPERENCE: 5382.500-02.
FILE REPERENCE: 5382.500-02.
FILE REPERENCE: 5382.500-02.
CURRENT FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 1480/96
EARLIER APLICATION NUMBER: 1480/96
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 0529/97
EARLIER FILING DATE: 1997-05-07
EARLIER FILING DATE: 1997-12-01
EARLIER FILING DATE: 1997-12-01
EARLIER FILING DATE: 1997-12-01
EARLIER FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 32
SOUTHARRE: FLASSEQ for Windows Version 3:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/08993359A Patent No. 6039942
                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
LYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petent No. 6039942
GENERAL INFORMATION:
APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
APPLICANT: Obmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Fuglsang, Claus C.
                                                                                                                                                                                                                                    37.4%;
66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.4%;
Best Local Similarity 66.0%;
Matches 33; Conservative
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.09
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Peniophora lycii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (123)...(1439)
; NAME/KEY: sig_peptide
; LOCATION: (123)...(212)
; NAME/KEY: mat_peptide
; LOCATION: (213)...(1439)
US-08-993-359-23
TELEFAX: 212-878-9655
                                                                                                                                                                    ; MOLECULE TYPE: CDNA
US-08-989-358A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-362-670B-27/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 23
LENGTH: 1593
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-08-993-359-23
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.0%; Score 22.6; DB 1; Length 1233; 64.2%; Pred. No. 21;
tive 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 02140.
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NOWER: US/08/362,670B
FILING DATE: December 22, 1994
CLASSIFICATION NOWER: 24
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPHONE: 617 498-8261
TELEPHONE: GARACTERISTICS:
FROUTHY OF SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
FROUTHY INTORMATICS:
FROUTHY INTORMATION SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
CLONE: peptide
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Wolfman, Neil
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/08333576C Patent No. 6027919
GENERAL INFORMATION:
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FILING DATE: Herewith CLASSIFICATION: 514
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
US-08-808-324-27
                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.0%; Score 22.6; DB 3; Length 1233; 64.2%; Pred. No. 21; trive 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding BMP2 propeptide/BMP-12 mature peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Mellon, Douglas A.
IIILE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
                                                                                                                  ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/333,576C
FILING DATE: No. 6027919ember 2, 1994
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: GREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: GENETICS INSTITUTE, INC. 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08808324
Patent No. 6284872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UDENCH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                    CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS
                                                                                                                                                                                                                                                                             435
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LOCATION: 1..1233
                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic STRANDEDNESS:
                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-808-324-27/c
                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCCAGATCTACATGCGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22.6; DB 4; Length 1233; Pred. No. 21; 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GENETICS INSTITUTE, INC.
PRELICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding BMP2 propeptide/BMP-12 mature peptide
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-N0Y-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US94-14030A-27/c; Sequence 27, Application PC/TUS9414030A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Cambridge CONTRIBUTE CAUCHER COUNTRY: USA ZIP: 02140 COMPUTER READABLE FORM: WEDLUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
                                                                                                                                                                                                                                           5202-D
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGIGSTRATTON NUMBER: 32,618
REFERENCE/CDCKET NUMBER: 5202-
TELECOMMUNICATION INFORMATION:
TELEFRAX: 617 876-8851
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.0%;
64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.2<sup>3</sup>
Matches 34; Conservative
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NAME: Lazar, Steven R.
REGISTRAINO NUMBER: 32,618
REGISTRAINO NUMBER: 5202D-PCT
TELEFONE: 617 498 8160
TELEFONE: 617 498 8160
TELEPHONE: 617 498 8160
TELEPHONE: 617 498 8160
TELEPHONE: 617 876-5851
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTREISTICS:
LENGTH: 1233 base pairs
TYPE: nuclec acid
TYPE: nuclec acid
STRANDENESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOLONE: DANA encoding BMP2 propeptide/BMP-12 mature
CLONE: DANA encoding BMP2 propeptide/BMP-12 mature
CLONE: DEATURE:
NAME/KEY: mat_peptide
FEATURE:
COATION: 447..1233
FCT-US94-14030A-27
CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
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CQUET/ MALCH
SAT...1233
FCT-US94-14030A-27

CQUET/ MALCH
SAT...1233
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CQUET/ MALCH
SAT...1233
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CQUET/ MALCH
SAT...1233
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SAT...1233
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FCT-US94-14030A-27

CQUET/ MALCH
SAT...1
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Sequence 6224, Ap Sequence 6227, Ap Sequence 67, Appl Sequence 2303, Ap Sequence 602, App

Sequence 934, App

Sednence:

Run on:

Searched:

Database

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APPLICANT: LINFORMATION:
APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Warklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3:
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NOMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                     Sequence 1, Appli
Sequence 27, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 476, App
Sequence 476, App
Sequence 2113, Ap
Sequence 2113, Ap
Sequence 330, Appli
Sequence 330, Appli
Sequence 7546, Ap
Sequence 7546, Ap
Sequence 7546, Ap
Sequence 7546, Ap
Sequence 7546, Ap
Sequence 2718, Ap
Sequence 2718, Ap
Sequence 2718, Ap
Sequence 2718, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
US-09-764-891-6227
US-09-738-658-67
US-09-923-876-2303
US-09-738-626-934
US-09-738-626-934
US-09-738-626-1
US-09-945-182-7
US-09-945-182-7
US-08-957-425-4
US-10-073-961-476
US-09-952-360-1
US-09-952-360-1
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US-09-953-360-1
US-09-953-360-1
US-09-898-751A-3
US-09-898-751A-3
US-09-898-751A-3
US-09-898-751A-3
                                                                                                                                                                                                                                      US-09-923-876-3718
US-09-815-242-7872
US-09-923-876-2600
US-09-294-093B-79
US-09-918-995-31548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 61; DB 10; Best Local Similarity 100.0%; Pred. No. 3.4e-14; Matches 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                US-09-886-607-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                               US-09-826-581-2; Sequence 2, Application US/09826581; Patent No. US20020142310A1
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; ORGANISM: Homo sapiens
US-09-826-581-2
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Sequence 1, Appli
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Sequence 11, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 15, Appl
Sequence 15, Appl
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Sequence 4, Appli
Sequence 23, Appl
Sequence 1, Appli
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Sequence 12740, A
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Sequence 3, Appli
                                                                          June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds (without alignments) 4579.068 Million cell updates/sec
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61
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-913-31A-19

US-09-931-381A-17

US-09-931-381A-17

US-09-931-881A-17

US-09-934-868-51

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US-09-917-800A-1694
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US-10-007-270-23
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US-10-265-593-3
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Maximum Match 100%
Listing first 45 summaries
                                                         OM nucleic - nucleic search, using sw model
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Sequence 31548, A Sequence 3, Appli

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Sequence 11, Application US/09909567B
Publication No. US20030022257A1
GENERAL INFORMATION
APPLICANT: Macina, Roberto A.
APPLICANT: Mair, Manoj
APPLICANT: Chen, Selyu
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT FILING DATE: 2001-07-20
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.0%; Score 25; DB 10; Length 1473; 64.9%; Pred. No. 2.7; tive 0; Mismatches 20; Indels
                  APPLICANT: Trawick, John D.
APPLICANT: Grant J.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Tedentification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMER: 60/191,078
PRIOR APPLICATION NUMER: 60/206,848
PRIOR APPLICATION NUMER: 60/206,848
PRIOR APPLICATION NUMER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR PRIOR RESED FOR WINDOWS VERSION 4.0
SOFTWARRE: FORSED FOR WINDOWS VERSION 4.0
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SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 14917
          Trawick, John D.
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Best Local Similarity 64.99
Matches 37; Conservative
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US-09-815-242-8004
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US-09-909-567B-11
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APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REPEREBRE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR APPLICATION NUMBER: US 60/195,665
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5.
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Publication No. US20030054522A1
GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Perret, Kavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
FILE REFERENCE: CARPO068
CURRENT APPLICANT: US/09/939,964
CURRENT FILING DATE: 2001-08-27
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Pred. No. 3.1;
0; Mismatches 21;
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Patent No. US20020061569Al
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PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
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Best Local Similarity 64.4%;
Matches 38; Conservative
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Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
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Matches 61, Conservative
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (20)...(1486)
US-09-826-581-5
                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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ORGANISM: Rhizobium
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APPLICANT: Pan, Juniang
APPLICANT: Pan, Juniang
APPLICANT: Soler-Ferran, Dulce
TITLE OF INVENTION: Method for Identifying Agents Which
TITLE OF INVENTION: Moduate Chemokine "MEC"-Induced Functions of CCR3 and/or
TITLE OF INVENTION: CCR10
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TITLE OF INVENTION: CCR10
TITLE OF INVENTION NUMBER: US/09/931,381A
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
ENGINE: 1244
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                                                                                                                                                      2 GGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGATCTACATGCGC 49
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILTE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILTE OF INVENTION: NUCLEIC ACIDS
CURRENT FILTNG DATE: 2001-01-17
Prior application darenewed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SEQ ID NO 166
LENGTH: 600
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                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/09931381A; Patent No. 0S20020131107A1
GENERAL INFORMATION: APPLICANT: Butcher, Eugene C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 166, Application US/09764864; Patent No. US20020132753A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kunkel, Eric J.
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; ORGANISM: Homo sapiens
US-09-764-864-166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: CDS
) LOCATION: (5)...(1093)
US-09-931-381A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                             US-09-931-381A-17/c
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US-09-898-751A-1
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                                                                                                                                                                                                                                                  TITLE OF INVENTION: Method for Identifying Agents Which
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
TITLE OF INVENTION: CCR10
CURRENT APPLICATION NUMBER: US/09/931,381A
PRIOR APPLICATION NUMBER: US. 09/638,914
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US60/136,570
PRIOR APPLICATION NUMBER: US60/13,858
PRIOR FILING DATE: 1999-10-27; PRIOR PAPLICATION NUMBER: US60/13,858
PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 6.5;
0; Mismatches 15; Indels
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                                                                        Sequence 19, Application US/09931381A Patent No. US20020137107A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09898751A Patent No. US20020160024A1
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APPLICANT: Kellerman, Sirid-Aimee
APPLICANT: Moraloy, Leslie M.
APPLICANT: Bowman, Edward P.
APPLICANT: Zlotnik, Albert
                                                                                                                      GENERAL INFORMATION:
APPLICANT: Butcher, Engene C.
APPLICANT: Kunkel, Eric J.
APPLICANT: Pan, Juniang
APPLICANT: Soler-Ferran, Dulce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Oldham, Elizabeth R.
APPLICANT: Soto, Hortensia
APPLICANT: Liu, Ying
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Best Local Similarity 68.89
Matches 33; Conservative
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Homey, Bernhard
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...(1086)
US-09-931-381A-19
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LOCATION: (1)..(1086)
OTHER INFORMATION:
                                             US-09-931-381A-19/c
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US-09-898-751A-1/C
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                                                                                        APPLICANT: BOTOWARY, Beth E.
APPLICANT: Gozzalek, Kristine L.
APPLICANT: Lakhlani, Parul P.
APPLICANT: Lakhlani, Natul P.
APPLICANT: Adhani, Natul P.
TILLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS; FILE REPREBENCE: 59138-A/JPW
CURRENT APPLICATION NUMBER: US/09/518,914
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 1999-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Borowsky, Beth E.
APPLICANT: Ogozalek, Kristine L.
APPLICANT: Lakhlani, Parul P.
APPLICANT: Adham, Parul P.
TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
FILE REFERENCE: 59138-A/JPW
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CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US/09/518,914
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: US 09/303,593
PRIOR FILING DATE: 1999-05-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10146835; Publication No. US20030073167A1; GENERAL INFORMATION:
                        Sequence 1, Application US/10146835 Publication No. US20030073167A1
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1508
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 3
LENGTH: 1541
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US-10-146-835-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                       GENERAL INFORMATION:
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US-09-917-800A-1694
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US-10-146-835-3
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APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Randar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
TITLE OF INVENTION: DATE: US/10/108,605
CURRENT APPLICATION NUMBER: US/10/108,605
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Patent No. US20020137190a1
GeneRAL INFORMATION:
APPLICANT: ACFES, Mattheos
APPLICANT: Odom, James M
APPLICANT: Schenzle, Andreas J
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REPERENCE: CLIS96 US NA
CURRENT PELING DATE: 2001-09-29, 858
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 81
SOFTWARRE: Mairosoft Office 97
SEQ ID NO 51
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GCCGAGCGCCCTACCACTGCGCCGAGTGCGGCAAGCGCTTCACGCAGAAG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 38.7%; Score 23.6; DB 9; Length 573; l Similarity 64.8%; Pred. No. 8.8; 35; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 10
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR TLING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                 ; Sequence 84, Application US/10108605
; Patent No. US20020160934a1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster US-10-108-605-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.7%;
Best Local Similarity 64.8%;
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Methylomonas 16a
                                                                                                                                                                                        APPLICANT: Broadus, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                       RESULT 10
US-10-108-605-84
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LENGTH: 573
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APPLICANT: Ramseler, Thomas M.
TITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas campestris FILE REFERENCE: 38-10[15824]8
CURRENT APPLICATION NUMBER: US/09/927,827
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/279,493
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2935 GCGCTCCGATGACGTCCTGGTGATTCCCGATGCCTTGCTGGACCCGCGCTTC 2884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_022220 US-09-917-800A-1694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.0%; Score 23.2; DB 9; Length 3627; Best Local Similarity 65.4%; Pred. No. 15; Matches 34; Conservative 0; Mismatches 18; Indels 0
                                                                                                        TITLE OF INVENTION: Molecular Toxicology Modeling FILE REFERENCE: 44921-5038-US CURRENT APPLICATION NUMBER: US/09/917,800A
                                                                                                                                                                                CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PLICATION NUMBER: US 60/222,040
PRIOR PLING DATE: 2000-07-31
PRIOR PLING DATE: 2000-07-31
PRIOR PLING DATE: 2000-07-31
PRIOR PLING DATE: 2000-11-02
PRIOR PLING DATE: 2001-05-11
PRIOR PLING DATE: 2001-05-13
PRIOR PLICATION NUMBER: US 60/290,645
PRIOR PLICATION NUMBER: US 60/290,645
PRIOR PLICATION NUMBER: US 60/290,745
PRIOR PLING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
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PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SEQ ID NO 1694
LENGTH: 1323
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Publication No. US20030036176A1
GENERAL INFORMATION:
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Johnson, Kory
Castle, Arthur
Elashoff, Michael
Gene Logic, Inc.
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US-09-927-827-4/C
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LENGTH: 3627
                                                         APPLICANT:
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Search completed: June 13, 2003, 09:00:41 Job time: 21.2903 secs

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June 13, 2003, 01:49:14; Search time 192.613 Seconds (Without alignments) 9216.782 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-826-581-5_COPY_1007_1067
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Listing first 45 summaries
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11 gb ba:*

2 gb_ltg:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	00000000000000000000000000000000000000	AX099776 Sequence	. ~		Homo	Seque	AF214520 Sus scrof	AX099800 Sequence	AX398331 Sequence	AX398333 Sequence	AX398335 Sequence	AX398337 Sequence	AX099804 Sequence	AX281580 Sequence		AC009974 Homo sapi		AC1260/U Kattus no	e s	mus	S	ω :	AC112001 KATTUS DO	ns	ຜ		ACOLSTON HOMO SAPI				AL//2255 Mus muscu	Mus	Homo	Oryza	Humar	HOMO	Oryze	ALO34548 Human DNA				linear PAT 02-NOV-2001				ertebrata; E	it; nominitage; nomo.	otein kinase gamma 3 subunit
ID	AY281582	AX099776	AX099802	AF214519	HSA249977	AX099774	AF214520	AX099800	AX398331	AX398333	AX398335	AA53055/ AX308330	AX099804	AX281580	AC027416	AC009974	AF214521	AC129703	AC127107	AF336381	AC129702	AE334948	AC112066	AC096427	0 AL663072	0 AC087332	AC013380 AC063943	HS75N14	AC129236	AC125616	AL//2233 AT:845470	AC101452	AC023022	AC108872	HSJ894D12	AC002	AC105	9 HS1103G7	100	ALIGNMENTS		1647 bp DNA	7305.	8833		Chordata;	בין דוווס רבי	an, H. and Marklund, S. an amp-activated protein kinase A 5 18-CT-2001;
Query re Match Length DB	100 0 1647	100.0 2109	100.0 2115	100.0 2115	100.0 2290	92.1 1867	92.1 1873	92.1 1873	92.1 1873	92.1 1873	92.1 18/3	92.1 16/3	92.1 2022	75.7 1722	75.7 152129	75.7 206854	71.1 5888	67 5 190183	67.5 192968	67.5 227724	48.9 196208	47.9 IDSI	47.9 166397	47.9 178452	46.2 249536	45.9 143720	45.9 154746	45,9 183861	45.9 187546	45.9 195325	45.9 204/6/	45.6 71165	45.2 75131	45.2 115004	45.2 119563	45.2 141990	45.2 143277	45.2 153170	0000T 7:0*			AX281582	5 from	AX281582.1 GI:166088:	, human,	Homo sapiens Eukaryota; Metazoa;	ו ו	Andersson, L., Luthman, H Variants of the human an Patent: WO 0177305-A 5
Result No. Score															16		8 5	2 5		22			2 5	27		5 6	31		33		3 3		38	39				44 27.6			RESULT 1		z	z		ORGANISM H		AUTHORS TITLE JOURNAL

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2115 bp mRNA linear PRI 03-JUN-2000 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3) mRNA, complete cds.
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TDFILVLHRYRSPLVOIYEIEDHKIETWREIYLOGCFREPVSISPUDSLEBAYTLI
KNRIHRLPVLLDPVSGVLHILTHKRLLKFLHIFGSLLDFSFSLYRTIDLGIGFRED
AVVLETAFILTALDIFVDRRVSALPVVNECGOVVGIYSREDYIHLAAQOTVHLDMSY
GEALRORTLCLEGVLSCQPHESLGEVIDRIAREQVHRILVLVDETQHLLGVVSESDILQ
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                                                                                                                                                                                                                                                                                                                       PAT 02-APR-2001
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2115)
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                                                                                 1 TICCIGCACATCITIGGITCCCIGCIGCCCGGCCCTCCTTCCTCTACCGCACTAICCAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              same, and uses thereof
Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
1. 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variants of the gamma chain of ampk, dna sequences encoding the
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  Length 2109;
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100.0%; Score 61; DB 6; 1 100.0%; Pred. No. 9.4e-10;
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                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                              Sequence 29 from Patent W00120003. AX099802
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AF214519
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AX099802
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VGIX SRFDVIHLAAQQYYNHLDMSVGBALRQRTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVLVDETQHLLGVVSLSDILQALVLSPRGIDALGA*
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LSPQAPFPKLGWDDELRKPGAQIYMRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFA
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
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/note="unnamed protein product"
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
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Sequence 3 from Patent W00120003.
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  Arexis AB (SE)
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/gene="AMPK gamma 3"
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Carling, D.
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Sus scrofa
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SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
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AVVI.ETAPTI.TALDTFVDRKVSAI.PVVNFCGQVVGI.YSRFDVTHLAAQQTYNHLDMSV
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                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger.V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                   Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFMQEHTCYDAMAISSKLVIFDIMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
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HOMO Sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
(AMPK gamma 3 gene).
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AJ249977.1 GI:6688200
AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
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/protein_id="AAF73987.1"
/db_xref="GI:8215682"
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Pred. No. 9.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="skeletal muscle"
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/db_xref="taxon:9606"
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LSPQAPPFKLGWDDELTKREAQYTYRRTEBETVCDAMATSSKLYIPPTMLEIKKAFFA
LVANGVRAARLWDSKKOSFVGMLT ITDF LLYLHKYRSPLVGIYETEGHTLETWREIY
LQGCFKPLVSISPNDSLFEAVTLIKNRIHRLPVLDPVSGNYLHLTHKRLLKFHIRF
SSLLPRSFETYRIQOLGTGFRENLAVULETAPILTAMLDIFVDRXYSALPVVNECGOV
VGLYSRFDVIHLAQQYTWHLDMSVGRALRKRTLCLEGVLSCOPHESLGEVTDRIARE
OVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDPSGPEKI
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SSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEATFPKTTPLAOA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867).
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
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/evidence=experimental
/product="%Anb_activated protein kinase gamma 3 subunit"
/protein_id="CAB65117.1"
/db_xref="GI:6688201"
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                                                                       (bases 1 to 2290)
Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of Amp-activated protein kinase gamma-subunit lisoforms and their role in Amp binding
Blochem. J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-0CT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, Ducane Road, London, W12 ONN, UNITED KINGDOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="AMP-activated protein kinase regulatory
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    .2290
/organism="Homo sapiens"
/db_xref="taxon:9606"

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AX099774
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TLEATE TO MEET A MEET BE SERVING SERSHGDOGNKASRWTRQEDVEEG GPPGFREGPORPYTESERSHGDOGNKASRWTRQEDVEEG GPPGFREGPOSRPYAESTGGEATPRATPLAQAAPLAEVUNPPFREDILESDCAASAS DSNTDHILDIGI IEFSAASASGDELGIVEEKPAPCPSPEVLIPRIGHDDELGRPGAQVYM FPWGEHTCVDAMATSSKLV IPDYALETKAFPALVAROYRAAPLAMDSKKOSFVCHLTT TDFILVLHRYTRSPLVQIYEIEFRKIFTLARFTLARGAFPALVSTSPRDE RANTHLHAULDVLDPVSGAYLHILTHRKILKFLHFTFGTLLERSFLYRTINGDGIGFFRDA AVVETAPILTALIFVDRAVSALPVNNETGGYNGINTGARGATTLCLEGYLSCOPHETLGENTDRIVERQVHRLVLVDFTQHLLGAOGTVHHLDMNY GEALRQFTLCLEGYLSCOPHETLGEVIDRIVREQVHRLVLVDFTQHLLGAVSLSDILQ
                                                                                                                                                                                        /translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
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FPMGBHTCVDAMATSSKLVTFDYMLETKKAFFALVNAGVRAAPLWDSKCSFVGMLT
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFERDIL
KNRIHRLPVLDPVGGAVLHILTHKRLHKFLHFFGTLLPRESFLYRTIODLGIGFFRDL
                                                                                                                                                                                                                                                                                                                                         AVVLETAPILTALDIFVDRRYSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLYLVDETQHLLGVVSLSDILQ
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Mammalia, Eutheria, Cetartiodactyla, Suina; Suidae, Sus.
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Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SB); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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                                                                                                                     /product="AMP-activated protein kinase gamma subunit"
/protein_id="AAF73988.1"
/db_xref="GI:8215684"
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Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
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    1395
/note="unnamed protein product"

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/db_xref="GI:13538835"
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/organism="Sus scrofa"
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       /gene="PRKAG3"
                                                                          /note="AMPKG3"
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                                                 /gene="PRKAG3"
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Matches 58; Conservative
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AX099800
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                           CDS
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                                                                                                                                                                                                                                                         /protein_id="cac35798.1"
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//db_xref="GI:3538809"
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ISPNDSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTHRRLLKFLHIFGTLLPRPSFL
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HLAAQCTYNHLDMNVGEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDB
TQHLLGVVSLSDILDALVLYSAGIDALGA"

583 c 529 g 375 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1873)
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, M., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Loif (EB); Looff, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Pred. No. 3.5e-08;
0; Mismatches 3;
                                                                                                                                                                                                                   /note="unnamed protein product"
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/chromosome="15"
/map="15q"
/tissue_type="skeletal muscle"
1..1873
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                                                                                                                                         /organism="Sus scrofa"
/db_xref="taxon:9823"
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Best Local Similarity 95.1%;
Matches 58; Conservative
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/db_xref="G1:21261111"
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KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
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GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETGHLLGVVSLSDILQ
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                 Rothschild, M.F., Giobanu, D.C., Malek, M. and Plastow, G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 022085-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 022086-A 5 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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/db_xref="taxon:9823"
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GPPGFREGEPQGRPVAESTGGEAFFKAPLAGAAPLAEVURPPTERDLIESECASASA
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: Wo 0220850-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220856-A 714-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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RESULT 13

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SNATDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGMDDELOKPGAQVYM
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Cetartiodactyla; Suina; Suidae; Sus.
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Novel prkag3 alleles and use of the same as genetic markers
reproductive and meat quality traits
Patent: WO 020550-A 9 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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    1. 1395
    /note="unnamed protein product"

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Pred. No. 3.5e-08;
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Sequence 31 from Patent W00120003.
AX398339 1873 bp Sequence 9 from Patent W00220850.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                       Query Match 92.1%; Score 56.2; DB 6; Length 2022; Best Local Similarity 95.1%; Pred. No. 3.5e-08; Matches 58; Conservative 0; Mismatches 3; Indels 0
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human AMP-activate PRKAG3 CDNA Homo	Human AMPK gamma s	Human AMPK damma s	Pig AMPK gamma sub	Pig AMPK gamma sub	Pig wild-type PRKA	Pig PRKAG3 polymor	Pig PRKAG3 polymor
SUMMARIES	ABA08485 AAH43685	AAD03296	AAD03320	AAD03295	AAD03319	AAD36456	AAD36457	AAD36458
DB	22	22	22	22	22	24	24	24
% Query Match Length DB	547	2109	2115	1867	1873	1873	1873	1873
% Query Match	100.0	100.0	100.0	92.1	92.1	92.1	92.1	92.1
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tissue regeneration; wound healing; infection; immune discell culture; drug screening; gene therapy; antiinflammat antiasthmattic; autiarthritic; haemostatic; antiartariosic cytostatic; osteopathic; vasotropic; cardiant; virucide; antifungal; vulnerary; antiulcer; ss.  Homo sapiens.  WO200157188-A2.  09-AUG-2001.  05-FEB-2001; 2001WO-US03800.	KW	doq	e disor	der; o	steopor	oŝis	vascular growth d	Lsorder;
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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
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/label= "C1037T"
/note= "Causes R340W"
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/label= "C230G"
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label= "T559C"
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                                                                                                                                                                                                                                           cequences habitoral-represent incleic acids encoding them. The invention also relates to vertoes and recombinant host cells comprising the nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides of producing the novel polypeptides, antibodies against the polypeptides of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving a insight into their probable biological activities, and hence poltential therapeutic applications. The polypeptides of the invention may differentiation activities; stem cell growth factor activity; hardward activities, and hence there are probable biological activities; and hence there are probable biological activities; namociated activities; chemotatic or chemokineic activity; tissue growth activity; infinity activith or inhibin-related activities; chemotatic or chemokineic activities; namostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or good properties and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or good properties and nucleotides or an error. International activities in the properties and nucleotides or are prompted activities in the properties and nucleotides in activities (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell useful growth, bolypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound repair growth, bolypeptides involved with tissue regeneration and repair for nucleic acids encodis involved with the activities may be used to augment or replace cells damaged by illness; that can be used to augment or replace cells dama
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                                                                                                                                                Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
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100.0%; Pred. No. 1.5e-10;
tive 0; Mismatches 0;
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03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A: in exon 4 variation may be a substitution of a T for a C at nucleotide 550, and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340M. There may also be conclotide variation in infrom 6. The numbering of these covariations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1007 ITCCTGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCCTTCTTCTACCGCACTATCCAA 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                    Disclosure, Fig 5; 25pp; English.
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WPI; 2001-244810/25.
                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAE00223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200120003-A2
                                                                                                                                                                                                                                                                                                        967 G 967
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                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                       Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New variants of the gamma subunit of verlebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rogel-Gaillard C;
                                                                                                                                                                                                                         gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human Prkag3 protein"
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                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                           AAD03296 standard; DNA; 2109 BP.
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1390..2109
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18-MAY-2000; 2000EP-0401388
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472..1389
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                                             G 1067
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                                             1067
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5'UTR
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                                                                                            RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                           Length 2109;
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                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                          Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
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                                                                                                                                                                                                                                                                                                     100.0%; Score 61; DB 22;
100.0%; Pred. No. 1.8e-10;
iive 0; Mismatches 0;
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(ANDE/) ANDERSSON L,
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18-MAY-2000; 2000EP-0401388.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism cuch as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a fransgenic animal and bost cell transformed with PRKAG3 or a beterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrkAG3 gene, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                           in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15; ss.
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0
                                                                                                                                                                                                                                                    Length 2115;
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                                                                                                                                                                                                                            Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
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1390..1867
                                                                                                                                                                                                                                                   100.0%; Score 61; DB 22; 100.0%; Pred. No. 1.8e-10;
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             AAD03295 standard; cDNA; 1867 BP.
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18-MAY-2000; 2000EP-0401388.
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Matches 61; Conservative
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                                                                                                                                                                                                                                                   Query Match
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5'UTR
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The present sequence is a cDNA encoding pig adenosine monophosphate

(AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform,
PRKAG3: PrkaG3 gane is located in the RN locus of chromosome 15.

Mutation in PrkaG3 results in an altered regulation of carbohydrate
metabolism, particularly in skeletal muscle. PRKAG3 is useful as
therapeutic for treating carbohydrate metabolism alsorders such as
therapeutic for treating and disorders associated with muscle metabolism

activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
cativity, and for restoring an annual AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
cypreferably a carabohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
cuseful for detecting a functionally altered allele of PRKAG3 or a
heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
concoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or
concoding PRKAG3 is useful for detecting mutations in a PrkaG3 domain
concoding PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                        Robic A, Rogel-Gaillard C;
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                                                                                                               Le Roy P, Chardon P;
                                                                     Looft C, Kalm E, Milan D, Gellin J, Le Roy P, Char
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1..1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 2; 71pp; English.
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                                                                                                           Iannuccelli N,
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(KALM/) KALM
                                                                        Andersson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-2001
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(ANDE/) (LOOF/)

(KALM/)

myopathy

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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                               AMP activated protein kinase regulatory gamma subunit, PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
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/product= "Pig PRKAG3 wild-type protein"
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Pred. No. 6.2e-09;
0; Mismatches 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace (599, A)
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95.1%;
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08-JAN-2001; 2001us-260239P.
18-JUN-2001; 2001us-299111P.
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                       Pig wild-type PRKAG3 gene.
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Best Local Similarity
Matches 58; Conserv
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                                                                                                                                                           Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a cDNA encoding pig adenosine monophosphate capturated Kinase (AMPK) gamma subunit muscle-specific isoform, complete PRRAG3 Presuls and isolated in the RN locus of chromosome is without in Prkag3 gene is located in the RN locus of chromosome is without in Prkag3 gene is located in the RN locus of chromosome is what is muscle presents in a latered regulation of carbohydrate metabolism disorders such as the reaching carbohydrate metabolism disorders such as myopathy and disorders associated with muscle metabolism cartuvity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3, are useful for detecting and dysfunction of carbohydrate metabolism resulting ranspenic animal and host cell transformed with PRRAG3 or a chectorinaric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                               Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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Pred. No. 6.2e-09;
0; Mismatches 3; Indels 0;
/product= "Sus scrofa complete Prkag3 protein"
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                                                                                                                                                                                                                                                (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
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95.1%;
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18-MAY-2000; 2000EP-0401388.
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es 58; Conserv
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RESULT 7 AAD36456

Query Match

Matches

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AAD36456;

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Sus scrofa.
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RESULT 9
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/product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
replace (89, C)
                                                                                                                                                                                                                        /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                              Pig PRKAG3 polymorphic variant DNA (PRKAG3-30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 89-91; 109pp; English.
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                                                                                                                                                             Location/Qualifiers
                 AAD36457 standard; DNA; 1873 BP.
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95.1%;
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08-JAN-2001, 2001US-260239P.
18-JUN-2001, 2001US-299111P.
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                                                          (first entry)
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Best Local Similarity 95.15
Matches 58; Conservative
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                                                         09-AUG-2002
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                                                                                                                                          Sus scrofa
                                                                                                                                                                                                     variation
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                                      AAD36457;
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RESULT 8
        AAD36457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Pig PRKAG3 polymorphic variant (PRKAG3-52)" replace (154, A)
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Pred. No. 6.2e-09;
0; Mismatches 3
                                                                                                                                                                Pig PRKAG3 polymorphic variant DNA (PRKAG3-52)
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BP.
AAD36458 standard; DNA; 1873
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95.1%;
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                                                                                                         (first entry)
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Best Local Similarity 95.17
Matches 58; Conservative
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                                                                                                                                                                                                                                                                            gene; variant; ds.
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                                                                                                         09-AUG-2002
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(first entry)

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AAD36460 standard; DNA; 1873 BP.
                                                                                                                                   09-AUG-2002
                                                                                        AAD36460;
    RESULT 11
AAD36460
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Matches
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                                                                                        NAME OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                      /*tag- a /*tag- a //tag- a //tag- PRKAG3 polymorphic variant (PRKAG3-199)" //treplace (595, A) /*tag= b //standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                          AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
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                                                                                                                                                                        Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Malek M, Plastow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 98-100; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                           AAD36459 standard; DNA; 1873 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-SEP-2000; 2000US-231045P. 08-JAN-2001; 2001US-260239P. 18-JUN-2001; 2001US-299111P.
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                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-393850/42.
P-PSDB; AAE22987.
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es 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rothschild MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200220850-A2
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                                                                                                                               09-AUG-2002
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                                                                                                                                                                                                                                                                                                       Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                    variation
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                                                                                      AAD36459;
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Matches
RESULT 10
                      AAD36459
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1 TICCEGCACATCTITGGIICCCIGCIGCCCCGGCCCTCCTTCCTACCGCACTAICCAA 60
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                                                                                                                                                                                                                                                                                                                                             "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "Single nucleotide polymorphism (SNP)"
                                                        AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig; gene; variant; ds.
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llarity 95.1%; Pred. No. 6.2e-09;
Conservative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ciobanu DC, Malek M, Plastow G;
Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
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                                                                                                                                                                                                                                                Location/Qualifiers
1..1395
                                                                                                                                                                                                                                                                                                                                                                               replace (599, A)
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es 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAE22988.
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                                                                                                                                                                                          Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                  variation
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Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;

g

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exon
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                                                                                                                                                                                                                                                                    RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. PrkAG3 gape is located in the RN locus of chromosome 15. Mutation in PrkAG3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as therapeutic for treating carbohydrate metabolism disorders such as clibetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic callist functionally altered mutants are useful for the diagnostic preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for defecting a distunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutanty. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrKag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                        PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kalm E, Milan D, Robic A, Rogel-Gaillard C; J, Le Roy P, Chardon P;
                                                                                                                                                                                                       gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Sus scrofa Prkag3 splice variant"
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                                                                                                                                                             Sus scrofa PRKAG3 splice variant DNA
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 69; 71pp; English.
                                     AAD03321 standard; DNA; 2022 BP.
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18-MAY-2000; 2000EP-0401388.
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Gellin J,
                                                                                                                   13-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                          Sus scrofa,
                                                                               AAD03321;
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RESULT 12
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9
                                                1 TICCIGCACATCITIGGIICCCIGCIGCCCGGCCCITCCITCCICIACCGCACIAICCAA
                                                                                                                                                                                                                                                                                  Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
                          Gaps
                         ö
Length 2022;
                         Indels
Score 56.2; DB 22;
Pred. No. 6.2e-09;
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/note= "5' portion of intron 10"
                                                                                                                                                                                                                                                                                                                                                                                    : = "Intron 4"
"3' portion of intron 4"
                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..dg= e
/number= "Intron 6"
737..782
/*far-
                                                                                                                                                                                                                                                                                                                                                                                 "Intron 4"
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r= "Intron 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g "Intron 7"
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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number= "Intron 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'number= "Intron 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'number= "Exon 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'number= "Exon 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ب
                                                                                                                                                                                                                                                                                                                                                                                                                                number= "Exon 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'number= "Exon 6"
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                                                                                                                                                                                    AAH43683 standard; DNA; 1722 BP.
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92.1%;
95.1%;
                                                                                                                                                                                                                                                           PRKAG3 intron 4 - intron 10.
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                                                                                                                                                                                                                                    (first entry)
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           Best_Local Similarity 95.1
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'number-
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/*tag= 9
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                                                                                              61 G 61
                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                           AAH43683;
Query Match
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intron
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or admittating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AASS41954 represent novel human call adjanostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2820 IGCTGCACCTCACCGGTTACGATCTGCCGATGCACTCCTTTTTTTGCCGCACTGCCCTTG 2761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoletic; immune/haematopoletic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruman immune/haematopoietic antigen genomic sequence SEQ ID NO:36006
                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23; Length 3238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                            Claim 1; SEQ ID No 13137; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28;
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2000US-0198123.
2000US-0205515.
2000US-0209467.
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Best Local Similarity 66.7
Matches 40; Conservative
                         P-PSDB; ABG13146
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2001;
                                                                                                                                       biodiversity
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24-FEB-2000;
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                                                                                                                                                                                                                                                                                                           New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CCIGCACATCTTGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 1e-05;
0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                          Marklund
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 3; 25pp; English.
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86.48;
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2000US-0649167.
                                                                                       06-APR-2001; 2001WO-SE00765.
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                                                                                                                                                                                                                          Luthman H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                    WPI; 2001-657170/75
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                                                                                                                                                                                 (AREX-) AREXIS AB.
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WO200177305-A2.
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                                              18-OCT-2001
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28-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0215135.
07-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0218296.
26-JUL-2000; 2000US-0220513.
14-JUL-2000; 2000US-0225267.
14-JUL-2000; 2000US-0225267.
14-JUL-2000; 2000US-0225267.
14-JUL-2000; 2000US-0225267.
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14-JUL-2000; 2000US-022527.
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14-JUL-2000; 2000US-022527.
14-JUL-2000; 2000US-02237.
14-SEP-2000; 2000US-02327.
14-SEP-2000; 2000US-02327.
14-SEP-2000; 2000US-02327.
14-SEP-2000; 2000US-02327.
14-SEP-2000; 2000US-02327.
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14-SEP-2000; 2000US-02327.
15-SEP-2000; 2000US-02327.
15-SEP-2000; 2000US-02327.
16-SEP-2000; 2000US-02327.
17-SEP-2000; 2000US-02327.
17-S
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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2000US-0249299.
2000US-0249300.
2000US-0250160.
2000US-0250391.
                                                                              20000S-0244617.
20000S-0246474.
20000S-0246475.
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2000US-0249215,
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2000US-0251988,
2000US-0256719,
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20000S-0251856,
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20000S-0251869,
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2000US-0241809.
2000US-0241826.
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2000US-0249212.
2000US-0249213.
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2000US-0249245
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2000US-0249265
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20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 20-0C
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased

Disclosure; SEQ ID NO 36006; 3071pp + Sequence Listing; English.

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c expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent.

C protein. (1) proteins and polynucleotides may be used to prevent.

C diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-altiden genomic.

C cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK84942 to AAK84950 and AAK84700.

C cancers from the present invention. AAK84942 to AAK84950 and AAK84700.

C sequence 9979 BP; 2496 A; 2022 C; 2532 G; 2929 T; 0 other;

Query Match 45.9%; Score 28; DB 22; Length 9979;

Best Local Similarity 65.7%; Pred. No. 10;

Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

A 7602 TCCTGCACATCTTTGGTTCACCACGCCCCCCTTCTTTTTACCCACTATCCAGG 7661
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Search completed: June 13, 2003, 03:00:00 Job time: 22.1613 secs

A1063338 GH03085.5 BG479057 602256134 BG290491 603288351 BE275257 601122081 BG291149 602287180 BG048516 952021601

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Scoring table:

Searched:

Minimum DB s Maximum DB s

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Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith PP.
USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
Fax: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 572)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E Stone, R.T., Heaton, M.P., Grosse, M.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                            BI344527 572 bp mRNA linear 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. BI344527
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AA009100
AA030295
BF470814
AI746867
AIS09176
BEG30622
BEG46793
AL661556
BI134085
                    BG479057
BG290491
BE275257
BG291149
BQ048516
BG174779
                                                                            BI735773
BI526922
BE307400
BG974543
                                                                                                        BI155021
BI664379
BF136865
BG288506
BQ715536
BF788164
BF788164
BF788164
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pig.
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AUTHORS
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                                                June 13, 2003, 02:37:44 ; Search time 151.839 Seconds
                                                                                          1 ttoctgcacatctttggttc.....cttctaccgcactatccaag
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       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                             16154066 seqs, 8097743376 residues
                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                            US-09-826-581-5_COPY_1007_1067
61
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                                   nucleic search, using sw model
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EST 30-JUL-2001

Casas, E.

BI134085 UI-M-BH3-BB618484 BB618484

AI726042 BNLGHil40

pass sequencing. Bases called and alt_trimmed with phred 104.e. Vector identified by cross_match with the -minscore 18

Email: smith@email.marc.usda.gov

v0.980904.e.

BM556730 AGENCOURT AQ997354 RPCI-23-2 BF528264 602043043 BE978092 bs73907.y BE408262 601302612

BM556730 AQ997354 BF528264 BE978092 BE408262

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92.1 48.2 45.9 44.9

26.2 29.4 28 27.6 27.4

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Score

Result No.

Pred.

BI344527 373008 MA

Description

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FORWARD: AGGAAACAGCIAIGACCAI and -minmatch 12 options. PCR PRimers

M03359 Za06909.r1 B173577 603357036 B152692 602924488 B2507400 601098995 B6974543 602844770 B1155021 60290543 B1664379 603289943 B1664379 603289361 B0715536 AGENCOURT BF58156 6021833561 BN917705 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN5648 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN56438 AGENCOURT BN5643

Gaps

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/Acex="Femmale"
// Alab_host="DH10B"
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// Alab_host="DH10B"
// Alab_host="Dr10B"
// Alab_host="
                                                                                                                                                                                                                                                                                                 389 bp DNA linear GSS 24-FEB-2000 RPCI-23-271P21 AD997354 AD997354
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Shao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genefics (info@resgen.com). BAC end page:
http://www.tlgr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: 77
Class: BAC ends.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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   70.9%; Pred. No. 1.5e+02;
iive 0; Mismatches 16; Indels
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-271P21.TJ
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Pred. No. 3.1e+02;
0; Mismatches 15,
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/organism="Mus musculus"
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/clone_lib="RPC1-23"
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   Best Local Similarity 70.9
Matches 39; Conservative
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/db_xref='taxon:9606"
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/clone_lib="NAMCE:873918"
/clone_lib="NHLMGC_88"
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Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM556730 1173 bp mRNA linear EST 20-FEB-2002 AGENCOURT_6540753 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737918
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National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ArC.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Bregeration: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov
Rate: LLAM12748 row: m column: 23

High quality sequence stop: 473.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1173)
                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
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Best Local Similarity 95.1%; Pred. No. 4.3e-06;
Matches 58; Conservative 0; Mismatches 3
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Email: oliver@helix.nih.gov,
http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digsetive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC); see http://www.nisc.nih.gov).
Sequencing Center (NISC); see http://www.nisc.nih.gov).
Seq primer: MISRPI reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/strain="y[*] w[67c1]/y"
/db_xref="taxon:7227"
/clone="bay3307"
/clone="brosophila melanogaster adult testis library"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plater LLCAB36 row: g column: 03
High quality sequence start: 7
High quality sequence store: 645.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 4.9e+02;
0; Mismatches 16
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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ilarity 69.8%;
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   BF528264 1-DEC-2000 mRNA linear EST 11-DEC-2000 602043043F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180619
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 626)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
Plate: LLAM9492 row: f column: 12
High quality sequence start: 130
High quality sequence start: 130
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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Ephydroidea; Drosophilidae; Drosophila.
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Andrews, J., Bouffard, G. and Oliver, B.
Drosophila melanogaster testis expressed sequence tags
Unpublished (1999)
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/clone="IMAGE:4180619"
/clone_lib="NCI_CGAP_Brn67"
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/organism="Homo sapiens"
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Length 619; Indels

DB 12;

28

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Metazoa; Arthropoda; Hachycera; Bucomorpha; Rophydroidea; Drosophilidae; Drosophila, Bridydroidea; Drosophilidae; Drosophila, Bridydroidea; Drosophilidae; Drosophila, Bridses 1 to 715)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlsen, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, J., Frise, E., George, R., Gonzalez, M., Guzalez, M., Guzalez, M., Garzin, H., Farfan, J., Parkse, E., George, R., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.

BDGP/HHMI AT Drosophila EST Project
Unpublished (2000)
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//db.bost="Plates Ar.10-MT.120: DH5-alpha. Plates
Ar.121-Ar.319: DH5-alpha TonA"
Ar.121-Ar.319: DH5-alpha TonA"
Site_2: Xhol; The mRNR for the testis library was made
Site_2: Xhol; The mRNR for the testis library was made
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTFV: Plasmid cDNA library."
                                                                                                                                                                                                                                      BF488250
AT23475.Sprime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster cDNA clone AT23475 5 similar to CG4714:
FBan0004714 located on: 2R 49F15-50A1;: 04/09/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003819: arm:2R [8082036,8314191]
hit genomic AE003819: arm:2R [8082036,8314191]
Pate: AT.234 row: G column: 3
High quality sequence stop: 674.
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  Gaps
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11; Indels
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/db_xref="taxon:7227"
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Mismatches
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Fax: 510 486 6798
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BF488250/c
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           /u__xi=_caxou:900.
/u__xi=_caxou:900.
/clone_lib="NIH_MGC_21"
/tlssue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: poTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAGGGG; Size-selected >500pp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).*
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/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage=resistant)*
/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/KhoI sites using the following 5' adaptor:
GCGACGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Supersoript II RT (Life Technologies). Note: this is a
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs.rfmail.nih.gov
Tissue Procurement: Dr. Daniel Movicar, DBS/NCI
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLLL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.llnl.gov
Plate: LLCMIG89 row: i column: 02
High quality sequence stop: 704.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity 75.6%; Pred. No. 5e+02;
Matches 34; Conservative 0; Mismatches 11; Indels 0.
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/db_xref="taxon:9606"
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Query Match
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60525214F NIH_MGC_21 Homo sapiens CDNA clone IMAGE:4649792 5',
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/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
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                                                                                                                                                                            Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 754)
1 (bases 1 to 754)
1 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubhin, G. M.
BDGP/HHMT Drosophila EST Project
Unpublished (2001)
0 no Jul 23, 1998 this sequence version replaced gi:3339282.
Other_ESTs: GH03085.3prime
melanogaster cDNA clone GH03085 5 similar to CG4714: FBan0004714 located on: 2R 49F15-50A1;: 04/10/2001, mRNA sequence.
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hit genomic AE003819: arm.2R [8082036,8314191]
hit genomic AE003819: arm.2R [8082036,8314191]
estimated-cyto:49F2-50A3: 04/10/2001
Plate: GH.30 row: H column: 1
High quality sequence stop: 754
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/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
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/db_xref="taxon:7227"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                      AI063338
AI063338.2 GI:13759449
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Db δλ

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/db_xrefa="taxongooffee"
//db_xrefa="taxongooffee"
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/tissue_type="choriocarcinoma"
/tissue_type="choriocarcinoma"
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/tissue_type="choriocarcinoma"
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/note="lorgan: placenta; vector: poTB7; Site_1: XhoI;
Site_2: EooRi: CDNA made by oligo-dr priming.
Directionally cloned into EooRI/XhoI sites using the
following 5 dadaptor: GGCACGAG(G). Size=selected >500bp
for average insert size 1:8kb. Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZaP-CDNA synthesis kit
(Stratagene) and Supersoript II RT (Life Technologies)."
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/clone=lib='NHH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/tab_host='-billow (phage-resistant)"
/note="organ: bladder: Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally, oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10409 row: f column: 13
High quality Sequence stop: 701.
Location/Qualifiers
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Cloud through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: IJCMA430 row: c column: 09
High quality sequence stop: 757.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.1e+02;
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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Tissue Procurement: ATCC
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BG290491
BG290491.1 GI:13047386
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75.6%;
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BG291149.1 GI:13048809
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/tissue_type="m_dalootic melanoma"
/lab_bost="mildb (phage-resistant)"
/nole="Cogan: skin, Vector: poTB7; Site_1: Xho!; Site_2:
ECORI: CDNA made by oligo-dT priming. Directionally
cloned into ECORI/Xho! sites using the following 5'
adaptor: GCACGAGG(G). Site-selected >500bp for average
insert size 18kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                           0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 921)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.2e+02;
0; Mismatches 11; Indels 0
                                                                          Length 913;
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                                                                                                                                              Indels
Note: this is a NIH_MGC Library.*
1 254 c 287 g 146 t
                                                                      Score 27.4; DB 12;
Pred. No. 5.2e+02;
0; Mismatches 11;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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/organism-"Homo sapiens"
/db_xref-"taxon:9606"
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High quality sequence stop: 742.
Location/Qualifiers
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75.68;
                                                                      Query Match
Best Local Similarity 75.6%;
Matches 34; Conservative
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Matches 34, Conservative
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BE275257/c
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/lab.host="Didder: Sistant)"
/note="organ: Diadder: Vector: pcWv-SPORT6; Site_1: Not!;
Site_2: Sall; Gloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 926)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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95203G01.y2 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.
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CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
flowed through the I.M.A.G.E. Consortium/Linn at:
http://image.lnl.gov
Plate: LLAM10406 row: p column: 19
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Best Local Similarity 75.6%; Pred. No. 5.2e+02;
Matches 34; Conservative 0; Mismatches 11; Indels 0
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/db_xref="taxon:9606"
/clone="IMAGE:4516098"
/clone_lib="NIH_MGC_93"
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Plate: 952021 row: G column: 01.
                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
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Contact: Walbot V
                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .926
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/note-"Vector: pUC19; Site_1: ECOR1; Site_2: ECOR1; The library was prepared by George Rudenko using poly (A) selector RNA and Universal Riboclone cDNA Synthesis System (Promega). CDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with ECORI addptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into ECORI-digested pUC19 vector. Blue/white selection on
                                             /organism="zea mays"
/cultiva="zwas Flack Mexican Sweet)"
/db_xref="taxon.4577"
/clone_lib="552 - BMS tissue from Walbot Lab (reduced rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG174779 887 bp mRNA linear EST 06-FRB-2001 602336043F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4459019 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Musinaes 1 to 887)

NIH-MOC Intp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs:r@mail.nih.gov

Tissue Procurement. Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov: f column: 12
High quality sequence stop: 30.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 CTTGCTCTGGTTTGGTTCCTTGCTTGCTTTGCTCCATTGCTCC 17
                                                                                                                                                                             /tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carbenicillin-containing plates was used to recover positive clones." 2 others
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/clone_lib="WOI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
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/strain="FVB/N"
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Location/Qualifiers
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/lab_host-"DH10B"
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TITLE
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COMMENT
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        199 c
        219 g
        220 t

        ORIGIN
        00 c
        219 g
        220 t

        Ouery Match
        44.6%; Score 27.2; DB 12; Length 887; Best Local Similarity 80.0%; Pred. No. 5.9e+02; Matches 32; Conservative 0; Mismatches 8; Indels 0; Gaps Qy
        15 TGGTTCCTGGTGCCCCGGCCTTCTTCTTCTCTCACGCA 54

        Qy
        15 TGGTTCTCTGATGCCCCGGGCTTCTTCTTCTCACGCA 54

        Db
        44 TGCTTCTCTGATGCCCCGGGCTCTTCTTACTCCAGT 5
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Search completed: June 13, 2003, 05:58:32 Job time: 155.839 secs

Mon Jun 16 09:56:15 2003

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Sequence 3, Ap
Sequence 3, Ap
Sequence 7, Ap
Sequence 25, Ap
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Sequence 6, R
Sequence 3, R
Sequence 3, R
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/cgn2_6/ptodata/1/ina/BC_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUB_COMB.seq:*
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Compugen Ltd.
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US - 07-866 - 979 - 3

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US - 09 - 201 - 746 - 3

US - 09 - 097 - 231 - 3

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version :
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993
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Sequence 11, Appl
Sequence 164, Appl
Sequence 4, Appl
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Sequence 7, Appli
             Sequence 3, Sequence 3,
                                                                                                                                                                                                                                                                                                                                        Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER TO STATE: US

ZIP: 07065-0907:

ZIP: 07065-0907:

COMPUTER TEADABLE FORM:

COMPUTER: The PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOUTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/148,708

FILING DATE: 08-NO. 6407207-1993

CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION CUNKNOWN>

PRIOR DATE: CUNKNOWN>

ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAME: CATUSO, Charles M

NAME: CATUSO, Charles M

REGISTRATION NUMBER: 30161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Length 387;
                                                                                                                                                                         US-09-576-160B-11
US-09-199-637A-164
US-08-200-016-4
           US-08-369-796-3
US-08-852-091-3
US-08-820-544-3
US-08-956-852-3
US-08-948-547-3
US-08-948-547-3
US-08-956-653A-3
US-09-364-970-10
US-09-087-465-1
                                                                                                                                        US-09-103-840A-2
US-09-103-840A-1
US-09-576-160B-10
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                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 18713
TELEDHONE: (908) 594-4830
TELEBHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: SINGLE
; MOLECULE TYPE: CDNA to mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-148-708-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000 CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score Pred. 1
                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08148708 Patent No. 6407207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 387 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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APPLICANT: Hess, John W
                                                     3943
3943
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Best Local Similarity
US-08-148-708-7
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686 TCCTGAATGTCGTGGGCTTCCTGCTGCCCCTGAGTGTCATCACCTTCTGCACGATGCA 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.6%; Score 26; DB 4; Length 1179; 65.5%; Pred. No. 4.4; tive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                           CURRENT PER PER COMPATIBLE
COMPUTER: IN PC COMPATIBLE
CORRENT PG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-NO. 640/207-1993
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/860,709
FILING DATE: CURROWN>
ATORNEY/AGENT INFORMATION:
NAME: CAUSO. Charles
REFERENCE/DOCKET NUMBER: 30161
REFERENCE/DOCKET NUMBER: 18713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BOLKOWSKI, JOSEPH A.
APPLICANT: Strader, Catherine D.
APPLICANT: Hess, John W.
APPLICANT: Chen, Howard Y.
APPLICANT: Trumbauer, Myrna E.
TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFFWARING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                         NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1179 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08759848 Patent No. 5750826 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: John W. Wallen III
126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                             COUNTRY: US
ZIP: 07065-0907
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ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rahway
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STREET: 12
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Matches
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                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                  Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
BK-2 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.6%; Score 26; DB 4; Length 909; Best Local Similarity 65.5%; Pred. No. 4.2; Matches 38; Conservative 0; Mismatches 20; Indels
  20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-No. 6407207-1993
CLASSIETCATION CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/660,709
FILING DATE: «UNKNOWN>
ATORNEY/AGENT INFORMATION:
NAME: CALLOSO, CHARTIES M
REGISTRATION NUMBER: 30161
REFERENCE/DOCKET NUMBER: 18713
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA to mRNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-148-708-9
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strader, Catherine E
Borkowski, Joseph B
Ransom, Richard W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                             Sequence 9, Application US/08148708; Patent No. 6407207
; GENERAL INFORMATION:
; APPLICANT: Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hess, John W
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NJ
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US-08-148-708-9
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  Matches
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TYPE: nucleic acid
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PCT-US95-09383-2
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                                                                                                                                            Query Match
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                                                                                                                                                               Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.6%; Score 26; DB 1; Length 1378; Best Local Similarity 65.5%; Pred. No. 4.5; Matches 38; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC compatible
COMPUTER: IBA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/148,708
FILING DATE: 08-NO. 6407207-1993
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/860,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 18713
                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281,393
FILING DATE: 27-JUL-1994
ATTORNEY/ACENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSES:
STREET: P.O. BOX 2000
CITY: Rahway
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strader, Catherine D
Borkowski, Joseph B
Ransom, Richard W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Caruso, Charles M
REGISTRATION NUMBER: 30161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4830
TELEFAX: (908) 594-4720
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SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1923.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08148708; Patent No. 640720; GENERAL INFORMATION: APPLICANT: Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NJ
                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-148-708-6
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                                                                                                                                                           20; Indels
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Borkowski, Joseph A.
APPLICANT: Strader, Catherine D.
APPLICANT: Strader, John W.
APPLICANT: Chen, Howard Y.
APPLICANT: Trumbauer, Myrna E.
TITLE OF INVENTION: BRADYKININ B2 RECEPTOR WODIFIED
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09383
                TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-148-708-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281,393
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9509383 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: John W. Wallen III
STREET: 126 E. Lincoln Avenue
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
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65.5%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1378 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: single
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New Jersey
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Les 38; Conserva
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APPLICANT: Lu, Dongsi
PAPLICANT: Chen, Wenbiao
TITLE OF INVENTION: Methods and Reagents for Discovering and
TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagon:
TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
CORRESPONDENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 CGTGCTCATCTGTGGCTCCATGGTGTCCAGTCTCCTGGCTTCTT 422
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tive 0; Mismatches 17; Indels 0
                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,906B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5849871nan, Keyin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154-H
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFENEN: 312-913-0001
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Kesterton, Robert A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1260 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
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APPLICANT: Fan, Wei
APPLICANT: Boston, Bruce
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Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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960..1260
                                                                                                                      COMPUTER READABLE FORM:
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GENERAL INFORMATION:
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Chicago
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; LOCATION:
US-08-466-906B-3
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FEATURE:
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NAME/KEY:
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APPLICANT:
APPLICANT:
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                                                              COUNTRY:
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Patent No. 5849871
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: Mountjoy, Responsible Correspondences: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESS
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Pred. No. 11;
0; Mismatches 17; Indels 0
                          Sequence 3, Application US/07866979
Relact No. 552347
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: And USES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: USA
COMPUTER: TITLIFOLS
COMPUTER: READABLE FORM:
MEDIUM TYPER: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Nolaber: US/07/866,979
FILLING DATE: 19920410
CLASSIFICATION: 435
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ATTORNEY/AGENT INFORMATION:
NAME: No. 5532247nan, Kevin E
REGISTRATION NUMBER: 35,303
REGISTRATION NUMBER: 92,154
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
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Best Local Similarity 67.3%;
Matches 35; Conservative (
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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15..959
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CITY: Chicago
STATE: Illinois
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; LOCATION: 960..1
US-07-866-979-3
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LOCATION:
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   US-07-866-979-3
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LOW, Malcolm J
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/097,231
FILLIGA DATE: 12-Jun-1998
CLASSIFTCATION: <unional content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the
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CITY: Chicago
STATE: Illinois
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TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
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Sequence 3, Application US/09097231
Patent No. 6278038
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
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Chen, Wenblao
                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                  INFORMATION FOR SEQ ID NO: 3:
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 35; Conservative
            312-913-0002
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; LOCATION:
US-09-201-746-3
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FEATURE:
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Patent No. 626821
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Mountly, Kathleen G
TITLE OF INVENTION: Melanocyle Stimulating Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 17; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive
CITY: Chicago
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PetchtIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281A
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APPLICATION NUMBER: US/09/201,746
                                                                                                 AFFLG. 04-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100048 nan, Kevin E
REGISTRATION NUMBER: 35, 303
                                                                                    JMBER: US/08/706,281A
04-SEP-1996
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01-DEC-1998
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: No. 6268221nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEPAX: 312-913-0002
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 67.3
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-201-746-3
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Gaps

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1 TICCIGCACATCTTIGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAA 60
                                                         GENERAL INFORMATION:
APPLICANT: YAAA, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
1.0CAPTION: (1131)..(2399)
1.0CAPTION: INFORMATION: Escherichia coli nucleic acid encoding
OTHER INFORMATION: Escherichia coli nucleic acid encoding
OTHER INFORMATION: folypolyglutamate synthetase-dihydrofolate
OTHER INFORMATION: synthetase
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: M32445/GenBank
US-09-347-878-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 2561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct) INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 COMPatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.7%; Score 24.2; 62.3%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: WORD fOF WINDOWS 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                Sequence 25, Application US/09347878C Patent No. 6376210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/099,242
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 62.39
Matches 38; Conservative
                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
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US-09-347-878-25/c
                                                                                                                                                                                                                                         SEQ ID NO 25
LENGTH: 2561
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Patent No. 5830760
GENERAL INFORMATION:
APPLICANT: Teal, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Recept
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA to mRNA DESCRIPTION: page 11, RAR-alpha N-terminal region; positions 103 to 363 of SEQ.
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                                                                                                                                                                                           Query Match 40.7%; Score 24.8; DB 4; Length 1260; Best Local Similarity 67.3%; Pred. No. 11; Matches 35; Conservative 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.7%; Score 24.2; DB 2; Length 261; 66.0%; Pred. No. 13;
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REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: F. FHCR-1-7190
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
NPORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows 5.01-t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                          LOCATION: 960..1260
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word for Windows 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/099,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,
FILING DATE: 0.11y 28, 1993
ATTORNEY/AGENT INFORMATION:
                                         15..959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Washington
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Best Local Similarity
                                                                                     NAME/KEY:
                    NAME/KEY:
                                           LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2800 P
CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101
  FEATURE:
                                                                FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-592-383-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                   US-09-097-231-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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Search completed: June 13, 2003, 06:01:18
Job time: 9.64516 secs
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                                                                TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: page 4,RAR-alpha403 dominant negative; deleted of 1311-1596 of SEQ.
                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARRELL JR, RAMMOND P
APPLICANT: WARRELL STANKEN
APPLICANT: FRANKEL, STANLEY
TITLE OF INVENTION: METHODS FOR THE DETECTION AND
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL.)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               6 GCACATCTTTGGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCC 58
                                                                                                                                                                                                                         DB 2; Length 2658;
                                                                                                                                                                                                                                                                 18; Indels
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Best Local Similarity 66.0%; Pred. No. 19;
Matches 35; Conservative 0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION 0435
PRIOR APPLICATION DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 38694-A TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400 TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08095728B Patent No. 5843642
LENGTH: 2658 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 2928 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: CDS

: LOCATION: 103..1488

: OTHER INFORMATION:

US-08-095-728B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: hRAR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-095-728B-3
                                                                                                                                                                        US-08-592-383-3
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39.7%; Score 24.2; DB 2; Length 2928;

Query Match

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                        Gaps
                                                                          6 GCACATCTTTGGTTCCCTGCTGCCCGGCCCTCCTTCCTCTACCGCACTATCC 58
                     18;
Best Local Similarity 66.0%; Pred. No. 20;
Matches 35; Conservative 0; Mismatches
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June 13, 2003, 04:39:50; Search time 19.2903 Seconds (without alignments) 4579.068 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1029858 seqs, 724030393 residues
                                                                                                                                                                                                                                                            US-09-826-581-5_COPY_1007_1067
61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:* /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Description	Sequence 5, Appli	Sequence 3, Appli	Sequence 159, App	Sequence 7, Appli	Sequence 5, Appli	Sequence 129, App	Sequence 1, Appli	Sequence 59, Appl	Sequence 2280, Ap	Sequence 6987, Ap	Sequence 21, Appl	Sequence 3, Appli	Sequence 19, Appl	Sequence 3428, Ap	Sequence 92, Appl	Sequence 21, Appl	Sequence 21, Appl	Sequence 11, Appl	Sequence 11, Appl
ID	0 US-09-826-581-5	0 US-09-826-581-3	US-10-255-536-159	US-10-045-815-7	US-10-045-815-5	0 US-09-925-297-129	US-09-979-593-1	US-09-979-593-59	US-09-764-891-2280		10 US-09-815-944-21	5	0 US-09-815-944-19	0 US-09-880-107-3428	2 US-10-044-090-92	US-10-269-353-21	0 US-09-790-264-21	US-10-269-353-11	0 US-09-790-264-11
% Query Match Length DB	1647 1	1722 1	566 9	2322 9	2416 9	1682 1	12043 9	12043 9	632	•	200 1	1260 9	1260 1	99014 1	733 1	741 9	741 1	819 9	819 1
% Query Match I	100.0	75.7	44.9	43.6	43.6	42.6	42.3	42.3	41.0	41.0	40.7	40.7	40.7	40.7	40.0	40.0	40.0	40.0	40.0
Score	61	46.2	27.4	26.6	26.6	26	25.8	25.8	25	25	24.8	24.8	24.8	24.8	24.4	24.4	24.4	24.4	24.4
Result No.	1	7	3	4	Ω	9	c 2	<b>တ</b>	6 0	10	11	12	13	c 14	c 15	c 16	c 17	c 18	c 19

RESULT 2 US-00-826-581-3 Sequence 3, Application US/09826581 ; Patent No. US20020142310A1

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Sequence 74, Appl Sequence 52, Appl Sequence 421, App Sequence 145, Appl Sequence 19, Appl Sequence 19, Appl Sequence 16, Appl Sequence 16, Appl Sequence 15, Appl Sequence 20, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Sequence 509, Appl Seq	ALIGNMENTS  81  THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 St 19,665  195,665  resion 4.0	100.0%; Score 61; DB 10; Length 1647; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0; TICCTGCACATCTTTGGTTCCTGCTGCCCGGCCTCCTTCCTCACGCACATCACA 60
US-10-764-898-74 US-110-073-865-52 US-09-764-898-146 US-09-764-898-146 US-10-269-353-19 US-10-269-353-12 US-10-269-353-12 US-10-269-353-12 US-10-269-353-12 US-10-269-353-12 US-10-269-353-12 US-09-798-264-16 US-09-798-264-29 US-09-978-192A-509 US-09-978-192A-509 US-09-978-192A-509 US-09-978-191A-509 US-09-978-608A-509 US-09-978-564A-509 US-09-978-564A-509 US-09-978-564A-509 US-09-978-564A-509 US-09-978-564A-509 US-09-978-564A-509 US-09-978-564A-509 US-09-978-608A-509 US-09-978-608A-509 US-09-978-608A-509 US-09-978-608A-509 US-09-978-608A-509 US-09-978-608A-509 US-09-978-608-509 US-09-978-608-509 US-09-978-824-509 US-09-978-824-509 US-09-978-824-509	ALIGNMENTS  1826581 10 For the HUMAN AMP-ACTITUS/09/826,581 14-05 160/195,665 17 18 Version 4.0	Score 61; DB 10;
10000000000000000000000000000000000000	-5 Application US/09826581 ORNATION: Andersson, Leif Luthman, L. Holger Marklund, Stefan Marklund, Stefan NUENTION: VARIANTS OF THE HI ENCE: 11145-007001 LING DATE: 2001-04-05 ICATION NUMBER: US 60/195,66 MG DATE: 2000-04-07 SEQ ID NOS: 14 Homo sapiens CDS CDS (20)(1486)	larity 100.0%; Conservative (CTGCACATCTTTGGTT
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1  US-09-826-581-5 Sequence 5, Application US/09826581 Patent No. US20020142310A1 REMERAL INFORMATION: APPLICANT: Luthman, L. Holger APPLICANT: Luthman, L. Holger APPLICANT: Luthman, L. Holger APPLICANT: Luthman, L. Holger TITLE OF INVENTION: CURRENT APPLICANTON VARIANTS OF TH FILE REPERENCE: 11145-007001 CURRENT FILING DATE: 2001-04-05 PRIOR APPLICATION NUMBER: US 60/19 PRIOR FILING DATE: 2000-04-07 CURRENT FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 14 SOSTWARE: PASLSEQ for WINGOWS VEFS: SEQ ID NO 5 FEAVURE: DAA ORGANISM: HOMO SADIENS FRAURE: NAME/KRY: CDS LOCATION: (20)(1486)	Match Local S es 61 1
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT US-09-09-09-09-08-09-08-09-08-09-08-09-08-09-08-09-08-09-08-08-08-08-08-08-08-08-08-08-08-08-08-	Query M Best Lo Matches Qy Db

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Pred. No. 2.3;
0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 43.6%; Score 26.6; DB 9; Length 2322; Best Local Similarity 71.4%; Pred. No. 2.3; Matches 35; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10045815
Patent No. US2002016498A1
GENERAL INFORMATION:
APPLICANT: Wadhwa, Renu
APPLICANT: Object, Akivo
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: 06501-091001
CURRENT PAPLICATION NUMBER: US/10/045,815
CURRENT FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 1999-04-26
PRIOR FILING DATE: 1999-04-26
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PASSEG for Windows Version 4.0
SEQ ID NO 5.
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: JP 11/118806
PRIOR FILING DATE: 1999-04-26
NUMBER: OS SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 129, Application US/09925297; Pattent No. US20020081659Al; GENERAL INFORMATION:
APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; LOCATION: 2282
: OTHER INFORMATION: n = A,T,C or G
US-10-045-815-7
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// LCCATION: 2376

USTER INFORMATION: n = A,T,C or G

US-10-045-815-5
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Best Local Similarity 71.4%;
Matches 35; Conservative (
                                                                                                                                                                                                                                                       LOCATION: (12)...(1637) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (12)...(2252) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
                                                                                                                                                              TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
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                                                                                                                                        LENGTH: 2322
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                            APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR PLIANG DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPPLICANT: Greenspan, Ralph J.

TITLE OF INVENTION: Methods for Identifying Compounds for
TITLE OF INVENTION: Methods for Identifying Compounds for
TITLE OF INVENTION: Methods for Identifying Compounds for
TITLE OF INVENTION: Balance and the Perception of Gravity
FILE REPERENCE: P-NI 3864
CURRENT APPLICATION NUMBER: US/10/255,536
CURRENT FILING DATE: 2002-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/168,579
PRIOR FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 261
SOFTWARE FRACES FRACES FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                            75.7%; Score 46.2; DB 10; Length 1722;
86.4%; Pred. No. 3.1e-07;
tive 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 44.9%; Score 27.4; DB 9; Length 566; Best Local Similarity 69.8%; Pred. No. 1.2; Matches 37; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10045815
Sequence 7, Application US/10045815
Sequence 7, Application US/10045815
GENERAL INFORMATION:
APPLICANT: Wadhwa, Renu
APPLICANT: Ohide, Akiko
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REPRENCE: 06501-091001
CURRENT APPLICATION NUMBER: US/10/045,815
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/JP00/02731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 159, Application US/1025536; Publication No. US20030087807A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Conservative
                       APPLICANT: Andersson, Leif
                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Drosophila
US-10-255-536-159
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                               LENGTH: 1722
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LENGTH: 566
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US-10-045-815-7
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Choi, Julie Y
Denton, R. Rex
Kliem, Stefanie E
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NAME/KEY: allele
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NAME/KEY: allele
LOCATION: (4110)
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LOCATION: (4141)
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                                              APPLICANT
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA105
CURRENT APPLICATION UNBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NO 129
LENGTH: 1682
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.6%; Score 26; DB 10; Length 1682; Best Local Similarity 64.4%; Pred. No. 3.7; Matches 38; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chew, Anne
APPLICANT: Chew, Anne
APPLICANT: Choi, Julie Y
APPLICANT: Choi, Julie Y
APPLICANT: Kliem, Stefanie E
APPLICANT: Lee, Helen H
APPLICANT: Nandabalan, Krishnan
TITLE OF INVERMION: HAPLOTYPES OF THE ICAM2
CURRENT APPLICATION NUMBER: US/09/979,593
CURRENT APPLICATION NUMBER: US/09/979,593
CURRENT RILING DATE: 2001-05-07
PRIOR PELICATION NUMBER: 60/201,946
PRIOR FILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application US/09979593
Publication No. US20030082555A1
GENERAL INFORMATION:
APPLICANT: Genaissance Pharmaceuticals, Inc.
APPLICANT: Chew, Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Genaissance Pharmaceuticals, Inc. APPLICANT: Chew, Anne
                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/09979593
; Publication No. US20030082555A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-1
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US-09-979-593-59/c
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                                                                                                                                                                                                                                                                                                                                   LOCATION: (24)
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Gaps
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            APPLICANT: Nandabalan, Krishnan
TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
FILE REPERENCE: WMH-0425 PCT ICAM2
CURRENT APPLICATION NUMBER: US/09/979,593
CURRENT APPLICATION NUMBER: PCT/US01/14714
PRIOR APPLICATION NUMBER: PCT/US01/14714
PRIOR APPLICATION NUMBER: PCT/US01/14714
PRIOR APPLICATION NUMBER: 60/201,946
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTIN VOICE: 21
SEQ ID NO 59
LENGTH: 12043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (7902)
OTHER INFORMATION: PS10: polymorphic base G or A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (7961)
OTHER INFORMATION: PS11: polymorphic base G or A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (8037)
; OTHER INFORMATION: PS12: polymorphic base G or A US-09-979-593-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: (7187)
OTHER INFORMATION: PS8: polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: (7155)
OTHER INFORMATION: PS6: polymorphic base G or A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (5302)
OTHER INFORMATION: PS5: polymorphic base A or
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: allele
LOCATION: (7181)
OTHER INFORMATION: PS7: polymorphic base T or FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (3697)
OTHER INFORMATION: PS1: polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (4141)
OTHER INFORMATION: PS3: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (7875)
OTHER INFORMATION: PS9: polymorphic base G or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATIÓN: PS2: polymorphic base C or FEATURE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (4221)
OTHER INFORMATION: PS4: polymorphic base T or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36; Conservative
Lee, Helen H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 36; Conserval
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapien
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US-09-815-944-21
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US-10-288-160-3
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                          9604 TEATGCCCTCCCCGGGTGCCCTGCTGCCTGGCCAGCCCCTTCTTCCCCAC 9552
ó;
                                                                                                                                     Sequence 2280, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOG6
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
FILING DATE: 2001-01-17
FILING DATE: DATE removed - consult PALM or file Wrapper:
NUMBER OF SEQ ID NOS: 10231
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PUBLication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO06
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper: NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.0%; Score 25; DB 9; Length 635; Best Local Similarity 64.9%; Pred. No. 8.2; Matches 37; Conservative 0; Mismatches 20; Indels
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Pred. No. 8.4;
0; Mismatches
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-6987
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Best Local Similarity 64.9%;
Matches 37; Conservative
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APPLICANT: AAllen, Keith D.
APPLICANT: Matthews, William
APPLICANT: Moore, Mark
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SEQ ID NO 6987
LENGTH: 22585
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US-09-764-891-2280
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ORGANISM: Homo sapiens
                                                                                                                            US-09-764-891-2280/c
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                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2280
LENGTH: 635
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Using Mammalian Melanocortin Receptor Agonists and Antaç
To Modulate Feeding Behavior in Animals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Methods and Reagents for Discovering and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.7%; Score 24.8; DB 10; Length 200; Best Local Similarity 67.3%; Pred. No. 9.5; Matches 35; Conservative 0; Mismatches 17; Indels 0
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STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: IRM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,160
FILING DATE: 05-No. US20030105024A1-2002
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION DATA:
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FILING DATE: 04-SEP-1996
ATORNEY/AGENT INFORMATION:
NAME: No. US20030105024Alnan, Kevin E
REGISTRATION NUMBER: 35,303
REFRENCE/DOCKET NUMBER: 96,886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                    FILE TERESTRENCE: R-654
CURRENT APPLICATION NUMBER: US/09/815,944
CURRENT FILE CATION NUMBER: US/09/815,944
CURRENT FILING DATE: 2001-03-22
PRIOR PELLOR DATE: 2000-03-22
PRIOR PELLOR TOWNERS: US 60/191,236
PRIOR FILING DATE: 2000-03-22
PRIOR PELLOR DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/218,075
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 200
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Boston, Bruce A
Kesterton, Robert A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen, Wenbiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
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Factor to US20020038467a1

GENERAL INCORPATION:

APPLICANT: Allen, Keith D.

APPLICANT: Allen, Keith D.

APPLICANT: MAITHEWS, WILLIAM

APPLICANT: MOOCE, MAIK

APPLICANT: Phillibs, Russell

TITLE OF INVENTION: TRANSCRNIC MICE CONTAINING MELANOCYTE

TITLE OF INVENTION: TRANSCRNIC MICE CONTAINING MELANOCYTE

TITLE OF INVENTION: STIMULATING HORMONE RECEPTOR GENE DISRUPTIONS

FILE REFERENCE: R-654

CURRENT APPLICATION NUMBER: US/09/815,944

CURRENT FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US 60/191,236

PRIOR APPLICATION NUMBER: US 60/215,214

PRIOR APPLICATION NUMBER: US 60/215,214

PRIOR APPLICATION NUMBER: US 60/219,167

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-13

PRIOR FILING DATE: 2000-07-13

PRIOR FILING DATE: 2000-07-14

SOFTWARE: FastERD for Windows Version 4.0

SEQ ID NO 19

LEWARD. 1260
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67.3%; Pred. No. 9.7;
tive 0; Mismatches 17; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.7%; Score 24.8; DB 9; Length 1 Best Local Similarity 67.3%; Pred. No. 9.7; Matches 35; Conservative 0; Mismatches 17; Indels
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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; Sequence 3428, Application US/09880107
; Patent No. US20020142981A1
TELEFAX: 312-913-0002
TELEX: <URKNOWN>
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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1..14
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Matches 35; Conserva
                                                                                                                                                                                                                                 LOCATION:
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Sequence 92, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILLS REPERENTE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTHARE: PERL PROGRAM
SEQ ID NO 92
LENGTH: 733
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APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scharf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-WO
CURRENT FALLING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3428
LENGTH: 99014
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
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OTHER INFORMATION: Incyte ID No. US20020137081A1 416842.32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.0%; Score 24.4; DB Best Local Similarity 63.8%; Pred. No. 13; Matches 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: unsure
; LOCATION: 665, 690, 698
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-92
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Job time : 20.2903 secs
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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